	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
5	GATCTTCAAA TGGGACAAAT GCAAGGCTAT TGATCTTATT CCCAGCAAAC AAGTGCGACA	60
-	TGTATOGTGT ATTITTGTTG GOCAACCGAC TOCTOGTGAA AACGGGCTTA AAATCTGAGC	120
	TAGTITITAAA GOCATCCTTC CAAAGTGTCA CATGTOGTCC TCTCGACACT GCAAGCAAGC	180
10	CCATGICAGA GATTITICACA TIGCTIOCIG GIATAGGCAG GTITTICAACG GAATGIAACT	240
	CCTTGAAGIT CCTGATATCC CACAGTCTCA TOGACTTATC TOCTCCOGIN TGTAGCCATA	300
	TAGTAACCTT GOCTATCTAC CGCGACACCA GTGACGGGCC CGGTACC	347
15	(2) INFORMATION FOR SEQ ID NO:59:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 673 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG101712	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
	GATCTICTIG GCGICGGGCA ICAGACAGGC GTAACTAATT IGATCATICC IGGIGCGGGT	60
30	GAGGCTAACT ATGATGCATT GGAAGITAAT CCTTACGAGA CGACGAAGCA AAGGAAAGAG	120
	CAGGAGGITA GAICOCTACT GAACAAATTA CCTGCTGATT CTATTGCATT AGATCCAAAT	180
35	GIGATTOGTA COGTOCACAA GOGTTCTOOG CAGATTAGAT TGACCOCCAA AGACCTGACC	240
33	CAAATCOCAA CTGATGAAGA CATGAAATCT AAGGAGAATA GAGACATTCC AAAAGCAAAC	300
	CCTOCTGTGA AGAGTAAGAA ATTCAGGTCT GCGTACATTC CTCCGTAAGA AGACGCAGAA	360
40	TGTTGTAGAT GAGAGGAAGT TGAGAGTACA GAAGCAGTTA GAAAACGAAA AGGNNGCCCN	420
	CTTGCGGAAG CANCANGCTG CTGAGGNGAG CTANCAGNAG ATNCGANCTN CCCTGNCGAN	480
	GOGICAGONA GICCACIOGO NVINNNCICA COONNATIO TIOGITINNON GANTICACNO	540
45	CANNACIOCT CCCGNICINI INICTINCCCN NCCINCINIC ACCINCINCIC TOCCINITICC	600
	NANCCCACNC CCCCONCONCC NNCCCCONNON CONNINNAN NONINCCCCC CTCTNCCCCON	660
	NCCCCCCCAL NCC	673
50	(2) INFORMATION FOR SEQ ID NO:60:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 523 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	

(I)

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1017RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
10	GATCAAOGTT GAAAACGAOC AGOGTGATAA AAAAGAOCAT GACOCCGATG TCCCTGAAGA	60
	GGAATTTAAG ATTAAATATA CCTCGACCTA CTATAAGGTT GAGAATATGA COCGTGTAGT	120
	ACCACAGCAA TTAAAATATA TTGCATTTCC AAAGGATGAG AGATTTACTC CCGCTCGCAA	180
15	GITTAAGGGT AGCAATGGCG TTATAGTGCT ATCGGACAAA ACTCCTGACG AGCCGGTCGA	240
	AGTAATCAAA ACCOCTAGAC AGGAAAAAGA GACGGATGCT CCTCTGCCTG CTCCCTTCAA	300
	GGITCAGGAT GACTTAGAAT TCTGAACTGA TAATTAGGAA GCGTCGATTA TGTTCATTAG	360
20	GAAAAAGGT ATTTTTCTA GAAACGAAAG AACTTACTGA TTGCAGCTCT CTCTAAACAA	420
	GIATATTATG AGGIGATTTA TITICAACTGA ATCIGOCTAA COCCCOGCAA CTAGGICTTA	480
	TOTTOTTGTA GTCACCCTAG AGGTGGTGGT CCCCAANCGG CNC	523
25	(2) INFORMATION FOR SEQ ID NO:61:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 493 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1017UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
	CATCTCCATC CACCTITICS COTOSTICCT CACCTCCTCT GIGACTICAT COTTCATACG	60
40	COCAATTAAG CCAGOOCCTC TGTATGCGTA COCAGTGTAG AGTTGCACAA AGTGCGCCCC	120
	COCTITIOGCA AACTOGATOG CATOCTOGOC ACTACTGATA CCACCACATC CAACCAAAAAC	180
	CAGGITCGIG TCCTTIGIGT ATTOGIGIAT CGTGCGCAAA GCTTTTAGCG CAAATGGTTT	240
45	CACCOCCTIC COCCACAACC COCCTCCCTC CITTITICACC TCCTCATCGA CACTCTACAC	300
	CCAGTCTOCC CTTTOCATAG TAGTGTTTOG AAACGATGAT ACCCCCAATA CTCGATTTTC	360
	THEOGRAPHIC ATTOCAMENT TOCKTOGTIC ANALYCCOGTIC CONTITUDAL	420
50	AGGAAAGTIG GTTATOGTTA CTGGACCAAG AAAATOCCNC CGTGGNCAAA GATTOGGTTA	480
	GCANAACAAG NIN	493
	(2) INFORMATION FOR SEQ ID NO:62:	
55	(i) SEQUENCE CHARACTERISTICS:	

_	(A) LENGTH: 523 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1018RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	GATCATCGIC GAGGAGIACA COCACTOGOT CIGOGOGIGO GIGAACITOG COGOGIGACA	60
15	CCCGIACITC TICCACGCCA CCGIGTICAG CAACCGGCAC CCGGCCGCGT CGIACAGGIG	120
	CATETTETCE CACOCCETTE COCTCAGAAG CTACTETCCA TOCTCCTOCA ACGACACCCA	180
	CONCANCORO COCTOTICCI ICIOCOCCAC CITGAAAGAC TIGACOCCCC OGAACCCCCC	240
20	CAATGIGICT TIGHTGATCC CGATACTCAT CCCGCTCGTC TTGCAGCTTC CGGTCCTTGG	300
	CCCTCTCGCC GCTGCTCTGC ACTGCTGGCT AGCAGAGCTC ACCAAAATTT TTATAGCCAT	360
	GOCCAGOCCA AACTICACTA ACTGOGGAAC CACAGGACCA CAGCAAGCAA TGCCCTCAGT	<b>4</b> 20
25	ATGROGREG GROCACOGT CORGRANCE CTACTAACCC GCACACTCA AGCAGATOGT	480
	GCACTICAGO GCCGACCTOG CGCTGGTGGC GATGGTGCTG GCC	523
	(2) INFORMATION FOR SEQ ID NO:63:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 770 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1018UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
	CATCOCCTCT ACCACTICAT OCOCATOCAC TACCITATICA CCCACATOCT OCTOCCOCCCC	60
45	GACTITICGET TCATGCGCGA CTACCTGGAG GTCCTGGCGCC GCCGGCTGGA GCAACACGAG	120
	TIGIOCCATG CCCGCATGIC TOCCGCTGIG CAACGGGACC ACATIGCCCG ATACACCGAG	180
	CTOCTGATOC TOTATOCOCG GAAGTCTOOG GATGAGAAAA TOCTGOCOGA OCTCTTTOCC	240
50	TCCTTOGTCG ATAGTCTGCC TCGCGGGATG GGCGGAGCCA CTCTTCGTCA GCCATTGCAT	300
	GAAGTCATGA CGTACCTGAT CAGCGAAAAC CAGCCGCAAC AGGTGCTGAA ACTGGTGGCG	360
	GOCATOCOCA AGOCOGAGOC CAATCOGOCGG CCGOGCAAAT CCTCCGTTCC AGOCACCTTG	420
55	GCGCTGGTTG TTTCGGCGTT GCGACAGTTC AACAATCCTA ATCTCGTCGT GAGCTTTATT	480

5	STOCAGOCAT ACAGAAAGAC GCAAACGAGA GTOCTOCTOG GACAACTCOG QCTATOGTCT	540
	CTGCCATTIT ATGCCCCCC TGTTGCGCTC TCTCCCGAGG CGGCGAAGTC GCCGCAGGAG	600
	CTGCCGCAGA TATCCCCTGT GGACCTGCCG AAGGACCTAA TACTGAAGTC CGTACCTGAC	660
	ACCIGATAAT GIGOGAGCIC TATCACCGAA TCTATCCCAG AAGCGATCOC AGGIGCCCCC	720
10	GGAGGAGTAC COCGAGATTT AATCCAGCTA TITTOCOCTTT ACCAGGACTT	770
10	(2) INFORMATION FOR SEQ ID NO:64:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 735 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1019RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:	
25	GATOCATGAC CCATGCTAGG TGGAAGGAGC CCTTACCCGC TAACTGGGAC TGCCTCTTCA	60
	ATTOCCTTAT CAGTITIGGTA TOCACAGCAC CCACGTOGTA CAACAACCGC CCCATCAGCG	120
	TAGACTITOCC COCATCCACA TOOCCTAGAA CAACAAACGA CATATOOOOC TICTICTICAC	180
30	GTACATATOC AGGGATGICG AATGGGTTCC GCGGGTTAGT GGGCTGCACA ACCTTCTTGG	240
	CCGACGGCTG TTCGCCCCTCC TTCGCCCGCG AATCCTCCTC CTCGTCCTCG TAGTTCTTCG	300
	GGCCGCGTC CTTGTTGTTG AATTTCAGAT CGGCCACCTT CTCGGCCCACC TGCTTAATCT	360
35	CAAAGGCTCG CTTCTGGGAT TCCAACACCA CGTCATCCGG CGAGGGCTTC ATGAAATTGG	420
	CACTOSCCTG CTTCTTAGCT CCTTTATAGT TGTTAGGATA AAAAACTGAG AACACCTCCT	480
	CCACTOSCCT CTTGAGCTGG GTTTTGCGTG GTTCTGCGCA TCCTGTCTGT CTCCACAGCA	540
40	OCACOCTOGA CAGCTGCAGT OCAGOCCOC CTOCAGOCTT GAAGGACGOC TGACGCTGCA	600
	GAAGAGCCCC CAGGGCCATC CACTGGTCTT GCCGTGCCTC GGTCGTTGCG GGGCGCGCTG	660
	CAACAGOCTT TGCCTCAGCG TCGCCGCGCG ACTGCTTCGC AGAGACGACA GCGTCTGCAT	720
45	CASCGACGCG CCCCGG	735
	(2) INFORMATION FOR SEQ ID NO:65:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 740 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1019UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:	
5	GATCOCAGAT TCATCATCOC TGTTATACCA GOCTCTATCT TCCTCGAGGT CCTCGGGACC	60
,	AAACCCCCCC CTCTCTTGTG TGCCAAGAGG TGCAGGACCC TCGGCCGGAT CCTCGGCCAG	120
	CAGAGTOGCA ATCTOGTCTT CATCCGCTAT COCTGTCAGC TTAGGCACAA AAGCCAGTTT	180
10	TICCGITTIG TCCCCGTGAT CATCCTGCTC GACCGTCCTC TTCTGATCTC TGCGACCCTC	240
	TGCAAACTCT TTGAGCTGCC TTGCTGCTGC CTTGTCAAGT CGCTTAAATC TCAGCGGTTT	300
	CTGTTTCTGG CCACCGCTCC CCAAGCTCTG GTCCGGCTCC AGTGCTGTTT CCAGTTCGTC	360
15	GTCCGAATCT TCGAAGCTCA GCGCGACCAA GTTTCTGGAT GTGTTTCCCT TCACGCGCTC	420
	CCCGTCAAGG ACAGCCTTCA CCGTGGTGTT TGTGCGCTCC TCCTGCGTAC TCCCCAGGGA	480
	TACTAGCAGC TCATGCAGGA ACTICICCIC CCCTTAAACT TGCCAAGCGC CATGCAGCTC	540
20	TTAGTGAACT TCACTOGATC GTATOCATGC ACOCCOCTA TATTOCATAT COCCTOCACA	600
	AACTITICIET GACATTGCAT GCGGATGTTG GTGGATCACT CCTTCAGCCG GGGTCATCGT	660
	CTTAGCTCCT ACCGTACTTG CTCTCTCAGA TGCATGATGT GTACCATCGC ATCTTCAGCT	720
25	TGACAGACTT CCATATACGT	740
	(2) INFORMATION FOR SEQ ID NO:66:	
3 <i>0</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 537 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1020RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:	
	GATCGITCCT GITTCTGCGG GCAAAGTTCA GAATTGACCT AGTGCCAGAC ATGACAGTAT	60
	CETTCAAACT CCTCGGAGAG TTAGCCTTGG ATATCCACCA TGAAGACAAA AACCAGAGAC	120
15	CAACAGOGGA TOCTACCAAA ATGGOCCAGAA TACOGAAAAA CCAGTGCAAT TCTCOGGTTG	180
	CTTCACCTOG GACAGTGACG TTCATCCCAA ATAGACCCGT AACAAGATTC AAAGGAACTA	240
	ACATTGTTCC AATCATAGTG ACCTTTCCCA ACATTTCAGT AACACGATTG TTACACCGGA	300
io	AGGACTCAAC TIGCAATIGI GCCAAGTAGI TACCATGIGA ACGGGGAGAAA ATCTICTCAT	360
	AGGACAGTAA ATTITIGAAAC ATCOOGAGGA CATGGTCCTG AATATCTCCC AAATAGAGCG	420
	CTATATCAGO TOTTOGITGA GTOCOCTOGA CATGATGATG TTGTATGITO GAGOCTAGOC	480
5	TOOCAGACAG ACCOTTOGTET CCOCTAGCCT OCAAGTTCOC AATGTTTATC TCGACGT	537

	(2) INFORMATION FOR SEQ ID NO:67:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 563 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1020UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:	
	GATCAGCACC GTGCCCTTCG TGTACGCCTG CTTGGACATG GTGTGCGACG ACCGTGTGTC	60
	OCATTICITÀ CACGIGAAAG CAATCATCAT CATCOOCTIG TCCACCTITÀ TAGACCCGAT	120
20	ATGCCGAAAC TCATCTGCAA TAGGCGGTTT CTGCCTGTTT TGCAGCTGCG GCGAACCGCT	180
	GTBGAACCGA TGAGCTACCA AATGCCCCCC AAACACCGGA CCCAGCACGT ACTGCATGCA	240
	GTTACGGCTT GGGCGCAGTA AACCAGCAAT CCTGAGAGGC CCCATCGAAC GTCTAAGCAT	300
25	TTTAAACAGT TATACGTAGT CAGCGGTTTT CCTAAAACAG GACATGAGAG TGCGTCGAAA	360
	GAAGGOGTCA TOTCAAATTT TICAACTITA GAAGCGCTGC COGAAAAAGC ACOGTCACCA	420
	TITATCTATT ACAAGATGAA CAGTTAGTOG TOCCOOCAAT TGTGTCAGAT ATATGTCTCT	480
30	GGACATGGAT ACAAGACACT CTCGCCACAG AAGGAGCAGG AGATAGCATC GAAAATCTTG	540
	CAGAAGOCTG AOCTGOCTCA GAT	563
	(2) INFORMATION FOR SEQ ID NC:68:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 346 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG102111	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:	
	GATCTCACCC TOCOCACCAT CGACAACCCT OCATACOCCG OCOGTGACGT CATCGOCAAG	60
50	GCCCGTGCCC GCACACTCGA GATGCGCCTC AATGCCCTGT CCGCTACCAA TGGCGCGGCA	120
	CGAACCCTCG AAACCGTGCC TATGAACATA CGCAAAGGCA TGGTTTCCAA GCACCGCAGT	180
	CGCATCCGGG AGCACGAGCA GCTGGCCCGG GACTCCGGCA CCGTCCTCGC CAAGGTCGGT	240
55	CECEGAGACT TOCOGRAGAT AGACGCAACC TACAAAAAAG ACATOGAGCG TOCOCATTOCC	300

	ACGACCATCA ACCCTGCACA COGTGCCCGC AAGAAACACC GCGATC	346
	(2) INFORMATION FOR SEQ ID NO:69:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 562 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG102112	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
	GATICTICCOCC CIGATICOCTICC CACTICACCC CCCCCAAGAT CTCTCACTCC TCCACAAAAAC	60
20	GCTGGAGCTC GATGTCCTGT TCCAGCAGCT GCTTCTCGTC GCGGTCGGCC GCGGCAGATT	120
	TOGGCCCGG CTCGGTCTCT AGGCCCGGGG CCTTGCCGGCT GCGGATGCGG CGCAGTTCTC	180
	GTGGAGAAGG CCCGCTGTAG GCATCTGACG CCCCGCGGAA CGAGATCACG CCCGGCGTAT	240
25	GSGCCGCCTC GTCGTCGGAG CTGGCTGAGG CGCCGTCCAT TTCGGACTGC TCGTCGGATT	300
	CAGACTETEC GGAGEGECE TEGESECTEC TETECOGGGTE ACTETEGETE TEGGAGGGG	360
	TOGTOCTICT GICCCICCIT TGTCCACCAC COGTCTTGTC TACATATCCC ATATCCTCTA	420
30	COGACCCAAA CTCCCCCTCC AACCCCTCC CCTCCCCACVICCTTC NATITATCTT	480
	CAATTGTCGG TCATCCNGGG GGGTTCTTGG GCCCCANGAA GINTNINANC AGGAANCCCT	540
	ACNANIANGG TITTICAAATT CC	562
35	(2) INFORMATION FOR SEQ ID NO:70:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 611 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1021RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
	GATCCTCGAG TTTGTGCGCG GCGGGTCCCG CTCATTTACC TAATCCTGTC TATAGTAAAC	60
50	ACCITETICI ATCTACATAG COCACCIGIT GIAACTTACG CIOCACOCAT OCOCOCOCC	120
	ACCITECCECA CEAGEGEEES GIAGAACOCE TOGECEGECE GEEGECEGEC CAGCATGEAC	180
	AGGCGCAGCC ACGGTTTICAT CGTGATCAGC AGGCCAGTCC ACAGCGGGCC CTGCACCAGC	240
55	COCATCAGCA CCACCACCACCACC TTGCCCACGA CCAGTCCCCT GATCCCCCGTC	300

	reactive degree engineering relations and the second degree of the secon	360
	TCCTTCGCCA GCGCTGCGCG GAACGTCTTT TTCGAACCTG ACGTCGGGTA TCGTTATTGC	420
5	TTGGGGTCCA TTGGAACGGC TGTTCGGGGT CAGAGGGAGG ATTCCTGCGC TGGTTTGGTT	480
	TITTACGAAGA CGACCCTCGG TGAGAATGTC AGTTTGGCCA CTNGGCAGCC CCAGGAAGGA	540
	CCGNGAATTC AAACCACCTG AGTHOGOCGN CGGNGTAAAA ACGCTAAGTT AGTGCNNTGC	600
10	ANACCONCCT C	611
	(2) INFORMATION FOR SEQ ID NO:71:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 346 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1021UP	
25	(vi) CDMINE DECOMENTATION OF TO NO 71	
20	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:71:  GATCGCGGGG TITCTTGCGG GCACGGTCTG CAGCCTTGAT GGTCGTGCCA ATGCGACGCT	50
	CGATGICTIT TTIGTAGGIT GOGICTATCT TCCCGAACTC TCCGCGACGG ACCTTGCCGA	60
30	OGACOGIOCO GCACTOCOGO GOCAGOTOCT COTOCTOCOG GATGOGACTG COGTOCTTOG	120 180
	AAACCATOCC TITIOGETATIG TICATAGGCA COGITTICGAG GGTTCGTGCC GCGCCATTGG	240
	TACCGGACAG GOCATTGAGG COCATCTCGA GTGTGCGGGC ACGGGCCTTG CCGATGACCT	300
35	CACCGCCGGC GTATGCAGGG TTGTCGATGG TGCGCAGGGT GAGATC	346
	(2) INFORMATION FOR SEQ ID NO:72:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 438 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1022RP	
50	(xi) SEQUENCE DESCRIPTION. SEQ ID NO:72:	
	ANNUMENTA NAMANGELOG GOCGLOGING AATAGIOGGI CITICIOCCG GOGICIGIOC	60
	AGAAAACGAG ATTCTGGGGA GTATCTGAAA TTCTTTGTTG CGCCGAGCCG TCTGGGTCTG	120
55	CGICAACCCA CACCGAGITT GCCACACGAA CIGAACCTAA TITICGITICCT GCACCIGITT	180

	TOOGGETTICG COTTTICAGE CITICAGGAA ATCTAGAGGG GCTGTGTGCT TTGAGGCTGA	240
5	AATCAGGGGA ATAGCCTGAA TTTGCGAGGG TGAATTGAGC GGTTATATGG AACTGTGGTA	300
	CATOGNOACA CTGTACCACG AGGACAGOGA ATATOTGACA GTAGGGOGTO CTTOGTAAGA	360
	ACACAGTGIA TOOCGIGAGA TAGGTGITIGA TIGAGTCTAG CGTOCTAGGT ACTCTTTAAC	420
	TTTCAGTCGG TGTTTTTT	438
10	(2) INFORMATION FOR SEQ ID NO:73:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 461 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1022UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
	GATCCAGCAG ACGITITAAT CACCGATTIT TITCGGIAACA TITCAAAATAT AATICTCGAT	60
25	GACAGTGAGA TAGATGGTGA AACTCCAGCT GGACTTACGG AATCTGGCCG GACTGGCAAT	120
	CIGCIAGAAT TOGCAAAAGC GAAATTITIT GOCANIGIAG ACGCAGAGA TAATGGCACG	180
	CATAAAAACG TGATTCCAAG CTATCCAGTG GTAAATGAGG ATTTACTAAG TGGGGNANCA	240
30	AATGCATCCA CAAACAAAAT GATAAAATTG TOOOGGATTA TCATCTTCCT GGCACTAACG	300
	TCATTAATGA TGAAGTACGC CAACACTGAA AACATATOGG GTAGTCCAGC ACTATTATGT	360
	TICICITAGA AAAATOCTIC ATOCTICATG GAATTAAGO GOCAACAAGT GCAAGGTAA	420
35	GAACOGAATT TTACTATAGG COCGAAATTT GTATATATTA T	461
	(2) INFORMATION FOR SEQ ID NO:74:	•••
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 213 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOFOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
<i>45</i>	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG102311	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
	GTCGAGAAAA CAGAGCTTGA GGTCCCACTG TTCTTTTTCA CTGCGGATGT CTCTGTCTGC	60
	TOCACGACCO COACTITICAG ATTGTOGTOC ATCAAGCOCT OCAAGTOGAC TTCGAGACGG	120
55	GIGTCTGGGA TGGTGCAGTA CGCAAACTTC TTGTGCTTGT GATCAGCGGG GTCTGTCTTG	180

	TGTACCGTAA GCTTGCCGGG CACCAGCTTG ATC	213
	(2) INFORMATION FOR SEQ ID NO:75:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 725 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG102312	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
	GICGAGOGAA GIAACCAATA TATTICACGAG GOCTACCTAT GOCATCAATG AGACGITCOG	60
20	AACCAAAGAT CGICGGGTCC TGGGTGATAG CGCTTCTGTG TGGGGGTCTTG TGTGCAAGCG	120
	ACAACCITICA TACACGCGAT ACTITOCTOGT TAGTIGTTAAT CTCAACAGCG GTGAAGTTAT	180
	CTTCGATGAC TTCAAAGAGG AGCGTTTTCT GACGGAGGCT TTGGAGACGC GAATAAAATA	240
25	CACAAACCCG AGTGAAGTTG TOGTCCGAGA TOOCCTTGGC TCAGAAATCG AAAAGGTGTT	300
	TCATACTICA GATICCGATA TCACTCTAAA TAGGATCGAG CTCGTCGGGT TGTATGAAGA	360
	AATCTTCAGT GAGCCGCACC CAGCCTTTAG GGGCAACGTT CCTCTGCAAA CAGCGCTCAT	420
30	GCTGGTGCAT GGCTACCTAA CAAACTTCAA AAATGAGAGT TTACTCTTCT TCAAGGAAAA	480
	CTITAAACCA TICTOCICCA AGACOCACAT GAITCITCCC TICTACCCT ATTOGAACCT	540
	TAGATATTIT GGGGACAGIA CAGATAGGAG CAGTAAAGGT CCCCTGTTAT GGGINTTAGG	600
35	TCAANCTAGA ANAACTAGGG TTAAGGACTT GGAGGACTGG NITGAAAGGC CITNTAATTT	660
	GGTCAAGTCA ANAGAGTTON GGNNGCCAAN GATTCACNAG GNGGGNATTN TCATGGCTCG	720
	CAATT	725
40	(2) INFORMATION FOR SEQ ID NO:76:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 659 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1023RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
55	TGCCCGGCAA GCTTACGGTA CACGAGACAG ACCCCGCTGA TCACAAGCAC AAGAAGTTTG	60

	NGTACTOCAC CATCCCAGAC ACCCGTCTCG AAGTCCACTT GCAGCGCTTG ATGCACCACA	120
	ATCTGAAAGT GGGGGTCGTG GAGCAGACAG AGACATCCGC AGTGAAAAAG AACAGTGGGA	180
5	CCTCAAGCTC TGTTTTCTCG ACGCTAGGGA TAACAGGGTA ATACAGATAT CAGATCTAAG	240
	CTIOCCICGI CCCCCCCCC TCACCCCCCC AGCGACATOG AGGCCCAGAA TACCCTCCTT	30C
	GACAGTOTTG ACGTOCOCAG CTCAGGGGCA TGATGTGACT GTCGCCCCGT ACATTTAGCC	360
10	CATACATCCC CATGUATAAT CATTUCCATC CATACATUTT OGATOGNOGC ACGGCGGAA	420
	GCAAAAATTA COOGTOCTOG CTGNAGACOT GCGAGGAGGG AAACGCTOCC CTCACAGACG	480
	CGITINGATTC TICCCCACGG CGNOCCCNIG TINGAGATNI AAAGGITIAGG ATTINGCAATG	540
15	AGGINCTCCT TICANITNCT CCCITTINAA ATONITGING GICAAGICNI CANATCAAAT	600
	TCCCAACATT AACACCNIGG TTAGGGAAGT TCANNITTCN GGGGCCNIGA TTANITCCN	659
	(2) INFORMATION FOR SEQ ID NO:77:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 646 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1023UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
	GATCTCAAAC CTCAGAATAT TCTACTTCAT CAATCTGGIC ACGITATGCT TICTGATTTT	60
35	GACCIGICAG TACAGGCAAA AGGAACCAGA AATOCICAGG TTAAGGGAAA TGCCCAGICT	120
	TOOCTIGIOG ACACAAAAGT TIGITCIGAT GOCTICAGGA CTAATICITT TGITGGAACG	180
	GAAGAGTACA TIOCACCIGA OGTCATCAGG OGAAATOGCC ATACAGCATC CGTOGATIGG	240
40	TOGACATTOG GTATACTTAC TTACGAAATG CTCTTTGGGT TCACTCCTTT CAAGGGGGAC	300
	AACACAAATC AAACGITCTC CAATATITTG GAAGAATGAC GITTATTTCC CAAACAATAA	360
	CGATATATCT COCACTIOCA AGGACTIOGA TIAAAAAGIT ATIOOGICAA GAAAGAGAGI	420
45	AAGCGACTIC GICAAAGTIT GOCGCCAAGT GAGATTAAAA AAGCATCCCT TICTITTAAG	480
	ACCOGNOCAG TOGOCOGNA THOGACOGAA CCAGGAACCT CCCTTITATC CCCGNATIGA	540
	CGGGAGATGG GTACGACTTT GGAAAGNTAT CACATTAAAG GATGTTAAAA AGGCCGGGAA	600
50	TCCGGCCCAC CCGGGTTAGT CTCATATTCA AAGGCGNGGT TCNNCN	646
	(2) INFORMATION FOR SEQ ID NO:78:	
<i>55</i>	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 557 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEDNESS: single</li></ul>	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1024RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:  ATNININGNI CANNICTOSS GCGSAGCGAN TAGTGCGTCA GCANGGTGCG CTCGGTGTGT	60
		-
	GCGCAGCCGT TGGCATGCTC GCGCATCCTC GCGTCCAATA TACCAGAATG CATCATGCTT	120
15	COCTOOCICT ATATIGACCI OGIOOCCATA TATGAAAAOG COGICCIIGA AGTITIGIAG	180
	AAACTOGICT GOOTGAGATG GOGTAGOGAA COCAAGGAAG CATTTATTGC GGCATTTACG	240
	ADOCCIOGAA ACACTAACTA OCCOGTACTT CICATCTAGC AGTOGAAGGG OCACGTCTGC	300
20	GGAAGGAAGC GGCTCTGGCA ACGTTTTCTC CGCCGATAGA GCATATGGGT TATCCTTGTT	360
	GATOGACTIC AACAGITGIC GAGCATATIC TATCCIGGAG GCATITGACG CTGCCAAATT	420
	TGACAGGTAG ACACTGGATG GCGGCGTTAG TATCGAATCG ACAGCAGTAT AGTGACCAGC	480
25	ATTCACATAC GACCOGACGC ATGATATTAC TTCCTTGNCN ACTTAANTIN CCCAATCTTN	540
	NOCCAGATIN ATTITCG	557
	(2) INFORMATION FOR SEQ ID NO:79:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 334 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1024UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
	CATCTAAATT CCCACOCCGC TOCOOCGGTT TCTCTGCGGAG TCTTTGCCGT GAAGCACGAC	60
	ATAATCGAGC CCAAACACAG CAAGATCGCA GAGAATCAAG CTTATGTAAG TCTCACGTGA	120
45	CTCGANGCGT GCAGAACGGT ACGGGTGTGC ACTGCAGGTG CCACGCCATG TCTCACATGG	180
	TTGTAACACG OCOCGACCOC GGTTCOGAAT ATCAAACAAA CATATGTTTG CCGCAAAAGG	240
	CACTOSTITCC COCACCTOCC ACCOSCAGOS GCACAGCOCG GCAATGCAGA GTCGCGTITAG	300
50	GELIGECELLEE CCCCCALLOCC GCAELLELCCC CCCC	334
	(2) INFORMATION FOR SEQ ID NO:80:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 621 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1025RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
	CATCAGCCCG TTCCCCCCCC CGCCGTTGTA CTTCTGGTTC TGGATGGACC CCGCCGTGAT	60
	OCCOCTCTCC TTOCCCTACT CCTCCCTCCT CCCCAAGTCC CACTTCACCC CCACTACCAC	120
15	CACCITICACE CCCICOCAGI GGICCOCAAT TICOCTCACC CACTIGITICI TGACGITICIC	180
	CACCGAGTICC CGCCAGTCCA CCCAGAAACA CACCATAATC GTGTGTGTGT CCCAGTACCA	240
	CAGCGATICGC AACCGGTICAA ACTOCTOCTIG COCAGCAGTIG TICCCACAGGC TICAGCGTIGAT	300
20	GIOCTOGTTG TOCACGAAGA TOTCATOGAT GTAGTTTTCG AATACCGTGG OCTOGTACAC	360
	CTTCCCAAAG TACCTCCCCT GAACACCTTC AACACCCACC TCTTCCCCCCA AGCACCCTCT	420
	COGAGGATGA CGATCTTGOG CTOGATAGGA TGCTTGGAGG ACGAGCTGGA CCACACAGAG	480
25	GCATCTTGTG TTTGTAGAGC TGGTGGTGGG AGCTCCTCTG ATGCCAGTCC ACGCTACAAA	540
	TACAGCGITIT GAGALGAAAT ACTAGCTGCT ACTGTCCTTT CTCTCTGACG AGGTGCACGG	600
	COCATCCCCG TTATAACTGT C	621
30	(2) INFORMATION FOR SEQ ID NO:81:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 522 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1025UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	
45	CATCCCCATG AGAATGAGCG CATCTTGGAT ATGCCGGGG CACCCGGTGG TAAAAACCACC	€0
	TATATATCTC CCATGATCAA GAACACTOGT TGTGTCTTTG CAAATGACGC CAACAAGGCA	120
	ACAACCAAGT CCTICATTOC GAATATICAC CGICTCOOCT OCACGAATAC AATTGICTOC	180
50	AACTACGACG CCCCCGAATT CCCTAAGGTT ATCGGTGGAT TTGACAGAAT TCTACTTGAT	240
	OCCCCTTOCT CAGGIACAGG TGITIATCOOC AAAGATCAAT CTGTGAAAGT AAATCGTACT	300
	GAGAAGGACT TTATGCAAAT TCCACACCTG CAAAAGCAAC TGATATTATC TGCAATTGAC	360
55	TOTOTTGACA GCAACTOCAA GCACGGCGGT GTCATTGTCT ACTOTACTTG TTCCGTTGCG	420

	GITGHASHM ALGHBOCCGI GGICGHMIAC GCCIACGSM GHGACCIAAI GICASCIGIT	480
	GAAACCGGCT GOCTATTGGT AAGGAAGGCT CACTAGCTAC GA	522
5	(2) INFORMATION FOR SEQ ID NO:82:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 508 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1026RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
20	CATCCAATTG CTOGTCATAC ATACOCATTA ACAGATTTTA TTACTATGTA TCCAACGTGA	60
	ATTOCTATAT GTACCITATT ATCOGTTTCA TAAAGATGCT TTAATTTCTT ATTCTGAATC	120
	GGAGTCGTTT GACCOGCGCT TAGACTGGTT ATGCCTCTTG CCATCGTTTT TCTCGAAAAT	180
25	GAAAATTCTA OCTTCACOCT COOCTOCAGG CTTAGTOGTA TCCTOCTCAT TGTTAGTTCT	240
	CCTATGACGG TATCCTGGGA AGGTATCCCA CTGGAATTTG TGCGACCTCT CAAGCTTTAA	300
	ACCATOCTICC TITOOCAACTA CCTTAGOCTG CCAAGAATOG TATOGATCAC COOCAAATAG	360
30	GGACAAAATG ATCCTCCCCA TATCATCAGA TGATTGTTCT TTTTTCCTACT TCATATCCGG	420
	AAAGATGGGC AACAACTACC TICTTATTCG CCAGCTIGAT AGTIGITTAC AGCTATCAAA	480
	AATATOCOGA TAGAGOTOTG AGOTOTOT	508
35	(2) INFORMATION FOR SEQ ID NO:83:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 594 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1026UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:	
50	GATCTAGCAG ACTAGACTOT CTATOGCATO AAGITTOTGT TITOAAGICT GOGITTOTTG	60
	AGCAACCTOG TOCCCCTATA CCTGTGTCAG ACGCACAGGG AAGCAGACGT CTATCGAGGA	120
	TGTCGAACTT ACAGACGAAA AAACAGCGCC CGCCAGCTAT TCCAGAGGCA GACGTATCAC	180
55	TOCAGGCTAT CAAGAAGCGG CGCATGTCCG CCAGGTCTTC TACCTCCCGT AAGTCGGGTT	240
	CTGCCCAGCG TATTAGTGTT GTGCCACGCG CCGCAGCTTC AGAGTCATAT GTGGTTCCAC	300

	CIOCIOGIOC TCCICIGAAG AAAGAGICIG COGAIGACIT ATTICAAACG ACTOCTICCT	360
5	TITIATGAACG TIACACTATT TOCACACTGA AAGAAATACC GAAAAACATT GCAGATGAGG	420
	ACTICTOCCCG ATATACCCTT AACGAGGATA GCATCACTAT GOCTGACCTT TGCAAACCTC	480
	TATTCCCGAT AGGIGAAGTA TCTGATAATT TCACCGGGCG AAAGAAGCTG CAAAAGCCAA	540
10	CATOGAAGCT COGAAGAAGC OCCOCGAACT CCGACAGATG OCTAAGCGTC AATC	594
	(2) INFORMATION FOR SEQ ID NO:84:	•
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 454 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1027RP	
	(A) Chomitan. FABIUZ/RF	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:	
23	CATATOGACG TACTOTOGOG TITGTTCTTC TITGTTCAGCA GGAACGCCGT COGGCATAGG	60
	CTTACTGACT TICACAGACA TGATTCTTTT GCTGCAAGTA AAGTATATTA ATGGCCCTGT	120
30	CAAAAATGGT AATAGTACGG AAAGACCAAC CTGAGAAGCG TCCAGGCCCT GCGATAAGCC	180
	GITTITIACCT AGACCAGTOG ATACACCTAA TGITTOGAATC AATGCAATOG CTCGTGTCAG	240
	AATTCTCCGT TTCCATGGGG TTATAGTCCA GCGTATATGG CCTCCGCATA CTATTTGTCC	300
35	AGCTATOGTA CAGACAATNC CTOCCGATTG GCCCGAGATT AAGAGTGCGA GCATGAATAT	360
	GETACCTOCC OCTOGTOCCA AAGTGTTOGA TAATAGGTOG TGTATCGTGT ATAGATCCGC	420
	ATOGATOGOT TOCOGOGIAT CATACAGIOC OCTA	454
40	(2) INFORMATION FOR SEQ ID NO:85:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 446 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1027UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
55	GATCAACGAG TAAAAAATGCC AGGIGITICC GITAGGIACG TGTCATGAGI GCTAGITITAT	60
<i>55</i>	GETTTOGTAC GOCTOCTOGG GOGCOCTTTC TOOGAGGTTC CAGCOCTCAT ACGITATGTG	120

	TOTAL SERVICE PROPERTY OF THE SERVICE SERVICE SERVICE SERVICES	160
	GATTGGTTCC AGAACGTCGC TGACTGTGTC AAATATGAAA TCATTGGGCG AAACTTAGCT	240
5	TOCTACOCAG TOCACCATOC AGAACCTOCG GCCGAAGCTA GCTGAGGCTC GATGAGACGG	300
	TOCCOGAAAT CCTTCGATCC CAGOCCAAAG CAGACGTACC TACCAGCTTT TAATGTGCCC	360
	OCCTACTAAC ATCATATACA GAGACGTTOC AGCTCAAGAG TTCATCAACG CTTACGCTTC	420
10	TTTTCTTOCA AAGACAAGGT AAGTTG	446
	(2) INFORMATION FOR SEQ ID NO:86:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 551 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1028RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
	GATCATOCAA ACOCAGAGAA OCAGAAGAAG TCTAAGAAAG ACOCCACTAA AGAGAAGAAA	60
	GCCAAAAAGC AGGAGAAAAA GGAACTGAGA AACATCATTG AGGACTCCGT TGAGCAAAAAT	120
30	AACCTAGCAC TGATAGAAAA GGTGGAGGAA GAAAGAGGCC GCACGAAGGA GAAAGACCTT	180
	CACATCAAGT TCAGGTATCG GGAAAGTTTCG CCAGAAAGTT TTGGCTTGAC CACCCGTGAG	240
	ATATITATOS CTGACGACOC TOCCTTGAAT GAGTATATTG GCCTCAAGAA ATTTGCACCA	300
35	TATAGAGCAA AGGAGTTGCG CAACAAAGAT AAAAGGAAGG TCATGAAGGC TAAGCGTCTA	360
	AAAGAATOGA OGAAAAAOGTI GTTCAATAAC GAAAATOOGT TOOCCGATGA OGATGAGOOC	420
	CTTGATACCC AGGCGGCTCC TAAAAAAGGAG AAAAGCCGTT CTAAGCACAA GACAAGTAAG	480
40	TAATATTACC GTCTTEATGT ACGUTCTGCC GTAATTATAT TUTGCTATAC ATATATATTA	540
	ATTIAAACTT T	551
	(2) INFORMATION FOR SEQ ID NO:87:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 628 base pairs  (B) TYPE: nucleic acid  (C) STRANDERNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1028UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	

	GATCCGCGCC CGGCACAGGC CTGGCAGCAC CCATCGCCGC ATGCTGTGCC TAACATGTCT	60
5	CAGAATTACG CGGCCGCTCA GGCGGGGCCC AGCCCCTCCA TGCTTTTIGGG CCAGGAAGCC	120
•	TTCCACGAGC TGGGCGACTC GCCTGGCATG TCAATGTACA TGTCGCCCCA GACCCATAGG	180
	CTCAAGGGCA ATGGCGGGTA CCTGTTGCCG ACCGCTTCTA TCTCCGACCC TTCGGTGCTC	240
10	GETCACACCE GEOCOCCICC GICTICICAG TCATICACAT COCACCTICT GOGIACCCCG	300
	AACTITIAACA TGAATGACTA TGTGCATAAC CTTTTCAGCC CCTCACCAAG AATAGACCCG	360
	CCAGGTAGCT CTGGGAATAT ATAGGGCCTC GCACACATTT AGGGCACAGT ATACTAGCTA	<b>4</b> 20
15	ATCCTACATT CTCTGTCATA GTAATGCCTA TGTCAGCACA CCTGCCGTAT AATTTCATTA	480
,,,	TTTCCTGTTT CATAAATGCT CACATATGTC ACGTGGCTGG ATCAGCACGT CATGGCAAAA	540
	TICTIATGAA TGAGCCIGIT CATCIOGICA GACAATACAT TATACACGCA TCCATCICIC	600
20	GGTATGATAC GGACTCTCTC ACACTGGA	628
	(2) INFORMATION FOR SEQ ID NO:88:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 655 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1029RP	
	( : )	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
35	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:88:  GATOGIAACA CTCTGGAGAA GTGGAAAGAG CTAGTCCCTC CGAGCTGTAA ACGATGCATG	60
35		
35	GATOGIAACA CTCTOGAGAA GTOGAAAGAG CTAGTCCCTC CGAGCTGTAA ACGATOCATG	120
<i>40</i>	GATOGIAACA CICTOGAGAA GIOGAAAGAG CIAGICCCTC CGAGCIGIAA ACGATOCATG GATOCOCTIC ATCACAACOG GIACGACACC GCCCAGTITIC COGAGCACAC OCTOGAGGAT	120 180
	GATOGIAACA CICTOGAGAA GIOGAAAGAG CIAGICCCTC CGAGCIGIAA ACGATOCATG GATOCOCTIC ATCACAACCG GIACGACACC GCCGAGTITIC COGAGCACAC GCTCGAGGAT GIOGGAAAAG GGGITCCGCG CGATGCAGTG GIATACCATA TIGCCCCACT GIGGCAATIT	120 180 240
	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAOCIGIAA ACGATOCATG GATOCOCTIC ATCACAACCG GIACGACACC GCCGAGTITIC COGAGCACAC GCTCGAGGAT GIOGGAAAAG GCGITICCGCG CGATOCAGTG GIATACCATA TIGCCCCACT GIGCCAATITI CCCGATOCCAC TGGATCCGCG CGTOCTCCAG AGCTCAAAGA AGGTTTGTGT GCTATTCTCG	60 120 180 240 300 360
	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATGCAIG GATOCOCTIC ATCACAACCG GIACGACACC GCCGAGITTIC COGAGCACAC GCTCGAGGAT GTGGGAAAAG GGGITCCGCG CGATGCAGIG GIATACCATA TIGCGCCACT GIGGCAAITIT CCCGATGGCAC TGGATCGGCG CGIGCTGCAG AGCTCAAAGA AGGTTTGTGT GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGGACGTAGG TGCATTTTTTT	120 180 240 300
40	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATOCATG GATOCOCTIC ATCACAACCG GIACGACACC GCCGAGIITIC CGGAGCACAC GCTCGAGGAT GIOGGAAAAG GGGITCCGCG CGATOCAGIG GIATIACCATA TICCGCCACT GIGGCAAITIT CCCATGGCAC TGGATCGGCG CGTGCTGCAG AGCTCAAAGA AGCTTTGIGI GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGGACGTAGG TGCATTTTTT CAGAGCTTGC TITTATCATGA CCTGCATGTC AAGATCACGA ACTTCCGCTT CTTTTCTGCG	120 180 240 300 360 420
40	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATOCATG GATGCOCTIC ATCACAACCG GIACGACACC GCCGAGTITIC CGCAGCACAC GCTCGAGGAT GTGGGAAAAAG GGGTICCGCG CGATGCAGTG GTATACCATA TTGCGCCACT GTGGCAAITIT CCGATGGCAC TGGATCGGCG CGTGCTGCAG AGCTCAAAGA AGGTTTGTGT GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGCACGTAGG TGCATTTTTT CAGAGCTTGC TTTATCATGA CCTGCATGTC AAGATCACGA ACTTCCGCTT CTTTTCTGCG CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT	120 180 240 300 360 420 480
40	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATGCATG GATGCOCTIC ATCACAACCG GIACGACACC GCCGAGTITIC CGCAGCACAC GCTCGAGGAT GIGGGAAAAG GGGITICCGCG CGATGCAGTG GIATACCATA TIGCOCCACT GIGGCAATITI CCGATGCCAC TGGATCCGCG CGTGCTGCAG AGCTCAAAGA AGGITTIGTGT GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGGACGTAGG TGCATTTTTT CAGAGCTTGC TITTATCATGA CCTGCATGTC AAGATCACGA ACTTCCGCTT CTTTTCTGCG CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT GGCGGGCCAA ACGCGGGCAA GTCGTCATTG ATCAATGCCC TGATGAAGAC TGTTGTTTAC	120 180 240 300 360
<b>4</b> 0 <b>4</b> 5	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATGCATG GATGCOCTIC ATCACAACCG GIACGACACC GCCGAGITTIC CGCAGCACAC GCTCGAGGAT GTGGGAAAAG GGGITCCGCG CGATGCAGTG GIATACCATA TIGCGCCACT GIGGCAATITI CCGATGGCAC TGGATCCGCG CGTGCTGCAG AGCTCAAAGA AGGTTTGTGT GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGTCG CACATGCCGC AGGACGTAGG TGCATTTTTT CAGAGCTTGC TITTATCATGA CCTGCATGTC AAGATCAAGA ACTTCCGCTT CTTTTCTGCG CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT GGCGGGCCAA ACGCGGGCAA GTCGTCATTG ATCAATGCCC TGATGAAGAC TGTTGTTTAC GAAAGTCGGC GTCTCGTATC CTCAAAGCAG TCCTCTGCGA CCTGCCTCCA	120 180 240 300 360 420 480 540
<b>4</b> 0 <b>4</b> 5	GATOGIAACA CICIOGAGAA GIOGAAAGAG CIAGICCCIC CGAGCIGIAA ACGATGCAIG GATOCOCTIC ATCACAACCG GIACGACACC GCCGAGITTIC CGCAGCACAC GCTCGAGGAT GTGGGAAAAG GGGITCCGCG CGATGCAGIG GIATACCAIA TIGCGCCACT GIGGCAAITIT CCGATGGCAC TGGATCGGCG CGIGCTGCAG AGCTCAAAGA AGGITTGIGI GCTATTCTCG AAGATCGATA TGGTGGTGCA GAGACCGICG CACATGCCGC AGGACGTAGG TGCATTTITIT CAGAGCTICC TITATCATGA CCTGCATGIC AAGATCACGA ACTTCCGCTT CTTTTCTGCG CTGAAGCAAT GGAACATCCA GACGGTGCGG AACGCTCTGA GTAAAGAAAG TTACTTACTT GGCGGGCCAA ACGCGGGCAA GTCGTCAITG ATCAATGCCC TGATGAAGAC TGTTGTTTAC GAAAGTCGGC GTCTCGTATC CTCAAAGCAG TCCTCTGCCA CCCCTGCCGA CCTGCCTCCA AAAGCCGCATT TGGACATCCA TTCTGCGGGT GTGAGCACAA TACCGAACTT CACTCGCCAA	120 180 240 300 360 420 480 540

5	(A) LENGTH: 638 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1029UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
	CATCTCCTCG TGTTTTCCAA CTTCGTCCCT CACCCCATAT CTCAGCCTTT CCCTCCTCAG	60
15	CATGATTATG AGGTGAACAA GATGCGCCGC GCGCTCTCCT TACTCCAAAA GCTGTATATT	120
	ACCIGATAGAA CCACCAATTT CCTCTCCCCC CCCAACCCCC ACCACTTCTC CCTCATTCCC	180
	GATACCACGG TGAAAAACTG CGACATTACA TCTCTCCTTC TTTACTTTCA TGAGTTCTAC	240
20	AGAGAACAGI TOGATTIGIT OCTOSCOSCAG GOCCGTOCTC GOCAGGAGGI OCCCAGGOGC	300
	GATCTCTIAG CCTCCCAAAAA CCATATAAAA GTAAAGTTCT TTACCCACAA GTCATCCCAAG	360
	CACGCTTCGT GOGGTTCCCT TGCCCTGCGG AAATTCCAAC TCGTACTGCG CGCTCCGTTT	420
25	CTGTTGCCCT TTCGCCAGCG GGTCGCCTAC TTTGAAACGC TGATACACCA CGACCGACGG	480
	COGTTOCAGG GACOCCACAC AGGACCAGCC TTGCOCCTGC CCCACCTGTA CTTCCCGTCG	540
	TOGOGGCGC AGCGTGCGAT TATCTCCAGG AACAACATCC TOGAAGATGC ATACSAGGCG	600
30	TATTATCCCC TOOOCGAAGA CTTTAACGAC CACCTOCC	638
	(2) INFORMATION FOR SEQ ID NO:90:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 688 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1030RP	
<b>4</b> 5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
	GATCTGCTTG TTGCGCAACG CTTCCCAATC GATGTCGCTG AGAAAGGGGT GGGCGCGGAC	60
	CTCTGCGCCG TCGTTGACCG CACCGAGGCG GTGCTTGGGA TTGCGGTTCA AAAGGCCCTT	120
50	GACAAAGGAG CGACCTTCCG OCGATAGCAC GTCCCTGGGG AATTTGACCT TGCCAAAACGC	180
	AATCTTCTOG TACATCTTCT OGTTGTCCTC TOCAAAAAAA OOCGACCAGC CACAGCACAT	240
	CTCGAATATC AAGACCCCA CCGACCAGAA GTCAACCATT TTCGTGTACC CCGTCTCATC	300
55	GAGCAGCAGC TCCCCCCTA GATACTCCCT GCTACCCCAG AACCTATTCC TCCCATCCTT	360

	TAGGTCCGCT TITGAGAGGC CGAAGTCACA TAGTGCGATA TIGCCGFTGG CGTCTAAAAG	420
	GATGITTICT GGCTIGAGGT COCOGTACAC GATATCATTA TCGTGAAGGT ATTCCAACGC	480
5	AAGCACCAAC TOOGCAATGT AGAACTTTOC COGCTCCTCC GOGAACCGAC CTTCTTTCTG	540
	AAGGTGCCAG AAAAGCTCAC CACCGNTCAG GAAGTCAGTC ACCAAGTATA AGTCTGTGGG	600
	CGTTTGAAAA GAAAATTTCA ACCAACAATG AAGGGACACG ACTTTGAGCA GTACGAACGA	660
10	GATGITICOCC TCACCAATAG TATGICCA	688
	(2) INFORMATION FOR SEQ ID NO:91:	•
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 751 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1030UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
	GATCGATTCC CTGAGCATGT TTTTCCCTAT GCTGCAGGTT TTACATGGTG ACATTGCGCA	60
20	TOCCGAACTA AAGAACCTTA TOTCTTTGAA ACTCTGGAAC ACTTACOOCG GAATTCCTGA	120
30	ACCOCTOCICA TICACTACTC TCTACAAGAA ACACCAAGIT ACCGTAAATG ATACCGTGCA	180
	CACTAGAGIGG TATCCTTTAC GOCCAGAGIT TGTAGAATCA ACCTATTCCC TTTACAGGGC  CACTAAAGAC GCATTTTATC TGAATATCGG ACGAAGCATC CTCCAGGCTC TATCAACGCG	240
35	CTTTAAAACG AAATGTOOGT TTOCOGOCAT ACAAAACGTC ATAACGOCAG AGCCACATCA	300
	TAGGATGGAA TOGTTOGTTT TOGGCGAGAC CITAAAATAT CICTATCTCC TCTTTGACGT	360
	ATCCAATGAA TTOCATACAC AAAAACOCAC TAACCAAATA TTTAGCACTG AGGCGCATCC	420
40	ACTIGIOGITIG ACTOCCICGA TGAAGGCTCG CTACGAAAAG AACAAGTACT GTGAAAACGA	480 540
	COTOTATATA CAGAACTIOC GTOCCCTACA GGACCTIGAC CACCTGAAAA GCOGTOCCAA	600
	TICATICACT GCAGAGGAAG CCATGATACC AGCITCAGAT TICAAAACAG AAGACTCCGA	660
45	GGAGICITIG AAGGACOGC TIGCAGOGCC ATACTAGAGG CCTACACGIA GATACGACAC	720
	GTTCGTGGAA CATGCAGACC TTTCGCGACA A	751
	(2) INFORMATION FOR SEQ ID NO:92:	
50	(i) SPQUENCE CHARACTERISTICS:  (A) LENGTH: 646 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: INVA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1031RP

5		
3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
	GATCTTAGTA ATGATCACGT GATTGGATTA CCGCTTGTGC GITTTGCTCT CCGCAAAGCG	60
10	ACATTIACAC GOGAAAAGCG GTGAACTCCC GCCGAAACCC AAATACTCGT ACACTATGAC	120
,,,	TATAGACGAC AATGICGATG ACGTGAGCAC AGTTTAACTC TAGTGTACAA TCACGTGCAC	180
	ATACCTICIC TGCCACCCAC ACATTRACCA TITATTIGIG GICACGIGAA ATGAATCGAT	240
15	GCATTITATA ACTGCAGGIT AGTIGAGCCA TCTCGCCAAC GATGTCCTGC GACAGCATTC	300
13	GCCCCACCCC CCCTCATCAC TCATTCCAAC CACCCACACC ACTCCACCCC CCCTCTTTAC	360
	TACTATAATT CGAAGGGGA AACGICATGG AATAAGCCCA ACGACACGCC AGTTGAGCTG	420
00	GAACCOCCAC TOGAAGAATG TOOCTOGAAA GTOOCAACGA COGAGGACGG TAACGTGTAC	480
20	TATTACAACA GOGAAACTOG OGAAAGCAGG TOOGAGAAGC COGAGTTOGA GOCAGCOGAG	540
	GAACTOCCCC GOGAAGARGA CGAACGCCG CCGGAGGARG AGAAGAACGA GCCGTCCCCCT	600
25	OCTGARGAGO COGGGGTCOG GATGGAACTG CTOCTCAACT CAAACC	646
25	(2) INFORMATION FOR SEQ ID NO:93:	
30 35	(i) SPQUENCE CHARACTERISTICS:  (A) LENGTH: 386 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1031UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
40	GATCANOGAN CAGCACOGAC AAATATAACA OCAGCACOGG CATTTGTCTA GTCCGCTGGT	60
	GYYYTGTGTC CACCGTGACG CTGGCGCTGG GCTGGAGTGC AAAAAACCGGA GCCACAAGCG	120
	TOCOCCTICCG ACCOCCAAAG CTCCCATCCT CCCACCACCA CACAATCCCT CCCCCCACTCC	180
45	YAGAGCOGTG CTOGGAGCGC GCGGACGCGC GCAGGCTGCG CGGGCCGCG CTGATGCTGC	240
	GCGCGGCATA CCGAATCAAG AAGGCACACG CGCGGGGGCA GCTGGCGATG CAGGTGGGGC	300
	COCTOCSCCC CCLOCCICAC CLOCCOCLOC CCCCCCCCCC CCLCCCCCLC CLCCCKCLAC	360
50	ACCCCGGTCT GGTGAACTTC GCGTAC	386
	(2) INFORMATION FOR SEQ ID NO:94:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 775 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1032RP	
10	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:94:	
	GATCHTRAAC CICTOGACTT CAATCHTCIG GGTAAAAGCA CAAGTITAGA GATGTATGAT	60
	CCAAGCACCA AACTACAGTC TCGAGACAGC AAAATAATCC TACTTATATA AACTGAACGT	120
15	TOCAATTCTT TAAAAAAATTT ACTAACTTCG ATTAATOCOG COCCOGTGAG COCCTCTGTT	180
	ATTACCTGAG TCATCCTGAG GGTTTCCCTA GGAAGCATCC GCTCTTACTA CGTATTTACC	240
	AAGOCACAGG AAAANGIGGT OGTATTCTTG ATTTCCCCCG CGITTTGTAC ATTACTCCAT	300
20	AGCTICATOGT CAGCAATICCC GTTICAATIGGA CATTTIGCTICA ATCGTICAGTIC TTTCCACTOGA	360
	CTTGAAATCC CGCAGGGATT TTCGGCTCCT GOCTCAACCA GGTCGCCCGG ACACCTACAG	420
	CCGAAAAAAT TOCTOCTTOG ACTAGGTCCG CTGACGTOGA CATOCGAGAT GACTTTAAAG	480
25	TGATACATTA AAACCAGGGC TGTATGAACT CAGCAAAGGT CTCTTTTATA CAGTGTGCAT	540
	ATAATATTIC GGGCGCTTGC AATTACCTCA TGCCAGGTAC TCGTAAGATT CGCCGTCCGC	600
<i>30</i>	GAGCOCTIGTA OCTATICCTT OCTATITAAG TIGTCGATOG CCTTCTTGAT AGAGATACCT	660
30	TIGCATTIGA COGITGIGAG ATTOGOCTAT GCATTOGICA CCAAAGTOOC ATGAGAGACG	720
	ACCOGNITION THICATAATH CHGACGATAC AASCINCAGA ACAATIOCHT TOING	7 <b>7</b> 5
35	(2) INFORMATION FOR SEQ ID NO:95:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1032UP	
45	.,,	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:	
	GATCCCGAAA ATAGACTACA TCTGCCGCAA GCAGCGCCC CTATCTGCAT TTCTCTTCTT	60
50	GGIGGTTGTC ATGTGGGTCA TCACGTTCAC CATTAGCATT CTAAGGGTAG TGGAACGGGT	120
	GAGTTCACTT TCACCCAGAT AAAAGTTAAC AGGACAAGTG AAAAAAAACG GGGATAAAGG	180
	CATCAGITAT GIAATAAAGA OCTATACOOC AATAAACATT TAAGIAACIA CCATOGIATC	240
55	TOCAGOGIAT TACTAGGITT COCHGAAGIT TOGAATGIGC CTICGITACC COGHGITICAT	300

	GCAGGCTAGC GCCACAAGAA AAATGCGGTC CCACCCATTC CACGATTAGC GGTGGCAAAA	360
	GTCCTAAAAG TTAGOCAAAT AAACACATAA CCATCCCTCA AAAAGCOCTT GAGCAAGOCT	420
5	ATCOCOCCTC AGACCACCTIC TAATATACAT TAGAAGTIGAG CGATGAACGA TAAATTOCCG	480
	AGACCAGATG ACTTOGAACC CACTTOGAAC TTTGTOGAGC CCGGTATCGG GCAGATCCTG	540
	COCCOGGATG GETCOCCCCA TOCAGGGGGA GTOCAGAAAC TOCTGTCAGC TOCGATGTAC	600
10	ATGGATGTCT ACACGGCTAT CTACAACTAC TGCGTCAACA AGTCGCGGTC CACCGGGCAT	660
	TITICACTOCC ACTOCOCCICA ACCOCACTOC AACCACTOAT CCATCOTOCT COCACGCACA	720
15	(2) INFORMATION FOR SEQ ID NO:96:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 602 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
05	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1033RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:	
20	GATCTICTOG AACAGGICGC CCCCGTCCCC CAGCTCCCATC GCGATCCATA GGTACTCACG	60
30	TGACACATTG CAGTOCAGCA COCTCACCAC ATGTCGGTGC COCGGGCACC GGGTCTGCAG	120
	CACCACCTOG COGGICAGAT CCTCGGTCGGT CATCCCTCGC GCTTTGCAGC GCTCGACGTG	180
35	CACGAACTIC ACAGCCACTA TOGICIGOGG GICIGOGGGC AGOGAGGGGG TITIGACGAA	240
35	COCCAACCTIC COCTOCCCAA TOCTICTOCCC CACCTCTACT TOCTTAATCT COCCCACCACCA	300
	TTCAGCCTOC GACGACTCCA TAGTAGCCCA AAGTCGTTGG ACGGCCTTCC AGGTGGCCTC	360
40	TAACTCCTCG TGATCCTTCG TTGAAAAACTG ATCCCCCAAC AATAGTCTCA AAAAACCCAAA	420
40	AGTOGGCCTT ACCCCCCAA CAAAACAAGT CCTAACTACA CCCAAGCACG AATTAATTTG	480
	GCAAGTGCCC TTGGAGCACG GTATAGGAGT ACCGGAGGTG GATATGAGTG TCGAACAGGT	540
45	GICTOGTOCG CACOCCTOCG AAGAACAGCT GOCAGOGTTT GAAGOCAATG TOGAGOCDCG	600
45	GA.	602
	(2) INFORMATION FOR SEQ ID NO:97:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 683 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1033UP

3	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
	GATCCGCCTC GTCGAAAACA GGTCCTTGGG GTGCGATACC GCCAGCACCT TGCACGACGT	60
	CCOCACCAGO TOGICGICOS TOTOCAGOSO COTGATGATG TOCTOCACOG AAAACACCTO	120
10	CAGCACOGTC TCAAACOGCG CAAGCTTCAC CACTGTGTCC AGCAGCGACA GAAGCCCGCT	180
	ATAGTOCAGO COACTOATOT COCCTIGOCGT GAGCACCTTT TTCATCGCCG AGACTAGTGG	240
	COGREGATOR GOSTOGAGAC GCACCATCAC COCCAGGTOG AGCTGCAGCA TGTCCACCAG	300
15	CCCGTTCACC GACCCCACGC CGTGCTCCTC GGGGGCCTCC AGCACATCCG CCAGCTGGCT	360
	CATTOGGICC TOGATOCTCC ATTICCTCCAT COCCATATOG ACTCTTCCCA AGTAGCGITT	420
	TOGOGUTTOT AAAAGTAAAG OGCACTTTTC CAGCACTTCG CCACTTAATG TCGTGAGOCA	480
20	CAGAACCGGG GCCCTATGTT GCCGGAGTCA AGGCTTGCCT CGCTATATTC CGACTTCAGG	540
	AAGCTGCAAG AGCTCAATCC AGATGGGTTC CAGGCTAACG TTCTAACATG GAAAGACCAC	600
	CTGATGAACA CAGTGTGGGG GGACGAGCTT CTGATAGAAG GGGGGGACAA GCTGCTGGAG	660
25	CGATTGAGCA CCAAGGAGAC GGG	683
	(2) INFORMATION FOR SEQ ID NO:98:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 653 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1034RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
	GATCATATIG GICTIGGCGC CAGCATCGCC TCTTCTGGTT CTGAGCCAGT AGTATGATAG	60
45	CATOCCOCCG ATGAACCTOG CAATOGAGAA ACTAGGTGAG TIGIIACATCC CGACOCCAAG	120
	GSCAACGCCT GAGGGTAACC ACTOCGCCCA TCTGTACTIG TCCTTATCAA TACAATTCTT	180
	TACGAGGGAT ATGACTGCAA AGATGCTTCC TAGGATGATC GAACATTCCA GTGCGTATGG	240
50	TOOGAGTOCC ATACCCATGA CCAGACGTGC GCAGTCTATC CATACGAACG CAGTTGGGAT	300
	CCGGAATTOC TOCCTGCGGA TTTCGTAGAC CTTGTTGTAA AAAATGTACA TTACGCTAGA	360
	CAACACGATC GACCAGCTGG CGCCGATAAT CTGCGCGGTA AACTGAGCCC TAGGAGAAGC	420
5 <i>5</i>	ACCCATTAAA TOCCCTGTCT TAAGATCTTG CATTAAATCG CCCCCTTGCT GAGCCCCCCC	480
,5	CTCAGCTATA CTTCCGGCAA CCAAATTTAT TAATACAGCG GCCTTGTGAT CCCTGGGTAC	540

	ACAAGAGGA AAATGATTTG AGCCAGCTTT CCGATGCCGC TGAACGGGTT GAGATCGGTT	600
	TCCCCAAGAC CCGGACGCCC AAAATCGATA GAAAGATGCT ATAAGGAGAG CCA	653
5	(2) INFORMATION FOR SEQ ID NO:99:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 670 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1034UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
20	GATCACOCAC ACCGACACC ACCAAAGCAG AACCACOGTA CCATATCTCT CACACACOGC	60
20	TOCCACTAGO ACAGOGOCTO CACCTIGGOCG COCTIGGOCTO GOCCCCCGGT COGCATAAGO	120
	ACGTCGGGG ACCTATITAG TICCAAAAAT ATIGTIGIAA CAGTAATAAT ATOCTCATIG	180
25	AGGACATTIC AGITGITACA CIGAAAAGAA CAGATACTAC ACTIGATCIA AGCCAAAAGG	240
	CAAAGAGATT TOGTTTICTAA AAGAAAGAGA AACATGCCTG TAAGAGGGAG GCCCATCCCA	300
	CATTITITCT CICCITATAT ACCAAGIAAA ATTIAGAAAA AGAAACGACG COOCTOCTIG	360
30	GTCGGCCCCC TCTGCCTGGC ACTCCAGAGC GGCTCACGCA GGAATCCTGC ATCCAGGGCC	420
	ATGCCATCAA GCTCTGAAGG CCCATAGCTG CCGCCATACA CGCCGCCATT CGCGAGCTTT	480
	CGTTGAGTTC GTAAGCCATG AAATCACAGT ATACGATTICT CGAGCGCAAG TTAAAGAGAG	540
35	CCCACTOGGC ATACTOCTAG GGCTACAACT GCGCACCAGC TGCGAAAGCG GAACTCCAAT	600
	AGITAAGGOC GOGTGOCAAT AGTATCTGCT GCAAGCAGCT TCTAGAATTT GGTAGATGAG	660
	TGCGITCATG	670
40	(2) INFORMATION FOR SEQ ID NO:100:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 558 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPCLOGY: linear	
,0	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG103511	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
55	GATCTTTTGT GGAACCAAGA TCACCACACA CGAATATGCG ACGCCAAGCG CCGCAACGAG	60
55	CCACACATGG GCCGCGGGGG TAGCGGTGGG CCCAAGCAAG CGIATTTTGA GCACCTGACG	120

	TOCTOTOGOT GAGCAATCCA GOGCATACTA GOCCCAGGIT GICAGCIGAA AGIGIGITAC	180
	CCGGTATCGG TATTACCCGG CTCGTATAAA TGTTACCCGG ATATGGTCAA GCCAAAATTT	240
5	TCCACCOCCT AAACAACAC AGAGTGTACG TOCATATOOC GOCAGCAGCT AGTGTACCCT	300
	AGTGAGAAGA AGGNCTGTGA GCTAAGACTA GCGAGGAGAC GAGGATTGGG CACTGATTGC	360
	OCCATCICCA TATTCTCTAC COCCCTGAAG ACCAATGING NATAINNOCH COCCCTNGIN	420
10	COCAACCIVEN CONCONGIVOS AGACIVACCGA CIVITOVITINA NOCINONOCOS CINCANAACCA	480
	ANUNVINCON CAATONOTTA ONATCAANNO CAANTINOON ONINCANOOC ONINCANAT	540
15	NAMED ALL DESCRIPTION OF THE PROPERTY OF THE P	558
15	(2) INFORMATION FOR SEQ ID NO:101:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 604 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG103512	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
30	GATCCITAAA AGCIGGCCIC CGCAGATAGA CCITCIGCGC AGAGOCIGGA AACCICAACT	60
	AGCAAGTOGC CACCOGAATC AGATAAGCAC TAGAGTOGTT CCAGTAACAG AGGAAGCGAT	120
	CAACGAACAT AGTAGAAGAG GACACTOCTG CCAGGCTTGA TCGGACAGAG GGTTTAGCTT	180
35	TCTGTTGAAT TTCAGAGTTT COOCCUTTG TTTACTTCOC TTCATTCTTT CGTGTAAAGA	240
	AGCTGTTTGC AGGATGTCAT CATTTGCCAG TCGCCAGGTA GGGTATTGCA GGGCCCACGG	300
40	AGTCGGTGAA ACAGAGTCAG GACCGAGAAC GCCGATAGAC AGGCGTTTGG TTTGTAAGCG	360
40	GIGAGAGCIG AAGCAGCICA AGAGGCCCCC CTIGGICAGG TIGIGCGGIG GCGGIIAGAGC	420
	ACAGCAGGGC ATCCCTCGTC GGTGGAGCGT NCGGNCAGNA GCCCAGGGGC NTCGAACAGG	<b>4</b> 80
45	GOGTIGITTAT NANGANONAC CGACCACAAA CACGCTIVINA TICGNACCGG CGGCCAGTIV	540
	CCTCANONTG GITCCCGNGA CITIGTITINN GAGCONATCC TITGGCNCTCC GCCNNAGNAA	600
	AAA	604
50	(2) INFORMATION FOR SEQ ID NO:102:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 480 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1035RP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
	GATCITAAAT IGIIGCATIG IGACCIGAAA GIIGCCCCGI AGACGCIGCA TATICAAGGI	60
10	TTCCATTTCC ACGGGACGTA ACCTAATCCG CTGCACTTTC GACAAACGAC TAATGTATCT	120
	GITCTCCCAC TCTCCCTCAT TCCCATCCCC ACTCCACTGT ACTTGTCCTG ACTGTAGTTG	180
	TIGAACCIIG ACGITAICIG CCICCAAIGA CICCAGIAGI AGICATTIIC GICICCCAAT	240
15	CGTTTCTATG GACCOCCTGA ACACCGAAGG TGCCTCCGCC TGCAAGGACT CGAAAAAGCCG	300
	CCGCTCCTCT GCAGAAGGCG GGAAATAAGA CATAACTTGC TCATCGCGTA GGTAAATCTA	360
	CGTCATTATC CGCGTCCACC ATGTTCGGCT GGGATAAAAT GGTGTTTCCT CCAGGGGGGCG	420
20	GOGAATACCA COCACTOTOC AATOOTOCOC COGTTANTGA ATNONTTINT TNATGOOGNN	480
	(2) INFORMATION FOR SEQ ID NO:103:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 482 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1035UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
	GATCIGGCGT ACGGTACCGA TATATTTCAA CTGAGGTATT CGTTAGAACA GCTACCTTCA	60
	GTGGTTCCAC GCTATATTGC GTTGCAAATA TGTTTGCGTA CCCTTCTGGC TTATCAGTGG	120
40	CATTAAAGAG CGCGCTAATG GGGACTATCT CTTTTACTGG GCCAGTGGTC TCCAAGAAGG	180
	AAGCATTCTC AATATATTTT CCGTGGTTTT TCAGGATGCC ATAATCTGGT ACACTCACAA	240
	ACAATTIATG TIGCACTOOG TGAGATGCAG GOGTATTAGT ATTIGGAATC ATGTGGGTGA	300
45	TTGTCCCGGA TGGGGTGCGC TTCACAACCG CAGAGGAAAA AATATCCCCA GGGGGATATT	360
	ATTNETCGAA GCAAGAATCG CITCGAGTAG GGATTGAAGA TTTCTTCTTG ATACTTAAAG	420
	CTGAATTOGT TCANATOGOG TCCAACGAAN GANTAGGNIG GATGGNCCCT TNGGGGGGGG	480
50	œ	482
	(2) INFORMATION FOR SEQ ID NO:104:	
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 645 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(ví) ORIGINAL SOURCE: (A) ORGANISM: PAG1036RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
	CATCATATTT CAATGCAAGA GCTCCATTAA TAGGTATTGT CTTGAGACAT GCGCTCAAGT	60
	CATTAATGTC ATGGGAAAAA TGCACCGTTC CACCTCCTAT CTCCAATGTA TATTTTAGCA	120
15	TITCAAAATC ATGITTTCTG TITACTATAA AGTGCAACCC ATTCAGGTCT GCGGCTTTCT	180
	TAGTAAAGCC TCTAAAGCCG TAATCCTCCT CTTGTATACT GCGTAGCTGT GGGTCAAAAT	240
	COGTAACAGG CTGTCGAAGA AGAGCGGTAA ATTGTTTCAG AAATTCGAGA TGCAATATTG	300
20	GTATOCCTTT AACAAGTOCA AAACAAATAC TITTTCOGAA TCTTOGTCAT CTTCATOOOG	360
	TCTTAATAAT ATGATGTGTA GTGGGCCTCC GAAAAAGAGG TCACCACTCG TATTCCTAAC	420
	CCTTAATTAC CTCAAGCAAA GCAGGGCTTC TTGTAACAAA GTTTCGGGAC CTGGACTCCC	480
25	CATGOGCCCC TOCCAATIVIGA TITOGNOOGAT NIGNNOCCCT TOCNGATANA GGNCTGGATG	540
	GCCANCOGAA NCCNICCTAG TGATNICCON CCCCTTCAGT GNUNCCNCIN GAGGTTTOGA	600
	NECONNITT TOOMINGOG GENVINICIG GNAACONOOC COINT	645
30	(2) INFORMATION FOR SEQ ID NO:105:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 613 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1036UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
45	GATCCCCTTT GGTAACGAGA GGTGTCCGCT TGTATTCACC GCACATCGTG GCCTATTTGT	60
	CATTACTOTG GCCCCGTCCC AGAGACCTAC AGGTATAAAT TCCCCATCAA GTGCCACCAG	120
	AAAGATATOC TATACTOGTT TTGAGCTTGA GOGACTGTTA ACTGCAACCA GOGGGACOGA	18C
50	ACCOCCIACO TITTACTICAT TIATTGAGOC TAAATTGGAA CCAGACATCA CAATTCTGCT	24C
	TCAGTGCGAA ATGGACGCAT ACAATCCAAA ACGCCAGAAG TATACTGAAA TAAAATCCTC	300
	TGTGGACTTC AATGTACGAA ATGTCCGGCA CCTGAGCAAA CTGCTTAAAA TATGGGAACA	360
55	AACAGGGGIG GICCCATCCA CIGATATCTT GIAGGGGICA GAGACCCATC AACCCATGIG	<b>42</b> 0

TTGAAACAGN COOCCCTTAT COCTOCTCAA ATCCNACCAA AATCTTTTTA COCTCCNCCN 480

	NACIOCANCAC TIMITITIAMI TATICOGAGIG CAANATOGAA ATAANCATCG TWAATTITOGA	540
5	AGCTATTICC COCCONCAAC CANCOCONC AANNVITTIN NGOCGINGAA AGANICAAAT	600
	TAAATINGGCC NGT	613
	(2) INFORMATION FOR SEQ ID NO:106:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 606 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1037RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:	
	GATCATCATT ATTTCCTGCG TTCGTGCCGA CGATTCGAAG GGCGGGGTCG GTTTCTTGAA	60
25	GCATTICAGG CGTATGAATG TIGCICTCAC CAGAGCAAAG GCCAGTCTCT GCATCCTGGG	120
	TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGCGAAAGG	180
	GOGTICACTICO CTOCCADATICG CATIGTICOGOG CTITOCTITICATI COACOGGAACA GAGOOGOCCA	240
30	OGATOCTCTT CATAOGITICA AAAATCACCA TAATTATATC GAGAACOCAG ATGATTATOG	300
	OCCTGAACCG GTGATGACTA AATCAAGAGG ACGCAATAGA TCATCCAGAA AACGCAAACA	360
	TATOGAAGAT AATOCAGATG ATAACTAGGA TOCOGTTOCT GAATTCAAGA AGGAAAATCA	420
35	AAGAGAAAGC AACACAGGCA CCGGTGGTTIA CCGTGCGCAT ACATCTAACC ACAGATTIGGC	480
	ACCTOCTAGG AACGATAGCA AGAAGGCCAA GACGTOCTCC AATGCCGCCG GTATTTCCCA	540
	OOCTACTICA NARGATOGIG ATCGAAGICA GAAAGGACAT GGAACIAAGA AGARICTICC	600
40	ATATIC	606
	(2) INFORMATION FOR SEQ ID NO:107:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 653 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1038RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:	
55	CATCAAAAAA AGAAATTACA ATTGACTGIT GCACCCACAC ATTCAACGGT TOCACCCACA	60

	CATTATGAGA TOCTTGATTT GOCGCGAACT GCGCTTTCCA ACTACAGTCC CGAGACTTTG	120
5	GGTGCCAACC GAAGCAGACT TCAACAGTGG TGATAACCAT AGTGTCCAAG TCTAGCGAAT	180
3	CTAAGGATAA TACCAAGAGA CAAAGCATAA TOGTATGTGC ACAGGATGGG GCGAAGTGTG	240
	GTCTAGAGCT GTCGGTGCGA GCAGAATACG GTGCGGGCAA TGAGCACGCC GCAGAGGCCG	300
10	ACCOTOTOCO CACCTCACCA COCCOCACC CCTTCCAAGC CCTCACACAC ACTACTAACC	360
70	CATTGCAGAC AAGATGGCTC ACGAAAACGT TTGGGGTCTC CCACCCNNAN AAACTACGGT	420
	AAGGGTCCC CCAGTGCGCG TGTGCGCTTC GNCTCTTGTT GGTCANAAAG TACGGGTTGG	480
15	ACATOTTOCC CAATGGTTCA NAGAGAAGGC CACGACATTG GTTCCCAAAT CCCCTAAGAG	540
,,,	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
	TATTTTCNA NACCOCNITT TITANITINA NNCNOGGINC CCAGNNGTTT GGN	653
20	(2) INFORMATION FOR SEQ ID NO:108:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 609 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1038UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
	GATCOGITCT COOCCITCTT TACCTOCCCG TTATTCAACG AGTCATCGAC TGAGAAAGAG	60
35	ATAAAAGCGC TCGATAGCGA AAATAAGAAA AATCTCCAAA ATGATATGTG GCGCCTTTAC	120
	CAGCIGOGIA AGICGCIGAC CAACCCCATT CACCCGIACC ACAAATICTC TACTGGAAAC	180
	TTTGAGACTT TATOGAGCAT TCCGAGATCG AAAGGCGTCA ACGTCCGTGA TGAGCTGCTG	240
40	AAGITCIACA AACOGICATA TICTGCAAAT CTCATGAAAT TAGTGATCTT GGGCCGCGAA	300
	CATCHAGATA CCHTGGGTCA GTGGGCATAT GAGCTGTTCA AAGACGTCCC TAACCATGGG	360
	ACCAAAGTGG CTGAGTATCA CGGCCAGGGA TTCACGGCCG AGACCTGATG AAGGTAATTA	420
45	AAGTGAAGCG GNIAAAATCT TAAGAGTGTG GAATTCATNC GNGGGGCAGA TTTGGTTAGN	480
	ATGGAGGCAG CAGTCGTATG NGCATTTATC GCCAGAGCAA GGTCCTCCCG NTCTGGAGAA	540
	AAAGTOGAAN CONONOCCT NOONNTCCCC TINAAAAGGAA AATNCCCCNC AANNOOCTIN	600
50	TVECAAVIVA	609
	(2) INFORMATION FOR SEQ ID NO:109:	

	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1039RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:	
	GATCATTICT CITCAATCCC ATTGACGTGA ATGATGAACC GCATTATCTT TTTAACAGCG	60
15	ACAACATOCC ACOGTATATA ATTIGTOCTTA OCTOGTIGATA TOCAGAACCA GGTGTTTAGA	120
	CTGGCAATAT CCCTAAACTG GTGTAATATG GTCTTCAAAA GTTTTGTGCT GTCCGAATGA	180
	GOCCACTITA GTAAATTAAC CTCGAATTTG TCTAAAGTAT CGCCACCGGC ACATCTTTTA	240
20	AACCOCACCA OCOCOCCCT TTTTATTOCC CATCOOCOCT GTGAATTAGC AAGTTGTAAA	300
20	GOOCTACTGA ATACGACOCC ATOCAGCTCT TCATCGATAT TCACAACCTC GTAATCATCC	360
	AATTOGTTAG CTTOGATTTT GONGGCATA TCTCTTATCC CTAAAAAGTG GGTTGGATGA	420
	TOCATAAAAC TGATCTTCAT CATATAGAGA AATTTOOOCT COCCCCAACG CAGACACAGN	480
25	CAATGTAGTT TCTTGTGGCA NAGTINGCIN COCAGGNATT ACTCGCANCC GGGGAGGINT	540
	CACCCCGGAG ACAAAAATTC CCCCTTTTCT NTGGAAATCG TNGTAGNNCC TANCAAGGAT	600
	GOGICAAGGA CCTGGITTOCC ATTCCANITT ACCATTITIN CCC	643
30	(2) INFORMATION FOR SEQ ID NO:110:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 635 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1039UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:	
45	GATCCTTCCA ATAACCCCTA AACATCCATG TGCTGGTTTT AACTATGAGG GAGITGCAGT	60
45	AATTICGOGG TCTCGCAAAG TAAATTGACA GAAAACCCTC AGATCGGTAA CGAAACAGCT	120
	GAACGACGGA GATTAAAAGG AAGAGGCAAA TAAGCTATAG ATAAGATCGA TAAATATTGA	180
50	GGGGGGATG GATATATTAG AAACTAGCTT TAGACTTGAA GATGTGCTTT CACGCTATTA	240
50	TAGACTICAA AACCICCICC GACTCAATTA TCAACACTIC CTACCCACGA CTCCAGATGA	300
	TCAATGGTGT ATCCAATCCG AGCTTCTTAA TCCGCAAGAA GGATCCGAAA GCCTGGTGG	360
<i>EE</i>	COCTITITIC GOOGGAACIC IGGIOCTITI ACCATCAAIG ACCAGGACII ACCCATICCC	420
55		

	GOOGITIOGAA GOGATIAGOCG AACCCCCCONC CTCGGAGAAG AAGGOCCACT TTACGGCAGG	480
	GTTTTCCAAG GCNAACCTGC AACGCCNVIG GATCTTTTTA AAGCNIGGGG GGATGVICAA	540
5	TAANAATTON GAGGCONAGA ACCTITIGGCA ATTIGGAAAAN ININTITICCCC GNAAGAAAGC	600
	NNAGOGANCC CCCCGGGNCN NATTTTTGGA ATGNC	635
	(2) INFORMATION FOR SEQ ID NO:111:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 648 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1040RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:	
	GATCCAGTGT ACCAGGTAGC GTCAGGCACT TCTAGCGCAA GGGCCGCCGT AAACCTTGGC	60
25	CTCTCACAGC ATTTGGGATG AGTATGGGCC ATCTTTAGGG CACGTGAGTG ATCATGATGG	120
	GTACAAAAAG AAATGATTTC OCCCAGGATC GAACTOGGGA CGTTCTGCGT GTTAAGCAGA	180
	TGCCATAACC GACTAGACCA CGAAACCACT TICIGCAGGC TCTTATIGGA CAGGIGATGT	240
30	TACCCCAGAA GAACATGAAC GTGATAATAA TTCAGAAACC TCTTATGCTA AAGTGAATTA	300
	CTATIOCTTA ATAACCIGAA GOGAATAGOC ATTOCCAGTA TIGAAAATCG GOCITTOOGT	360
	TTATIGOCTA ATTATATTAT TANCANTATA TATATATACC AACAAGGIGA AGAATGGNIG	420
35	TOGNIGGITT GOOGGOGATA COCNAGAACC AAAGTAGAAG TIGACAAGIT GGTOGNAGNG	480
	GITCAATICA GNACIICAIG GCAACNITIA CNAINVITIN NINAGAACCC CCNAITANIC	540
	TTINNCTICG GOOGGICTON NONAACCOGA AACAATIVITIN CNGAACIGAG TINGOOGGAN	600
40	GITCNICGGT NITITIONNOC TITGGGTCCA AATTGGGCCG GAANCCCT	648
	(2) INFORMATION FOR SEQ ID NO:112:	
<b>4</b> 5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 613 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1040UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:	
	GATCAGCAAC CTTCTCCGCC GTCTGTGTCC TCGCTTTACC GAGGATACGA AAATAGCCGC	60

	GOCTOTOTT CHAMICOCCA TOCTOMECHO CHAMECHEGI CITCIGNIOC MAGCAGIACI	120
	AGTTACATTA TTCTAGAGAT GGAGGCAATG COGACAGCTC TGCGTCAGTA TTTGAGGGCA	180
5	ATCTOCCAAG ATOCAGAGGT ATCCOCCAGT CTGTCCCTAA CGAAATTCCT ATTCAAGAGG	240
	ACGATAGACA ACOGTOCTIT TACCCCAGAA ATCCTOGAAG ATAITGAATC TCGGGAGCTT	300
	ATGGATGTAT ACAACCTCGA AAATCAAGTT AAATTCCAAA AAATGGCGGT TTGGATAGAA	360
10	CTGTGAAGCT ACAAGTCCTC GCTAAAAGTCC CTAAAAGAAA AAATCTTGCA AGATATGACT	420
	ACATTATGAG GTTTTCCNCC AATTTAAGGA GAGGAGGATC CCAGNGACNA TTTAGCTCTC	480
	ACAGATICTT CONTCOCCAA AATTITTTAG GTACCNATNC ACGITICCCCG AATNAATGIN	540
15	NATINITIAC ANICOCOCNG AAATATOCTC ANAGNINAAG TTTGOOCACC CCCCCCCCCT	600
	ATCANGITIT GIC	613
	(2) INFORMATION FOR SEQ ID NO:113:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 649 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1041RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:	
	GATCCTCCAC CAGAGCGTCG GCGTCCCCATA CCTTCTGTTC ACGCAGTGGC GCGTTCTTGT	60
35	AGAAAACGCC CAACAGITIGT TIGIAGGIGA ACTOGICGCG GAATITICTIGG GCGCGAATTIC	120
	SCICCASCIC CICTICOGAA ASCITTICAC GCOGCCACCA GCITICICATC COGTICAACC	180
	AGCOCTITIC GIOGAGIOCO COCTIGITOCG COCCITICIOC COCAGCAATA TOTCOOCCA	240
40	GATGCCGTAC GCGCTCCGCC ACTICATGAC GCATGACGCC CTGCCGCTCT TCTGTGAAGA	300
	ACTOGRAGIC CAACCCAGCT TOGAACAAAC AACTGCTTCA OGTATOGCCG OCATACTTTC	360
	ATOGACGTCT CGAGATAGTC GGCCGGAGGA GGGGCAACAA ACAACGCGAG CGGCCGGGGT	420
45	TTOGGGCATG TGTCANGING OCTGCGCCTG OCCCTTCACC AACGACGAAT AATGITGGAT	480
	TINGCCCING TCCCINIGGCG GWINCAATCA GAATGCCGGN TCAACCNAAN CAAAAGGGAC	540
	AATINIOCOGG AACCAAGGGG GITICCANGOC GAAAGTGTTT ATTINIOCONAC TINITIOCOGTA	600
50	NAATTITINT TINICNCTOG GONIGTONNI NACCNCCACC CONAAATAA	649
	(2) INFORMATION FOR SEQ ID NO:114:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 645 base pairs  (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1041UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
	GATCTOCTTC CTGAAAAATG OCGTCTCTGT CTTACTOGTA CTCTCAAATA OCTACGTCTA	60
	GETACAGGGC CATTITOCGGA TOCCAGGCCAC GGGTCCACTG CAGGAGGTAC AACAGGATAT	120
15	COCACGICIC GCCCIOCOCA CGICACTIGG ACCCTCCCGT TCTCGTCCTG ACGTCTCAAT	180
	AAGGTACGCC GTTTCTCTTC GCCGATGGAC TGCGCTAACT GTATGGCCTG GCTACAAGTC	240
	TGTTGGTTTC GAGCAGCCCA CTTCTTTATC CACCCTCAAG GTTTACCGCA ATCCAGCAAT	300
20	TTT00GTCCT GGCACAGCCG GATATCATGT GACTTAATTA CGTCAACGTT CAAGAGTTGG	360
	GSGCGGCCGC AGCAAATTTA ACGGGGGCGN CGGTCGTCCC CCCCGATCGG GGGGGGGGA	420
	GOGNATTANC ANTICCANTOC COOCCAAATC TINGTITTACA NAAAGCAAGC ANANTCATAG	480
25	TGATTIGOOG GAANANCCCA AGGITNNGGC CNCCANGGNI CAAANICNCC CNI'INNI'TIT	540
	TOOGTTCCCG NCOGAAAANN CCATTCNCCG ACCOCCCNAG GNCCOCCAAT TTTCCCCNGT	600
	TINIVAGOGGAG TICHNYTTINGGG GGGGANNICNG CICANIAGGAAG GNOGT	645
30	(2) INFORMATION FOR SEQ ID NO:115:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 682 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1042RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
45	GATCCGTGCT GCGGACAACC GCCAGAGCTC GCCTACAGCC GGTATATATA GGCGGGCTGC	60
	CGGCCTGCCG CATGCGATTT GTCCCACCTC GCTCTGCTTC GTCCCGCCTG CCGTTGCTCC	120
	ATGGGACCIT TCATTTAGTG TCTCGCGAAC GTTTCGAATG TACCCTATCG TGGTACCACG	180
50	TIGCCIGCCG TOCCGITACT ACATCTICTA GCGCGGACTG AGTCACATGT CTGGCCGCGC	240
	ACTOCTITIC TOTAGATAGT CAGACGACAG ATAGTOGATA GITGGAGATT TOGGCAACAA	300
	TAGCOGTOGC CATTACOCCT GCCCATTGTT CCCATGTCAT TOGGAGGCTG GGNCCCACCC	360
55	ACCOCAACTC TINCCCCITT AANCCTNANA GNCCCNOCCA ATGNAAAACN CITTCTTING	420

	INDIGONGCAA ACGOGCCTINI AGGINGATTIC TITIGINOGATT NGGGANGCAC TGAGAATICCA	480
	AGINGGAAGG GOOCTINIAAA AATINGCTCCG GOOCANNOCT NOOCAAAGGT TTNAAAANCN	540
5	GENTAAATNA GOONCAGAAG AACONGGGGA GGAANCANAC ANAAANTNOG COCCNOCTIGA	500
	AGGAAAGGG CNGNUNIGGG GNCGAANCCC CNGNAACGNI NITICTTAAA GGANAACAAA	660
	NOSTINCAAAA AAAATOOOOG NC	682
10	(2) INFORMATION FOR SEQ ID NO:116:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 649 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1042UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:	
25	GATOGOGTOC TOGAGOGACT TOTGAGOGTG AAGCTOGATA COGTGATOGT OGTOGTGATG	60
	GLOGLOGICY LOCLOCICLE CICLOCCCLE COGLYLCYCC LOCOCLELLE CCGLLOCOCL	120
	GITGCTGCCG ACAGCAGCAC CTGTATCCGC AATGCCCCGAT ATGCTAGAAT GGAGCAAATT	180
30	AATGGACTGG TCTGCATTCT TGCAGAGCGG AGCCTCGCAC ATGCTGGATA TGCTTACGAG	240
	ATCGCCGGAG GATCTTTATG TCTGTTTCGC TATTCACCAC GTGGTCGTGG CAGTGCTGTT	300
	GITICATGAC CAGCCOGTAT CITICANAGGA GICGTAGTIC ACGCATTGIT GGGCAAAGCC	360
35	AGTOGAAGGA GOOCATOCTO CACGGTOGGG GAGTOCOCGG GOGACGTTTC CACAAGOCAA	420
	GGTACCTAGA AGATGAATCT TTTTTGANTC ANCNGTTGGG CCNCTNGGCA ATTTNAAGTC	480
	GNAANIGNIG AACTICOGAA AGTIOGAAAT TOGNOONAGG NOTTOTTOOC COONCONONT	540
40	TNOONAAGCA AAAANAAANA ATTAATTOGN CCCCCCCCCC CAAATTTGNG GTCNGAGAAA	600
	TITICCAAACC TIGGGITAAT AGTAAGGNCC COGNIGNCIG GGCCGNCCC	649
	(2) INFORMATION FOR SEQ ID NO:117:	
<b>4</b> 5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 648 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1043RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:	

	ADDIAGAN ARATHAN CENTRATION OF THE ADDIAGNA ARATHANA	60
5	GATOGATTGT CCAGAAAAAC CGGTTTTAAG ACTCGTTCAT CAAACTTGTT AAACCATTGC	120
	CCATCOCCTT CCACTATATT CCCCAACCTT TCCCCCATAT TTCTTCTGIC TAATGATAAT	180
	COCCCCACAG OCTOSTICADO OCCTIGATISCA GASCOCIGAAG ACOGTICOGTIC TATICATAGGA	240
10	GCAAACCTTT CTTCATCCGG GCAGCCGGTC GGGCTGTCGG TTAAAAATGG AGGTGCGTCT	300
10	ANTCANGACA TUAGCUGGAC AGGUCUAGOG OCTUCANTAT CANATUCATC ATCCGUTUCC	360
	TECTIGITETT CTACGEACCE TGTCTTTATG TTTAAGATET CAAGCATACE CGCAGGAGTA	420
15	CCTCCAAATA TGATAACGGT GAGAACCACA ACTACCAGCA CAGTGGCCAG AAGAGGGGAA	480
,,	CTTGGANCTC GCCCNNNGA COCNTAGCCA GNCNCACTCC AANAGNAACC CCNAANCCCG	540
	NCCNNINGG NAACNICCIN INTITINGINT TOGATNICCC CNAINIANINN AAAACCCCCC	600
20	CCCCGGGAIN TIMMOGGCNC CCMMMMCCC MMAANGGGN AAAAMMC	648
20	(2) INFORMATION FOR SEQ ID NO:118:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 419 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: 1043UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:	
35	GATCAGATTG TCTTGTGATG GAGAAGCTGG CGCATCAGTA GAGTGCAGAG AAGACCCATG	60
	COGAACAACT GIACCACCCA GOGACTOCOG TCTTCCCCGGA ATGITGCGAA AAACAACAGC	120
	ACGECCIGAG TCACTTACAG TCGCAGTGGG TTGCGAGCGC GACAGATTAA AAGAAAAGCG	180
40	CTCGGGCTTT GTGAACAGNT CAGACCAAAA CCCAGGTCCT GGCTCGCGGA ATTCCTCGCT	240
	TACCITICACA TACAACITAG TGTGTTCGCT GTCCNAAATA TACTCCAAAA TCTTGATCGG	300
	COCACCTOTIC TOGITICATOT COTOCACAAG TIGACCACTG TATITCCAGTT TGACATCAGA	360
45	GGGCGAAATC ATCAGIGIGI GGCGITCACA GAGCAAATAA ACTCCTITIAC TTCCTGCAC	419
	(2) INFORMATION FOR SEQ ID NO:119:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 606 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1044I1

ATCOCCCTCT GTAGTCGCCG TCATGCTCAT	
	60
OCAAOCTICAA TOCTCOCAOC COOCGACTOC	120
CCCTTCACSG CCCGGCCCGCC ATTGGAGTCC	180
CACCCATACA TTOCAGOCCG TACATTTCAA	240
COCACACOCA ACOCOCOCAC CCACOCCOCOC	300
CCACCACCCC COCCCTAGGC CCACCGCCAGC	360
AAAAATATAG TOOCTACAAG AGGGATAGGI	420
AATTAAGCAG ACGAAATGGT TGTTTGCAGG	480
CAAAAGGITT TTGANICGGG GAGGICGWIG	540
NGAAGNGANG GNAACNCAAG ANNOOCCAN	600
	606
):	
5: mirs de mmic)	
2	
EQ ID NO:120:	
CACAACACAA ACCCCTGAGA CCCCACCCCC	60
COCACAGOOG GCOGGOCTICG ACTICOGGOCGA	120
CCCCCCCCCC TCCCCCCTCC CCACCATIACC	180
CCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCCCCCCC	240
OCCOCTTOCT OCCOCCATG COCACGGCAG	300
ACCOCCEAGE ACCITEMENT COCCECTCOCC	360
GGAGCTITTIG TOGGTAGNOG TGTTCAACTN	420
NACINANCAG TONINNACON NGAGCIGAGN	480
ACGCCCINCCA ACCCININGAN CCCINITITIT	540
GGACCITTIC TOOGTAGNOG TGITICAACTN	

	ANTINICATT TICCCCCCTT CONACONTIN NI	632
	(2) INFORMATION FOR SEQ ID NO:121:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 626 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE; (A) ORGANISM: PAG1044RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
	GATCOCCTIOC CTACTIOCAC CTCATGCACC GCTTGGAACT GCCGCCCCAC CCATGTCAGC	60
20	ATCTITATICT TOCTOGACCC TGTGACCGAG TAAACAAGCA CCGTCATCCA CGTCTCAGCC	120
	TICCCACATG GATGITCAAA CAGCCAGGCA TGGTCAATGC CTCGTTTGTC AACTATCTTG	180
	TOGTAATGIT GTAAGTTOCT OGAATGAAGT AOCAGTAAGC ACTTOGTOGT GCOGACGAAT	240
25	ATTGTCCGCA GCCGTTCGGA GTACAGCAGC TCTTCTACAC CATAATTCGG GCCAAGCAAT	300
	TCTGTATATG TCTGAACTAG ACGCAGOCCT CTCTCGTCCA TACTGGAGTA CACCAAGAAG	360
	TCCCTATTAT TTCGGACCAC CACAAGTTGT CGAACGCAT CAACCACAGG GACACACTGA	420
30	OCACCITOGG ACOGAATOGG ATTTACTAGC TCAGCCCTAA GCATCTTATG ATGAGGGCTG	480
	CCCTTAGCIT GCTGAGTGCT TCGGGCTGCC TGCTTGTGGT TGGTGGGTCC TTTCTTAGAA	540
	CGATTGTTCA AAACCATGAT GATGGGGTTT GGTCCGGCCN GGTGATTTGA AGATTTAAAC	600
35	COGTINECAAG GAATTGACON TOODOG	626
	(2) INFORMATION FOR SEQ ID NO:122:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 545 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
<b>4</b> 5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1044UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
	CATCICCTIG ACCOCCCGIG OCCCTCTCTT CTICAACGIG ACACCGIGCA ACTOCTACIG	60
	TTAGTATOGG TCCOGTCTGC GGCTCCGCTC CACGCAGCAG GGAGCCCTGC TCCGCACTCA	120
55	ACATACCCTC TTGTGCAAGT TAATGGTGTA CTCGCGAGTA ACAACGTCCT TCAAACCAGC	180
	CATTICGOCT OCTTAATIAT CICITACGAG TGAGTICIGG TATATCCAAC CTATCCCTCT	240

	TGTAGCCACT ATATTITITCA TGAAAAACCG CGCCCGCGCC TCTGGCCTGC TGCCCTCGGC	300
5	CTACCOCCCC CCTCCTCCCC COCTCCCTCC COCTCCCCAT TOCCCCCCCCC CCCCTCCAVIC	360
	CCCCCINCOG CTCCINCCAG NTCCCCACGA NTCQNENCCA TNENNGAAAT GTACOGNITG	420
	AANGNITGNI GINAAAGSCA NAAAAGAATC CCCININGGI GGNITNNAAN MUUSOONNN	480
10	NUMBOGGAN GUCCCACCIN ANIMACAANT TTAANAACHG MUNTMIANA THUMTNGATN	540
	NANAA	545
	(2) INFORMATION FOR SEQ ID NO:123:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 723 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1045RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:	
	GTGGATCCGT AATGTGGGTT TGTAGGCCAG AGGGGATTCG ACGGTGGCTG GGGGCCATTC	60
	TOCCCOTTAA TTAGATOCCA COCAATTGTT TTCACATCCC AGOCGAAGGT TOGCATACCG	120
30	CCCACATACT TOGGIAATIG ATAATOCCOC CACATGACOG GATACTAAAC AAAGCAAAGT	180
	GICACATICT TATTITICTGT TGTGGTCAAA AATCGGGGGG TAGGCGATCA ATTTGCATAT	240
	ACAACACGAA ACCOGATCOG AGATTTCTAG GTCACAGGAC AGTTTGCCGT TTTTIATTGCG	300
35	TGTCTTTGTG AAACCATAGG CACTTGACAT AGGAGCCCTC TTTAGAGTAC AATAAGCAAC	360
	TGGCAGCAGC CCTACAGCTT GGGCTAAACT TCTCCATTAT GTGAAACGGG AAAGACGACA	420
	ATGCCTCTGA ACOCTTTCAC GCCACTTTTG GTGOCCCCAAT TOCATNGNIT COGNAANTAN	480
40	ANINECCOCO ECCOCAAAA ANNOCAAAA AAANNECTT TTTINECCNT NNINTTINN	540
	AAACCANGAA TAMITTITIT NGGGANGGGGG GGGGCCCCCT TITMINAAAN CCANNOCCCC	600
	TIMMMOOM VECHITITIN MINNMMIT AAAAAMINED MINITMMED MAAAAMIND	660
45	NCCCCCCCNA NNCNCCONNIC COMMINITIT TITTININNIA MIAAAMINCC CINDOGNIGG	720
	œ	723
	(2) INFORMATION FOR SEQ ID NO:124:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 502 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:	
	GATCTAATAA CCACCCGITG TATATTTOOG COGTTAACTA TATATOOGAA TCATATAAGT	60
10	GCTTAAAAAC ACCTCACCCG CAAGGGGGTC ATCTATAAAC AAGCCATAGT GTGTGTATCT	120
	TIGOCTACAT AGCATCATGA CTATGTTOCG CACGCGTCAT TTGCACTGTT TTAGCATGTA	180
	ACTOGCAGAG CCAGCAACGA ACAGAGCTAA TTTTGGAGGC TTACCATACT GTTGTCGCTG	240
15	GATGITGAAG CACGGCTGIT GTGGATAAGT TTAGAACCOG TCGCCAGCAC ATTCATACCC	300
	TGAAACTACC AGTTCCAGGG GACATGITCT TCGTGGCTTT GACAGAATTA TTATTGTAGT	360
	CCAGTTAGAT GTACTACCAT TGTTGCGCTA ACATAATCAC CATTGTCATC TCTGGAATCA	420
20	CGIGICOCCA ACCATATIAA TGITIGIACT TAAACTCGGI ACTCCCTTIA TCCAAAGCCA	480
	TCACGGAATC GCCCTTCACT AT	502
	(2) INFORMATION FOR SEQ ID NO:125:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 515 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1046RP	
35		
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:	
	GATCGCGCGC GCAAGCCCGT GCGCGAGCTIC GAGCAGGTTC TCGAGGTCGC GGGGCAGCGC	60
40	GTCACACGAG TAGGCGTAGG GATAGAGGAT CTCCTCCGAG TACGAGTGCA GGTCCAGGTA	120
	GOOGLAGATE TOCAGCTOGE CCTTOGICTT GITCACGIAG TCGTTCCAGC TGCGCGCCTC	180
	CACGGCCTCG AACGGCTGCT GGCCGCTATA GTCGCCCGAG CAGGGGTAGG CGTGCTGGCC	240
45	GETCCAGTGG TAGTCGAACG AGTGGTCAAT GTCCACGCCA TCGCAGCCCG GCATGTACGT	300
	999CTGCCGG TTCTTGC9CC ACAGGCGGTC GTGCGTCCAC GTGTACGCGT AGCCGTCTGG	360
	GITGAACACA GGCATCACCA GGAAGTCGAG CGCGTCCAGG TAGCGCGTCT CCTTGGGCCC	420
50	CCGCCCATAC CGCGAGAGCA GACGCTCCAC GACAAAGCAC GCCGTGCTCA CGCCAATCCA	480
	CTCGCGAGCA TGCACGCCGT CCGTAATTAC CACCG	515
	(2) INFORMATION FOR SEQ ID NO:126:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 561 base pairs	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1045UP

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: LINA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1046UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:	
	CATCCOORGAG CICCATCATT AGAROGICIG GACTICOOGA AGACACOCAG TOGIATGICI	60
15	GRACTITOC AATTICAAAT TAATTCTCCT TICATCGTAG TICGGGCTGC TGGGGCATCT	120
	CCGACACAAA CGGCTGAGTC GCTGACACAA ACAAAAAACTC GACTACGGAA AACGACTAAG	180
	CGTCGCAGAT GCTATATATA TACAACTTGG TTCCTAATTA GGGTTAGATC CTTGCGAGAA	240
20	ACAGACGTIG ACCTIGICCA CITCACAATT TTAGICCCGT CTCCGAAGTT TCCAGGCAAC	300
	ACGAATAACA ACACATATTG CCATGOCATC GGTAACGTTT AAAGACAATG CGGAAGTGAT	360
	AATGATAGGT GAGCAGGATC GGAGAAGAGA GCAAGGTATG GCCAGGCCCT GGATAACGGG	420
25	ATTCATCGAC OCOGATATCA TGTOGCAAAA OGACGGTCCG TAACTCATAG TAGACATCGC	480
	CAAAGAGAAC TTCGACAGCT TATATTGACA TTCGTCCTCT TGCTCTACAT TGTTGAGGCA	5 <b>4</b> 0
	AAGATATAAG AGAGTATGGT G	561
30	(2) INFORMATION FOR SEQ ID NO:127:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 685 hase pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1047RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:	
45	CATCGAGTAG ATGTTCCGCA GCGCTGGCAT CTTCAGGTCC CGGTACGTCA GGATGAACTC	60
	GCCAATGCTG GTATCCAGCG TGAACCCGTT GACGCCCTGC CCCGTCGTTA GCATGACGTG	120
	CGTGGACGCG CCGTACATCG CGTAACACGC TGCCACGATC TCCCGGCCCG ACCGCAGCAC	180
50	ATCCTIGATT GTCCCGCTCG AGTCCGGAGT CAGCTTGAAA ATCGAAACGA TCGTGCCCAC	240
-	CGACACACOG GCGICCAGGI ICGACGACCC GICAATCGGG ICGCAGCACA CCGCATACGI	300
	CCCACCOGTC TCCCGGGAACA CGATCAGGTC CTCCTGCTCC TCCGACACCA GCACCTTGAC	360
55	GITCCCOCTG GCCTTCATCG CATTGATGAA GATCTCATCG CCCAGCACAT CCAACTTTTT	420
	CTOCTOGTCC CCAGTCGCGT TAGACGCGCC GGAGAGCCCA ATCAGGTTCA CCAGCTCCGC	480

	GOGTOTGATO GTOTOCGAGA TGAACTTGAA COCAAACGAC AGTGAGTTGA OCAGCAGGTT	540
5	GAACTCGCCC GTCGCGTTTT TGGCCCGAGCT GCGCTGCGAC TCCAGGATGA AACGCGCCAG	600
	CGTAATGATA TCCGTGTCGA TAGCCTCTGC GGAGTCGCGT CTCTGTGGGT TCACGGTAGC	660
	CATTICTOCT TGAGTOCOCT GTOGT	685
10	(2) INFORMATION FOR SEQ ID NO:128:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 678 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1047UP	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO:128:	
	GATCACTCCC CTCGCTTGAA ACAATGCCGT ATAGCGGAAT CTGGCCGAGC ACCAAGAAGA	60
25	TCAGCAGCGA GACGGCTGTC CAGATCAACT TCTGGTTGTA TGGCACTTTG CGCTCGGGCG	120
	CGATCACCTC GOOCAAAAAA GOOTCGAAGG GTTTGAATAG ATCCAACAGA CGCCCACTCA	180
30	TTTCAGGCTC ACAATGTTTG TAGGTAGCTT GCTGGGCTTG GATTGGCTAC ACAGTTGGAA	240
30	CCACACAAAG TCACTATTOG GCGAGATGGT ACTCTAAATG ACTGCAAGGA GAACTOGTCG	300
	GTITOGITIC CTGAACAGCT TAATTOGACT GAGTTGCAGT AGCTGTACTG AAAGGAACAC	360
35	GTATCTTGAA AAAATTATAA ATCTCAGTAC CACGTGACCG GATACGACGT GCTATTCCAT	<b>4</b> 20
	CTCCCTAGAG CACCTATATG CCTAGTCCCC GTACCCTTCG TGAGTAAGAA TACCTCTCTT	480
	GGACAATAAT COGTGATGAC CITATTATGC TATAAAGCTA TITTACATAG CAATGGATCT	540
40	COGTIGUITAG ACCUTUGOGO COCCAAAAGA CCAAGTACAT CAGCACCGAG AACAGCAGGC	600
	AATCOCCAGG COCTTOTOGA OCTOCAGAAG ACATOCTOGA TOCAAACCOG AAGAACGCCG	660
	NTCGGAGTAC AGTTGGCG	678
45	(2) INFORMATION FOR SEQ ID NO:129:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 638 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1048RP	

55

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
	CATCCTCATA GICCOCCTCG TCGTATTOGT TCCTTCTOCG CCGGCCCTGC ACCGGCATAC	60
5	CCATCGCGTC CACCTGCATC TIGICATCCG CGTCCATGTC GTCGTCCAGA AACACCTGGC	120
	TATCCTGCAG CATCCTGTCC COCOCATTGA OCTGCCCGTC CATCCGTCGC CGGTCCGCCA	180
	ACCACACTIC CTCGTCCTCC CCGTCGTCCA CCCCCTCATT TTCATAGAAG TCCTTGTTCC	240
10	CATTOSCOST ATASTCCOCG TACATGTCGT COCCCACCAS GTCGACCTCG TCTATOCCCT	300
	CITICIOCOTO ATCCAGOTOS TOTTOCAAAC TOGATOCOCT OGTOGOCOTO GOTAATOCOC	360
	GITCTCGAAG TCGATCTTCG TCCCGGGGAC CCCAGGGGGG ATTATTCCCC CATACGGGAA	420
15	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	480
	TGTAATANIC CNCTGTCTTT TTCGGTTCAA CINTAGCCCT CNGGGCCNGG TINACCCCCC	540
	ATCCCGTATG GAAGCANCCA ATAACAAATG CCTCCGAAAA NITTGTTNIT TTCCNATTIT	600
20	GGAANAAGNA ACTTCTNANA ANGAATTTTIN NANTINNN	638
	(2) INFORMATION FOR SEQ ID NO:130:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 621 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1048UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:	
	GATCGCGCTC CTCAGCCATG GCTTCCTCTA ATAGTAACAC ACGCCCTGCT TCGTAGTCGT	60
	CGAGGTGCAC ACCTACCCGC GCAAATAATG CCTCATCTGA CAGCTGCACC TGGTAGAACT	120
40	GTGAGCACCG GAAGTGCAGC TTGCTGCAGA AGCTTGTGAG ATATTTGTAG GGGTTGTTCT	180
	GIGICAGAAA GITOCTCACC CGICGATICT CGIAGOGATC ACGGATACGA CCTIGOCTCT	240
	OCCOCCACAG COOSTACCCG CATACCTTGT TTAGATTGCG CTCATCTATC AAGTCTGAAT	300
45	ATGTCGGCTT GGGGAAAGAA CCTTCCCACG TATTTTAGTG TCTCGGGTGT GCATTCTTGT	360
	CTTOCGAAGA OCAGTTCOGA GCAATTCGAC CGTCAGAAGG TCCCCCTCCT TTAGTGAAAG	420
	NNOCCATCIT OCTGATAGCA ACTTAAAACC CCTTTTOCNT TNTCNCAATA CNAGCCANNA	480
50	CCTTANGTAC GGININCCGT TCTTAACCCC GCCGGGICCC NGGGNGGITT CAAGTICTIG	540
	GIBBGANAAG GINCCONINC CCGBBGGINC GCCTACTTAA GNGANGCCAN AAGGNAAAAG	600
	NCCCCCNGAA AAGIGGNITT T	621
55	(2) INFORMATION FOR SEQ ID NO:131:	

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5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 480 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) Original source: (A) Organism: Pag149RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:	
15	GATCTITICAG CTITGGCGTG CTATGGCAGG CAGCCTGCGC CTTTATGGCC TCAATGCCTC	60
	OCTGACGACT CTCATGTOCC TGTGGGCAAT CTGGTCACGT GGGTACTATC CAGCGACGGG	120
	ACTOCCTATG GCTGTTGCAG ACAAAGCGAA ACTCAGCATG CTCTACGTGC CCTACTTCCT	180
20	GATTOCTCTG COCCTOGICT TIGTGTGAGG TCTGGAGCAA TGCAGAAGTG CAACACTCTA	240
	TATATAATCA CCTGACTATG TACCTATTTC TOOCATAOCA CGTTACGTTT TGTCACGATT	300
	CCAGTCAGTT AGCTGCCTCG AGCAACCGGT GAGCTCCGAA AAGGGAATTC GCTACAAGGT	360
25	CITAGOGCAT AGNOCTOCAA CIGGOTTIGG CTAGGICAAT IGGITTICIT GGAACCANIC	420
	TTOGTATAGA CICTTOCGTA TIGATCOSOC TGAOGAGTGT TITINGNOGNA GNCAAACACC	<b>4</b> 80
30	(2) INFORMATION FOR SEQ ID NO:132:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 477 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1049UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
	GATCGTCTCC TCCCCCCACAG CCCCTTCTAG ACCCTCCACG CCCCACACACCT TCATCCTCCT	60
45	CTCCCTCTCA AACCTACCCA GACCCTTGTA GTAGCTGACG CCGTTTTTCT TGAAGAGCAT	120
	CTCAATACCG CCAGTCAATT GCTTCACAAC GGTGTCCTTG GCCTTTTGCA ACTGGGGCAT	180
	GITCACAGIG ACCICGCCCI IGACGICGAT ACCGCGCIGC TIGGCATCGA GITGCATCIG	240
50	GTGCAGCAGG TGCGAGTTGT TTAGCAGCGC CTTGGATGGG ATACACCCCA CGTTCAAACA	300
	OSTGICACCT AGACOGOGOG OCTTICTICCAC ACACOGOGOG TOGAAAACCA GTTTGTTOCA	360
	OCCITOGATG OCCOCCACINI TTAACCACCG GOGACCINOCA COCATCAACC ACAACGTCOG	420
55	GETTTCTT TGTTGGGAAT TCAACCAGGC CONCTTINNT GGGACGACON CTTANNC	477

	(2) INFORMATION FOR SEQ ID NO:133:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1050RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:	
	NNNTTINIGG TOOOCCIGI AGANIAGIGG TOOOCCACCOCCACATI CICCATOCIC	60
	ACCACCACGA CAGACTOGAA GTACAGGAAA AGOGACATTG TOGTOGCAGA GATGTGOGAC	120
20	OCCOCCUTTOG AGTITCCCAAA AGCAGACAGC GTTGCGGACG CCAGCAGTCC AAGCCCGCA	180
	ATTGTCGCCG TCGCCCACTT CACAGGTGTT TGGGCCACGG TGCGGCCGTT CGTGAAGTGC	240
	GTCTGGATGC ACGACACCTG GTCGTTCGAC TGGGTTTCGT GTACCATCAC CTTGAGGTAG	300
25	GCGLCYLLGI CCCGCCYCCLC GLYCGLCYCC CCCGCCYYLCL INLLIGIGLI CLCCCCGCGCLC	360
	ACATACTOCA COOCCTOGAT CTGAATGTCA CCGOGTGTCA CAGGACAAAA CTGCTTCTAG	420
	CCCATCCCAT ACATGTCCTT CCC	443
30	(2) INFORMATION FOR SEQ ID NO:134:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 400 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1050UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:	
45	GATCCTTTCG TATGAAGTAT GCAGCTGTCG ATATCCTTAG TTAACTTCTG CCCAGCTATT	60
•3	TAAOCTOCAA TTGAATCOOC OGTGACTCAG CTTOCAAAGG GTAOCAGAGA GGACOCGATG	120
	OCTITATICG GAAAGGATAG AGGIGAACGG ATACCIGAGT TICCGIGTIA CCTOCTAGAG	180
50	ACCINGAACGC ATCTGGTGCC GNTGNCAGGG GATTCTATAC AACCTTGTGA TCGAGCGGAC	240
	ATATINOCGAG COGATACTAG GOCAGNICCC TOOGATAOGT GAGOCTINTAG ACCOGGCCCT	300
	GACCOCCCCT TTTGAGSCCG CAGAGGTACC CCCCCCGGGTT GCGGAGGTGA TGAAGGCGTT	360
55	CCAGGAGGGG TACGACTCCC GGGGACAAAA ACGCAGGCCC	400
j <del>a</del>	(2) INFORMATION FOR SEQ ID NO:135:	

(i) SEQUENCE CHARACTERISTICS:

5	(A) LENGTH: 713 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1051RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:	
15	GATCAAATIT GACATGTAAT TAATATATTG AGGTAAAATC TAGATAATAA ATACTGCCAG	60
	CAGTOCTGAC CAACTTOCAT TAGCAAGCAT ATAAGAGGTC TTAAATCAGC CGAAGGTATA	120
	TOCGAGOGAA GATAGATCCC CCCCCCTCCA GGAATTCGAT ATCAAGCTTA TCGATACCGT	180
20	CCACCTCCAC GCCCCCCC GTACCCCAATT CCCCCTATAC TGAGTCGTAT TACCCCCCCT	240
	CACTOGCCGT CGTTTTACAA CGTCGTGACT GGGAAAAACCC TGGCGTTACC CAACTTAATC	300
	CCCTTGCACC ACATCCCCCT TTCCCCACCT GCCGTAATAG CGAACACCCC CGCACCGATC	360
25	GCCCTTCCCA ACAGTTGCGC ACCCTGAATG GCGAATGGAC GCGCCCTGTA GCGGCGCATT	420
	AACCCCCCC GCTGTGCTGC TTACCCCCAC CCTGACCCCT ACACTTGCCA CCCCCTACC	480
	CCCCCCTCCT TICCCTTTCT TCCCTTCCTT TCTCCCCACG TTCCCCCCCT TTTCCCCGTCA	540
30	ACCICIAAAT COOCCICC CITTAGOGIT CCGAITTAGI GCTTTAGOGC ACCTGGACCC	600
	CAAAAACTTG ATTAGGGTGA TOGTCACGTA GTOGGCCATC GCCCTGATAG ACGGTTTTCG	660
	CCCTTICACG TIGAGICCAC GITCTITAAT AGIGGACTCT TGTTCCAAAC TGG	713
35	(2) INFORMATION FOR SEQ ID NO:136:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 703 base pairs  (B) TYPE: flucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1051UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
50	GATCTATCTT CCCTCGCATA TACCTTCGGC TGATTTAAGA CCTCTTATAT GCTTGCTAAT	60
	OGAAGTTOGT CACCACTOCT COCAGTATTT ATTATCTAGA TITTACCTCA ATATATTAAT	120
	TACATOTCAA ATTTGATOCA CTAGTTCTAG ACCOCCCCC ACCOCCGTGG ACCTCCAGCT	180
5 <i>5</i>	THIGHTOCCT THAGHGAGGG THAATHOOGC GCTHGGCGHA ATCAHGGHCA HAGCHGHTHC	240

	CTGTGTGAAA TTGTTATCCG CTCACAATTC CACACAACAT ACGAGCCGGA AGCATAAAGT	300
	GTAAAGCCTG GOGTOCCTAA TGAGTGAGCT AACTCACATT AATTGCGTTG COCTCACTOC	360
5	COSCITITICCA GTCGGGAAAC CTGTCGTGCC AGCTGCATTA ATGAATCGGC CAACGCGCGG	420
	GGAGAGOCOG TITIOCGTATT GGOCGCTCTT CCOCTTCTCG CTCACTGACT COCTGCCTC	480
	OGTOGTTCOG CTOCOOCGAG COGTATCAGC TCACTCAAAG OCGGTAATAC COGTATCCAC	540
10	AGAATCAGGG GATAACGCAG GAAAGAACAT GTGAGCAAAA GGCCAGGAAA AGGCCAGGAA	600
	CCGTAAAAAG GCCGCGTTGC TGCGTTTTTC ATAGGCTCCG CCCCTGACGA GCATTACAAA	660
15	AATCGACGCT CAAGTCAGAA GTGGCGAAAC CCGACAGGAC TAT	703
15	(2) INFORMATION FOR SEQ ID NO:137:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 595 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG105211	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:	
30	GATCTCCCCT TCAAACCACC TACCCCACCACC CCCACGTCGT TCCACGAGAAA GTCAACAATC	60
	AATATOCTOG GTAAAOCTAG CACCOCCGAA CTACTTOCTC TTGGCACCAC CGCAAAGGCA	120
	CACAACGAAA ACTOOGAAGA TGAACTGAAG AAACAACAAA COGTCACOGT TGATGACCAG	180
35	GTTGTTTCOC CAGAAGATTC GCCCTTTCCA GAGCCAGTCC AGGAACCAAA GACCTCAGTC	240
	TCCGGCTACA TCAAGAGGAA ACTATCCCTC AAGCGTGATA AATCCACAAG ATCCAATCGT	300
	TCGCAATATG ATAGGITACA GGACTAGATA TGGATGITAA GTATAGAAAA ACTGTATATT	360
40	ATTTGACGTG CTCCCCGTTA CCCAAACATA TAAAGATTTA ATTACTCATG CCCCGATCGT	420
	ATTITITICAT GEOCCCCACT GGACTICCATT TGGGCAGTTG GAGGACGAAG TAGGAACCCA	480
	ATTGCTGGTT ACAAGCOCTC GGTTTCATGT ACCCTATACA CAAGTATCCA TTATTNGGGC	540
45	TTATTGATTT GIGTCTNTGG GCCGGACTTT TANCITTICTC ACTGGGGGAN GTCCT	595
	(2) INFORMATION FOR SEQ ID NO:138:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 625 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG105212	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:	
5	GATCTOOGIT OCOCCTGAAG ACCACCAATG CGATOCACAC GAGTATCATG ATCAGCAAGA	60
	TTAAAGAAAA GACAGCGTTC AAAATAAAAA ATACCCATGC CATAATGGAG CTGACGCTTG	120
	CAGGCTGTCC AAAGAGCCCT GAGAAAAATA AGAAGAGGAA CGAATTAACA AGAGTAACAC	180
10	TOGATATCAT AATGITCAGG ATGITAGICG COCOGTCGAG GTACOGCCTG CATTIAGCCA	240
	GAGCTGCCAG GTATATTATT TCAATCACAA ATAGAGCGAC GGCCTGGGTT TTACCGCAAT	300
	TETEOGCAAA TOCAATAAAT ACCOCTTTCA ACAAAATATG COCGAGGATC ATOCAGGACC	360
15	ACCAGTAGTG TGTCGCACTG TACATTGTGT AGAAGAAGCC GTATTTGTGT AGCACATTTT	420
	CATTOCCOCA TAGAATOOCA OCTOOGITCG AGTOCACACC AATOGAAGCC CTTCCACNGT	480
	AGATAGTOCG GCAGOCAGCC CANCCCATAA TIGACAAGAT AAANGTNGAG CTAAGNCTOC	540
20	CAGAACGACC NCCGCCGGGG ATCANCGTTC ANTGATTCCC CACCAGCAGA GATCGCNATT	600
	GANTGACCCC GGCAGTTNIN CGCAA	625
	(2) INFORMATION FOR SEQ ID NO:139:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 486 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1052RP	
35		
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:139:	
	GATCOCOGAC OCCITOCOCOC AGAACCITOOC GIOGAOCATG COCCIGATCC GAGTOGAATT	60
40	CATGCAACGC ATCTTCCGGT GGTACGTCCA GGCGAGCGGC GGCGAGCCGT CGCTGCATTT	120
	GACGICAACG ACCACGICIG TGCTTGCCCA ACGCTCACTG GATGCGCTAG TGGGCCGGCC	180
	CGTGAGCAAG GCGACACAGT CGCTATTTGC CAGCACACAC ACGATGATCT TCAGAGGGAT	240
45	CCGTAGACTG GCCTACCGTG CGAACATAGA GAGCTCATCG GTTGTGTGTA CCGGGCTAAC	300
	GITCTTCCTT CIGTTCGGCT ATTTGGATTG GCGTGGCGGT TTACATTTGT TCAAGCGGGG	360
	CTACTOGAG CTGCTTATCC CGCATGAAGG TCAATGAACC CAGGTCCGGG TCCCTAGACT	420
50	TCCAAGAAAA ACGIGGGIGA TIGNOCICAA AGGIGIICIT TIGGGGIANA TCITCCCCCG	480
	NGTTCA	486
	(2) INFORMATION FOR SEQ ID NO:140:	
55	(i) SEQUENCE CHARACTERISTICS:	

5	<ul><li>(A) LENGIH: 468 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEINESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: ENA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1052UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:	
	GATCCAGCTC TTGCGCGGTA TGAACTTTCC CGCCCGCACC GGCGCCTCGC ACACCGAAAT	60
15	OGACCICACC TOCCITCICC TOTOCIACIT CCAAATTTOC GOCCCCCC ACTACACCT	120
	GATCAGCACC CACGGCTCGC TCGGGTGAAA GTCAATGCCC TTCACCCTGT CTGTCCTCGA	180
	GACAAACGIT TICTACTCAC GITAGIACIT GCTCCGCGCC CTGGATAGCA TGGTCGAGCT	240
20	CTGCGGGTCC GCCCCCTCCG TGGGTGGCAA AGATGGTCTT CAAACACACC GTAATAGGCC	300
	GIGCOCCACC ATGCAGOCCC CATTCGTCCT CGGACACACA CATACCTTCG TTTCCAAACT	360
	TCATTGGTCC CCACTTGGGA TICCTAGTAG CIGTTCAACT CGGCTTTTTG GGTTCTTGTG	420
25	GAAAANTAAT ATTOOONTOG ATTATTTAAA TAGOOGTOON TTTTINTTT	468
	(2) INFORMATION FOR SEQ ID NO:141:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 672 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1053RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:	
	GATCATAGIG ATTGATATOG OGAGAGOGIT TOGTATGIGA CAGOCTGTAT TCACGTATCT	60
	GGICCITCAC TICATATATT TCTTGTGGGA GCTGTGAATA TATCTCCATG CGTTCTCTGT	120
45	TOCATITITIC GROCATITIG TOGAATOCAG COCACTICIC GIACGITGAA GIACOCTICG	180
	GTACTAACGA TCCCTGAACA GOGAGGAGGC ATGTTGCGAG GGAGAATATT AAGGAATCAT	240
	ATCTCATTIT TACGTCTGAG ATAACTAGTA CTAACTGCAA TGCGGCGTCC AAATACCCGT	300
50	CGTAGTAATC GTATAGGAGC AAAGCTTCAT CICTTATACG ATGTGGAGTT GATTCAGTCC	360
	ACTOCAGOCC TIGGTATITA GOCAGCATIC CATCATATIT GGACTGATAA TATTCGAAGT	420
	TCTTCCACGC GTCCTTATAC GGATCAATTA CTGATTTTAC AACATCGAGT AATATGGAAA	480
55	GATATAACTC TGGATTGCCC TGTATGACTT CCAGCACGCC ATGGAACATA TCCCGAATGC	540

	CGICGCGCA CTIGGAGACT AACTTIGGCG IGIATATCIG CICTICGACT GTCCCATGGT	600
	TGAGGTAGGT ATCTTCAGGT AGAATGAAGT CAATGAGCGA TAAACTGACT TGCTTGAATC	660
5	CTCCCAAACA GT	672
	(2) INFORMATION FOR SEQ ID NO:142:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 609 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1053UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:	
	GATCTCGGCT CGCTGCTCGC GCTCGAGCCC TACTGGGCAG AGCGCTACCC AATAAACAAC	60
	GCCCTAATCG GCGGTGCAGA TAAATTGCAC AAGCTCTACT CAACCGATTT TGCGCCCATC	120
25	GTOGOCOCCA GGACTITICOG CTIGAACCTC GTOGACAAGC TTOGACCOCT GAAAGACCTC	180
	ATAATOGCAA AGGTCAGCGG CCCAAATTAA TAGTCACGTG TACATAAAGG TTTTCCTAAT	240
	AGCTATACAG CTTGCCCGCG TCCTCAGCTT GCAGCGCGCA ACCGGCGTGC AGCCATGAGC	300
30	GICCTACTOG AAACTACCAT TOOCGACCTT GTAGTAGACC TOGACTACAA GACATOCAGC	360
	GCCGAGAGCT ACAACTICCT CAAACTCTGC AAAACTCGCT TCTACGACTG TCAGTGCATC	420
	TACCGACCTC CATCCTGAAG GCTCAGCACG CCCTCGGCGA TCCACAGGTG GCCTTTGCAT	480
35	TCCGCACGGA TTTGCCTGTA CACAATACCT CGATCGAAGG CCTGCGCGAC ACACGGGCGG	540
	TCACCCCGAA GCTCATTGAA GCCTCCGTTG CCGCTCAACC CGCAGAGCGC TTCGGACAGG	600
	TCGCCTTG	609
40	(2) INFORMATION FOR SEQ ID NO:143:	
<b>4</b> 5	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 594 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDELNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1054RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:	
55	GATCCGTCGC CGGTCCGCCA ACGACAGCTC CTCGTGCTCC GCGTCGTCCA CGCCCTCATT	60
	TICATAGAAG TOOTIGIIGO GATIGGOOGT ATAGIOCGOG TACATGIOGI CGOOCCACCAG	120

	GICGACCICG TCIATGCGCT CITCIGCGIC ATCCAGGICG TCIGCAAACT CGATGCGCIC	180
	GTCGCCGTCG TTATCGGGGT TCTCGAAGTC GATCTCGTCC GGCGACCCCA GCGGCGAATT	240
5	ATTCCCCCATA COCCAGCCCC OCCCGCTCCC AACTTGTGCC GACGATGGTG GGTGCTCGTA	30C
	OCTOTOTICAC CIOCUGICAC TACTOCOCTIC CICUGIATOS TITUCATOTO TACCOCTICT	360
	OCOCCOGTOT GAACCCTICCA TICCOGTTATG CGAACCCATA CCCAAATTIAC CAAATTICCCC	420
10	TTCCTGAGAT CTTGAATACT ATCTCCCAGA TGTTTGACAG ACGCGCAGCT TCTCACGATA	480
	CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT GGATTGGATT	540
	AGATITICAG TCATATIGAA AAATTATTIC CAAACAGGGC AATIGGATGA GCTG	594
15	(2) INFORMATION FOR SEQ ID NO:144:	
20	(i) SDQUENCE CHARACTERISTICS:  (A) LENGTH: 545 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1054UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:	
30	CATCGICGCG TTOCOCAGGG CTGCCCAACG AAGCCTTGAC ATGICAAACC GCTTGAAAGA	60
	AGAGGIGATA TGGGCCACCC ACGAGGCCAA GTGGGAGCAA CIGCTGGCTA CIGGGACCCT	120
	TCCCCCAGAT GOOOCCAAAA GCGACTGGAA GCCTGGCCGA GCATGGCTGG AACCATATGA	180
35	GOCCOCGTTT COGAACCAGC TTGCAAATCG CAAGCOCACG AGCCAGAAGC TCAAGCOCTA	240
	TAGTOCCCAA ATCAGCAAGG TACACCTCCC GTATTACATT AAGTGCAGTG CTGCTATGCA	300
	TACCCGTCGC GCCAAACGCT TCGAGTGTTT CCAGAAAGAG CTCCACACCG TTAATCCATT	360
40	CGTTCCAGGC AGAGATCTCG GTTCCCTACT CTCCAAGTGG CGAATGGTGA ACGGAAAAAA	420
	CTACTATCGC TGAATGIATA TAGITTATAG TCCTATTCCT TCATCAGGTC TCCCAGCAGA	480
	GOCGOCCOCT COGTICTICAAC TATGCOCACC TCGCTCAGCC ATTCGCTGAG GTCCTTCTGA	540
45	GITCG	5 <b>4</b> 5
	(2) INFORMATION FOR SEQ ID NO:145:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 532 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1055RP

5	(X1) SEQUENCE DESCRIPTION: SEQ ID NO:145:	
	GATCCGTCGC CGGTCCGCCA ACGACAGCTC CTCGTGCTCC GCGTCGTCCA CGCCCTCATT	60
	TICATAGAAG TOOTIGITOO GATTOOCOGT ATAGTOCOCG TACATGTOGT COCCCACCAG	120
10	GICGACCICG TCTATGCGCT CTTCTGCGTC ATCCAGGTCG TCTGCAAACT CGATGCGCTC	180
	GICCCCGTCG TTATCGGGGT TCTCGAAGTC GATCTCGTCC GGCGACCCCA GCGGCGAATT	240
	ATTICCCCATA COCGAGCCOC GCCCOCTCCC AACTITGTOCC GACGATOGTG OGTGCTCGTA	300
15	SCICIGIGAC CISCIGICAC TACTOCSCIG CICIGIATOG TITICATOTO TAGCOCTICI	360
	GCGCCCGTGT GAACCCTCCA TICCGTTATG CGAAGCCATA CCCAAATTAC CAAATTGCCC	420
	TICCICAGAT CITGAATACT ATCTCCCAGA TGTTTGACAG ACOCOCAGCT TCTCACGATA	480
20	CGAAATATCG TGATTTTACG TGACTTTCAA TACCTCATTT TGGATTGGAT	532
	(2) INFORMATION FOR SEQ ID NO:146:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 553 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1055UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:	
	GATCGTCGCG TTGCCCCAGG CTGCCCCAACG AAGCCTTGAC ATGTCAAAACC GCTTGAAAGA	60
	AGAGGIGATA TOGOCCACCC ACGAGGOCAA GIGOGAGCAA CIGCICGCTA CIGGGACCCT	120
40	TCCCCCAGAT GCGCCCAAAA GCGACTGGAA GCCTGGCCGA GCATGGCTGG AACCATATGA	180
	GGCCGCGTTT CGGAACCAGC TTGCCAAATCG CAAGCGCACG AGCCAGAAGC TCAAGCGCTA	240
	TAGTIGOCCAA ATCAGCAAGG TACACCTOCC GTATTACATT AAGTIGCAGTG CTGCTATGCA	300
45	TACCCGTCGC GCCAAACGCT TCGAGTGTTT CCAGAAAGAG CTCCACACCG TTAATCCATT	360
	CGTTCCAGGC AGAGATCTCG GTTCCCTACT CTCCAAGTGG CGAATGGTGA ACGGTAAAAA	420
	CTACTATCGC TGAATGIATA TAGGITATAG TCCTATTCCT TCATCAGGIC TCCCAGCAGA	480
50	GOCGOCCOCT COTTCTCAAC TATGCCCCACC TCCCTCACCC ATTCCCTGAG GTCCTTCTGT	540
	AGITICGICAC CCG	553
	(2) INFORMATION FOR SEQ ID NO:147:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 556 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1056RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:	
	GATCATCAGC GCGAGCTICC AATTITGIGGG CTTICTGTTG ACATACATCC TCCACACCTC	60
15	SCATSCOSCG COCCAGGGCT COCCCTTTOG CCTCGGCCTG ACCTTCACGG GATACGGGTA	120
.0	CASCATGATT CCTAGCGACG TGACGAGCAA GGTCGGCAAG GACCGCGACA TCGCGCGCGT	180
	GSAGCTGGAC GACCCCAACG AATTCGAAGA TTCGCACCTG TACTCGCCGC TGGCGCAGCC	240
20	GOCOCAGGAC COCTICGAAT CACAGCTCTC GCACGGGCTG ATGGAAAAAAC GGCGCAGAAT	300
	TCCCCCCTC CCCATCCTCC TAGAGATTTT CCCCCTTCCA ATTATCTCCA AAACCCTCTA	360
	CGACTACATT GTGGTCAAGC GCATGGAGCG CCGCATCTTT ACTGCGAGCG ACAGCGAGAG	420
25	CCCCCCATAG ATGTTCATAT AACTTATATA TCCCTCATTG ATCTTCGCTT GCGCCCCGTC	<b>4</b> 80
	TAGGGAGCAG ACCAGCAGTT TOTTCGTTCG COCTNAAGTC GATGCCGCCA GAGAGACCAG	540
	ACGCCCCAGC GCGGIA	556
30	(2) INFORMATION FOR SEQ ID NO:148:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 550 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1056UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:	
	GATOCAACOC AGGACTTCTC GAAAGATAGA ACTCCGAACA CAGCCACCGG CAGGAACTTC	60
45	TCATCAGCTA GCAGCAATAC TAAGCAGACC TTCAGCGAAA ATGAAGAAGA ATCTGATGCT	120
	GAGITOGAAG ATGIATAGIT GIACCCGIAT ATTOCATTIT TITTITTITT TITTITTITT	180
	TTTTTTTTGGA GATGTCAAAA GCTCATCTCA ACTCCATGAC CAGCCAGTAG TGACTAAAGC	240
50	AGIGIGICIA GITCTICTAA GIGATTITAA GGACTATGAG CITTAATGAG AAGGTGAAGT	300
	GOGTACTAGG CACTOCTGTT GOGACTCTAG TTACGATAAA GTCTGTCGAA GCCGTATATC	360
	GCCTICTATGC AGCTAAGCAG AACACTAGCA GGAGCATTTC TGGGGAGGAG AAGGACGTAA	<b>4</b> 20
55	GACTOGOCCAA ACOCATTCOT CACTCTAGGG COTACGATGA GGAATTATAT COGGAGCAGT	480

	IABCICOGAA CIACOCAITI IOSSCGAALA COSTATOSCA CGACTACAGG AACAGTACTC	540
	ATATOGTOGG	550
5	(2) INFORMATION FOR SEQ ID NO:149:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 653 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	•
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1057RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:	
20	GATCAGGGCC AAATCACTGC TAAGTACAAA CACAAAGGGC CAAGTATTAA GGTGAGAGAG	60
	CGTTACAGGT GCATTGATAA TACCGCAGGT ATATATCAAG GCGCACAGTG AACACATTCT	120
	GCAGACGATA GATATGTCTG AGACGAAGTA GGTTGAGATA TTTACGCACA AGCCTCATTT	180
25	GTAAGATAAA TOGTCATTAC TAACGTTTTT GOGTTTAGCA GCAGCAGCCG GAGCAACAAC	240
	CACCOCACCA ACCACCOTTOC TOCTOCACAG CCTCCACCAG TCGACCATOC CCCCCACCA	300
	COCCCAGGG CGAACACGCG CAATGTGACT GTGGCAATCC AGTACTCGTG GCTCCACGAC	360
30	ATGAGGAATG TCGGGGGGAGA GGGGAGAGAG CGGGGGGGGG AACGGAGATA	420
	CONTROL CASCUTICACO CACCIOCOCO ACTOGACCIC GAACCATCOC TUTCACCAAC	480
25	TGATCOSCAT TOCOSCOCAG TITISCATTGA COCOCCITOCO COCOCCATIC ACCUTOCITOC	540
35	GGGGGCTCTC GAAGGAGTCC TITIGAAAACT CCCTCTCAGG AAGCTCAGCG AGCTGGACAG	600
	CGAGCIGIGC AGIATATGCT ACGACGACTT TGAAGACGAC ACGICGATCG GGT	653
40	(2) INFORMATION FOR SEQ ID NO:150:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 668 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1057UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:	
	GATCTAGGGG TICTICTICC COCCCTACGG GCCCCCTCG CAGCCTCGCG CTGGCTCCCC	60
55	COCCAGAGOG GATCOGCAAG OCTOCTOGCA GCCGCACACT OCGTCTATOC CTGGACCGTC	120

	construction of the second construction of the s	100
	CTCCCCTCG TGTTGAATTT TCCTAAAACT CGTGAAATTG TACCCCCTCG CTCCACCCCG	240
5	COCCTGTCGA TTGTACACGG GAATAGCGGA TCAATTGGAT GGGGACGCCA GTGTTACCCC	300
	CGAAACCOTE CCCACCOCT COCCCCCA CCCCTCACCT CCCCCTCCCC CCCAACCCCC	360
	ATTICCTOTO GACTOCAGAG CTCCAGGAGC TGTTGAAGGC GCAGGACAAG TTCCAGCTGT	420
10	ACCTOCCOG CTTCTCCGAC ACCCACCAC CCCACAACCC CCTCCACCAC CAACCAAAAC	480
	ACCTROCTER ANTACROCRA ACCTITROCRE COCTROCANCE CONACCACNE COCCTROCNCE	540
	ACCOSCIOGA COSGIATCAG AGOCTAATGI TOCOGIACCA TGAAGCGIOG CAGCOGGIAR	600
15	ACCIOCOTOC CGCCCCOTT ACAACCACCG CTTCTCCCCCC CCCCCCTCCA CAACAAATCC	660
	SCECTEGG	€68
	(2) INFORMATION FOR SEQ ID NO:151:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 614 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG105811	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:	
	GATCITCACA TICOCATOCA OGTICITICIT GITTITAGTA GCACCCICCG OCOCCITOTI	60
35	990CTTCAAC TIGAGITCAT CCGCACTIGG CITGATAAGA CCAGCITTCA AGTACACCAT	120
	GATGTCGTCG TCATCACCGT GCTTAAAGCA ACAGCGCTTG CCATAGCGGC AGTIAGCCTGT	180
	CITACTCCAA TIGATACATG OCTTOGIGCG GAATTIGICC GACCOCTCCT TGAACTTIAA	240
40	CTCGTCGAGA CCATCCCCAA ATTCCCACTT GTTATCGTAC TTCCACCCCC CCGTAGTCCC	300
	AAATGATTOG CATAACTCTG TCTTGTAAAG CATCTTGTTG ACCTTCTCCT GCGATGGCTG	360
	TOOCTOCTOC TGTGGGGTGG CGGGGGGGGGGGAAAACTT CGGCTCCGGC	420
45	IGIOCOCCIG CICOCCCIGG GCCCCGGGI CCTCCCGACG GAIGCTOCAG GACCCCAGGI	480
	TTTCGCCCCT CAGGGTAGTA TCCCATTGGT AGGCCGVTAA TGAGAGTTTA TCGCCACCTC	540
	NAAGGTAGGT TCCCCGTTCC GNAGGGCCAA GOGNAATCAN TNGCCGCCCA AACCGTNAAC	600
50	anaccanac anac	614
	(2) INFORMATION FOR SEQ ID NO:152:	
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 634 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEINESS: single</li></ul>	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG105812	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:	
	AACCTTOCAT OCCTOCAGET CGACTCTAGA GGATCTTOCA AAGTATOCCT TOCTAGTGTG	<b>6</b> 0
	GIGATOGITA TCTOCAGITT CAATTOCTTT GITAGITAGI GTATCACATT CTTCTOGCTT	120
15	TOGCCGATTA GAGTOCTOGG CCTCATOGAT GOOGATCTCC GGTGTATACA CGTATATTTA	180
	TICICITICOC CCAAGIOOCG GAGIACAAIT TICCTCTAGC TOGACCTATT TCGGITGIAI	240
	TICAGTAGTG AAATAAAACT ATCAATTAAG TACAGCTTTC GTATGACTCT GCCACAGGAT	300
20	GAGAGCAGAC ACTICTOCAAA GTACCOGATT TCAAATAAAT GTTTAGGAAT AAAATCAAAG	360
	OCGIACAATT ACATAATTAT AAAATOCTCT CGTACCTATG TCTTTCCOCGT CTTTTTTTTA	420
	TOTTANAGIG AACATCGAGT CITGICCTIC TTAGGIGITT AGATGACAAG CITACATGCC	480
25	TOCHENDENN ARACAGTING TOGRATICCET COGRETCOTON CCANGIRGNA AGGNANITACO	540
	NIVEAGEAGAG TEATTACENE NACCEACEGG ETTOCEANCE NAVITNETIN GENNENAGNG	600
	GENNERAL TENACONANN TITIENNOCHI NECC	634
30	(2) INFORMATION FOR SEQ ID NO:153:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 475 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
00	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1058RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:	
	GATCATTCTT GAGAATOCTC ATAGTTATOG TITAACOGTT CTTCAAACOG AAGAGTATCT	60
45	TCAATTACAG AGTAGTTTOG AGAGAGAACA OGTAACGTCC TACAACATTG COGAGAAACC	120
	AACTACAATT GOCTACGTTG CACTTCCAAG AACCGAGTAC GATGAACTTG TAGCTTCGCA	180
	AGCITCTACG AAAGAACAGA ATTITIGAGGT ATACOCCGCG GAAAATGGCA AGGICATAGT	240
50	GCATAAATCT GAGTATCACG ATTTGAAGAT CAAAGCTATC CCAGTGATTT CACCATTGCC	300
	TCAAATGAGC AAAGAGCAGA TOGTTGAAAA GOCCAAGGAA CTTGGAATGG TAGCTTTGCT	360
	CCATTGACGA GTATGAGAG TTAAAGAGCC CTATTTICCCG ATAACGCTTT GGATTGCAAC	420
55	AGCGAAGGAC COCGGAAAGG TTGGTCTCCT AAAGGAGGAG TACAACCCCT TATTG	475

	(2) INFORMATION FOR SEQ ID NO:154:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 476 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: ENA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1058UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:	
,•	GATCTGSCGC CCCGACASCC TGCCCAGGTG CGCCTGCATC CGCCGCTCCT GGTCGCGCTC	(0
	GTCGAGCCCC AGCTCCTGCC GGAAGCTAGC CCTCCAGCTC ATGTACGACT CATGCGTTAC	60
20		120
20	CTICGITCCG CGGAATTICT TCTOCTCTIC GAGCICGCGT TCGCGTAGCT GCCGCTCGTG	180
	CICCITCICT COGCOCICAA GCICCTICIG AAACCACCAC TCCGCGTCCT CCTTTAITGA	240
25	CGAGATCAGC GCAAAACACA TCIGIATICC CAGCAGGAIG TCCICCTCCA CCIGICGCAT	300
23	GGACTGGCTT GGAAAGACCG TCCACCTCGC CGGTCAAAAT GAAATGCTTG TCCGGAATAT	360
	TCTCCAGTT CGCAACACAA GOGTTCCCCC GTGCTCGTCC GGACTTCCTN GTTCCTCAAT	420
	COCNOCTICAA COTOCTOGGN TITIOGOOGGG GAAGGINCCA NOOGGOTTIAA TUTCAC	476
30	(2) INFORMATION FOR SEQ ID NO:155:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 644 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1059RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:	
45	GATCTGTTAC OCTOCAGOGC GAAACCTOCA ATGCTCTGGG CCAAGGTTGG CGGCTGGGAT	60
	TCTTGGGCTC ACTGCATGCT TCGGTTTTCA AGGAACGACT GGAGAATGAA TACGGCTCGA	120
	AACTCATTAT CACACAACCC ACTGTTCCAT ATGTCGTGGA GTACTCCGAT GGGACCCAGA	180
50	TAACAGTAAC AAATCCAGAT GACTITTCCTG ACCTGACACT TOOOCGAACC AAGATAAAGA	240
	ATTICCAGGA GOCATATGTA GAAGCTATAA TGACTCTTCC ACAGGATTAT CTCGGAAGGG	300
	TTATCACTCT CTGCGACGAC AACCGTGGCA TACAGAAAGA GATAACGTAC ATTAACACCA	360
55	COCCEANCE GATOCTGARA TATGATATCC CATTOCCACA TCTAGTAGAC GACTITITITG	420

	GTAAGCTCAA GTCTGTCACG CATGGTTATG CTTCCCTAGA CTACGANGAT GCAGGCTATA	480
_	AGCCGTCTGA CATTGTCAAG ATGGAGTTGC TTGTAAATGG AAAAGGTGTG GATGCACTTG	540
5	CACAAGTGAT GCATCGCTCC CAAACCGAAC GARTGGCCAA AGAATGGGTT ANGAAGTTCA	600
	AGCAATATGI CAAATCCCAG TTATACGAAG TGGTTATCCA CCCC	644
	(2) INFORMATION FOR SEQ ID NO:156:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 649 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1059UP	
20		
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:	
	GATCGTGGCG GACGTGTTTG TGCGCACCGC GGACGTGCTG CTCAAGATGT CGCGGTACGA	50
25	RGAAGCCAAG GCGGGGGGG ARCGCGGGCCT GAGCCTGGAG CCGGACCACA TGAAGCTGAA	120
	GOCOCTOCAC CIGGAGTCTG TOCOCAAGTT GOCCGACTAT AACGOCGACA TCTAGTCCGC	180
	GCGCCGCCC CGCGCGGGCA CCACGGGTAT ATATACACAG CCGGTCTCCG CGCGCCATGC	240
30	COCCOCCOG GACCOCAGAC ACACOCCCCG ATCTTCCCCCC CCCCCCCCCC ATGACCTCGT	300
	GCAACCCTCT TGGCCCGTAC CCTGCTAAGG AGGGTAATCT CCCACCTCAG TACTATAAAA	360
	AATTITTAAG TTAGCCACTT TCGAGTTACA ACTCCCCGCC TGTCGGGTAA CGGATCTCAA	420
35	CTIGIGAACC CCCTAACCCT CCTCTACTCC TTTTCCCCTA AGCCAATATC CCCCCATGTC	480
	TICGICOGAT AICAATGICA COGFIGATIC GITTATIGAT AGGITGAAGC GGAAGCAGAT	540
	TACTOGCACG TACAATGIGT COCTOGAGAC GITACAAATT CIGATGCCTT ACGIATCTGC	600
40	CATCCOGTOG TCGACGAAGG ACGARCTCAT TGAACAGATC CGTCTACTC	649
	(2) INFORMATION FOR SEQ ID NO:157:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 641 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 <b>0</b>	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1060RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:	
55	GATCIOCICA TACTGAGCOG CCAACTOGTC GTACTCCGTA TOCAAAACAT CTGTGGTTTC	60

	CTGGAAGTGC GCCACCTTGA GCGATATCTC ATTAAACTTG GTAACCAGCT CTCCCAACTG	120
	ATGATTGACT GCACTOGTITT COGTCAGCAG GTCCTCCAGT TCGCCAGTTC TGGTGTCCAC	180
5	TICCGCCACG TATCCGCTGT ACAATGTATA CTCGTCGTTC GCAGACCCCA GARCAGAAGC	240
	TOGOCGOCAC TOTGOCGOCA OCAGOTCAAT TACOTGAGGT TOAATOTOTG TITICAACOGT	300
	TGCCAACAGA GTGTCTACTT TTTGGCGTAA CGAACTATCC CCAAAAAAGCG GAGGCAGCTC	360
10	ATOGTGAGAR GARGCACOGG GATTTOCCOC TACATOCTGT ATGACTGART TCTTOCGGCT	420
	CCTAAGCATG GTGCAGTTGC TGCCTCAACG GCTTTCTTCC TGGTGCARGT CTGCAGTGGT	<b>48</b> 0
15	TOGTOCTTAT GOGCAAGCAG AATACCATGT TGACCCGCG AAATCTCATC ACGTGATCAT	540
73	CATCTIGCAA COGCTCOGAR GACRCTGATG CACTGTTCCA TAGGCTTAGG GCGCAATTAT	600
	ACOCTAGCTA GITATATTGA TAATATGTAC ATGATOCCTT C	641
20	(2) INFORMATION FOR SEQ ID NO:158:	
	(i) SPOUENCE CHARACTERISTICS:  (A) LENGTH: 649 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1060UP	
30	(A) CHANTAN. PARTOUCE	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:	
	GATCTTOCCG TOCTTCTTGT COAGCTGTAG GTCCOGATGA GOGTACOCCT CGCTCAGGTA	60
35	CTCCAGCCGC AGCTCGCCGC TCTCCATGGA CGCCTCCAGG ATCGAAGGCG CCGGGCACAGC	120
	CTCOGAGOGG ACCCCCCCT CCAGGAGOGG CATCTCCTGT COCTCCTGGT CCATCTGCAG	180
	COCCOCAGOG CTCGGCTCCA GCGCCGGGTC GAAGTACTTC ACATTCGTCA GGCCCGACTT	240
40	GTACAGATTC AGGATGCAGC CCTTGAGCTG CGCACGGTGC AACCGGTACG CAGTCGCGAC	300
	ATACTOGIAC COOCTOGICC CCCCTCCCGT GAAGTGCGGC COCTCCGATC CGATCGAAGA	360
	CAGTGACGCT GTTGGCTGGT GGCTGTATCG CCCCTCGCGC GCCGGCCGCTG CGCCCTGCGC	420
45	CITICITICACC CACCOGACCC GAAACACAGT OCOGTOGTAC GICTOCCOGT TCAGCOCGCC	480
	TOCACOTOGO ACCODOGARO COGCODOCTO OGARCAAGGO GACACOTOCT COTOGOCAGOG	540
	COCACCOCC TICATORCCT CACATORCAG COTOCOCTTG TOCOCTTOCC CCGTCNOCAC	600
50	CTGITAACTG CATCCGCGTC TGTTGCCTGC TGCTGCTTGC TGCTTGCTT	649
	(2) INFORMATION FOR SEQ ID NO:159:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 570 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1061RP	
10	(vi) SECTENTE DESCRIPTION, SECTOR IN NO. 150.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:	
	GATCIGCTTT TGIAAGIATI CATCAGCTAA ATACCGTAAA GCIGGTTIGA ACGGAGGTCC	60
15	TOCCTTGTOC TCATATATTA TAGAAGTATC AATGACGAGG GGATGCCGCA TTTTCAAGAC	120
	GITCAAGTCG GCCTGCAATG AATGGCCGAT AAGCACATCT GITGCGCTTA TCATCCGCAA	180
	GAGATOCTGT TOGACGICTT GCAAAGTOGT GGTCACCCCG ACCAACTTCT CCTCTGTAAT	240
20	ACCOCTOTAC TICGICAAGT AGTCCACAAT GOOCTCATCT GOCTTGACAA ACTTGTCATA	300
20	AACTAAGITA CAATCAAAAT OGACGACGCT CACACGCGTC AACACGTATC OGTTTTTAGA	360
	AAGGCACATC TCACAGTCGA TGGCAAACGT GTGAGAACCG TCGTGTTGGA AACTGACAGT	420
	GTOCACCCAC CCACTGCACT TCTCCTTATT CTGATACTTT ACCAACAAAG CCTTTTGGGT	480
25	ACTOCTOGGA TAAGOCAGGT GIGTTTAGAT GGATGGGGTA CTCATTATGC AATAAGTCAA	540
	CAACGGGCAT AGCAAATCAA GCAAGTGATT	570
	(2) INFORMATION FOR SEQ ID NO:160:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 522 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1062RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:	
	GATCTCOGTG ACGTOCCOCT GGTATCOCCTT CATCCAGTCG CCGTTCAACA AGAAGTTTCT	60
45	GITTAACGICG AAGITTACAGC TOGTIGAAGGA ATCAACCTCT GOGCCCACGG CCTTIGATICAC	120
	CTCTOGTGTG TTCAAATACT CCTCACTGTA CTTCATGTCA TCGTAGCAGA GCTGGCCCTC	180
	ACACTCCTTG CGAACGTCGT AGACGTTCTT ACCACTTCTC TGGAACGGCG TCAACTGGTT	240
50	GCCATTACAG TACAGAGAG CTOGAACACA CGACCACAG TTCTGCAGG TGTAGCATGT	300
	GCGGATCAAA CGCAAGCACC GTGGCAAGGT CTCGTTCATT GCCGAGCATT GCTCTGGGCC	360
	AAGAATGGCG GGTTCGCCGC CACCACCGCA GGCCATACGC TCGTAGTAGG GGTACTGTGT	420
	CAATOGGTCT GTCAACCCGT TCCCAATTAG CACAGAGCTC AACTTAAACG AGCGCTCCTC	480
<i>55</i>		

	GCCTGGGTGC GACAAGATCT CGGCAGCAAT AGCAGGAATG TG	522
	(2) INFORMATION FOR SEQ ID NO:161:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 633 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1062UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:	
	GATOCTOGTT GTATCATAGA GAATGAACAT ATTGATAAAA AAATOCTACT GTGTACAGTA	60
20	ATGICTGAAC ACCAACATOC TCTTTTCTTG TATTAAATGA TOOGATAACG AAGTCTTQGA	120
	AGAATCCIGG GCGGAAATAG TAGACATGIT TAGAGAGATT TITGTAATGG CTAGAGTCGG	180
	TITTGATGOC CGAAAAAGAA GTOCCAACAT TIAATTICGA AGGITTATCA GGTAGGICAG	240
25	GGAATATACT ATCCTCGTAT AAACCCTTGA TIGTACTTOC AAGGAOCTCC AAGTCGTCTG	300
	AGITAGOCCA TOGITCATCT TTAGIGICAG CATOGACCAG GACCICACAT GIGATICCTG	360
	AGICAATTOC ATCTATGACC TOTOCATTCA CAATCAAGCC CATGOGTOCA ACCTCCTTIGA	420
30	GAGCCGCCTT GATAAGCTCA GTACGCAGCT CGACCGAAGT ATCCAACGTA ACTGACTCCT	480
	TTATTTCGAA TTOCAGATAT TCOOOCCOCA CTOCATGTAT AGATCCCCCA TGAATAAAGG	540
	AGAATTOCTG CACAGTAGTA AACOCAAATC CCCCCTAATT AGTTGGTTGG CTTCTTAGGA	500
35	AGTCAGTGAA CCGATTATTT GCGTCCTGAT CCT	633
	(2) INFORMATION FOR SEQ ID NO:162:	
40	(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 505 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1063RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:	
50	GATOGACTIG ACOGICACOC GGTACTOGIC GTACTIGTOG ATGAACTOGI CCTGTAGTIC	60
	CCCCAGTICG TAGATGAGCA COCCCAGTIT GTCGGTCACG TCGGACACAT CGTCGTCGTT	120
	GTOCATOCCC CACATOGACA OCTOCCOCOC AGOOGCOCOC COCTCATTIGG CCACCACTTC	180
55	CAGCGCACGT ACCACCCCCT TITICCGTCTT CACGAACGAA GACACCTTCC GTGCCAACTC	2 <b>4</b> 0

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	CACCOCCANA	300
5	GAACTTOGAA CGTGTOGAAG AGOGTGOOGG AGGGGGTGAC TOGAGGTCTG ACGCAGTAGG	360
	COCCTICIOG TITICICAAAG AGTATGTICT GIGCATATIC TCGIOCTTAG ACTOGICIOG	420
	CAGTCGGTAT TTGTAGGTCC CATAAGATTC TCAGACGACA OCAAGTAAAG TACAACGGTG	480
10	GICOGIOCCC CICCAACGIC TITIT	505
70	(2) INFORMATION FOR SEQ ID NO:163:	
15	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 631 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1063UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:	
	GATCTTAATA GCAATAGTOG ACTACAGGAA ACACAAGCTT TCATAATGTO GAAATCTTTA	60
	TCATOGGATA CACTAGACTA TACTOTACAA CCATGGATTC GTACTGCTGT TGATGCCATG	120
30	OCTTATICAGA CCATICACACO TICTACAGOCA TOGACGATICO COCTATITTICO CAGAAACAAA	180
	CATGIGGING TAGAANCIGN CACCOGNICG GOGAAGACCG TGGCANTIGN CATACCTGNA	240
	TTGGAGAGA TGATACAGGA TGATGCCAAT AGTTCAAAGC TCAAAAAAAGG CCACTTCCAC	300
35	ACCATAATAA TCTCCCCTAC GCGGGAGCTT GCATCACAGA TACAGGGCGT GATTGAAGCG	360
	TTTCTGACAT ACTATCCAGA TOGAGAATAT CCTATAAAAT CACAGTTGCT TATCOGTAGC	420
	AATACCAGTA GIGICAGAGA TGATGITGCA GCGITTTTGG AACATAGACC GCAAATTTTA	480
40	GITOGIACOC CTOGAAGOCT ATTAGACTIT CITAAGATOC CAAACATCAA GACGICTICA	540
	TGTGGCGCAG CTATTCTTGA TGAGGCCGAC AAGTATTGGA TATGAATTTG AGAAGGATGT	600
	CCAGACAATA CTGGAGATGC TACCAAGCCA A	631
45	(2) INFORMATION FOR SEQ ID NO:164:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 626 base pairs	
50	(A) HANGIA. 020 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG016411	
55	(A) CHARLET. PROCEEDIT	

561

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:	
	SCAGGAANTG GOTAGCCAAG AACCCGGCAA GACCTTCCCG AGCTACAACC GCCTCATCTC	60
5	GCAGGTGTTT GGCATCTGCG TCAGCATGGC CGGCTGTATC GGGTACGGCT GGGGAATTCA	120
	ATTICACTAT CACATOGOTA TOGTOCTATT CTTTTCTTTC CTAATOGOGT TOOGTATGAC	180
	CTOGTOCTCT AACTOCACCA TGACCTTCCT TACOGAGTCC AACCCAAAAA GACCTOCOGG	240
10	TACCATTOCC GTAAGCAACA GOTTOCGCAA TATCGCTGCC GOCATCAGCT CCGCCATTAT	300
	TITICAAACTA TOCAACOCCA TOOOCOTTOG ATOGIGINIT ACAGOCITOG GTCTAATOGA	360
45	CITOCTATCC ATGTTGACCG TCTATTACTT GATCCGTAAT GGGCGCGAGA TTACAAGGAT	420
15	AGCTOCTGAG CTATGATATC ATAACACATC COCATTTTTA COGATTTAGA TAACCAAAAC	480
	ASCATANTTA GCATGITITAG AATCTATCAG AAGAACCTCC CTIGITICCTT TAATCATTAA	540
20	TITGAACAGT CATTGATTCC GICTTTCGAC CAAGAAGITA GCACGIGATA TCCOCTGACG	600
20	COGAAACOOC GTOCCTIGIC TITICAC	626
	(2) INFORMATION FOR SEQ ID NO:165:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 394 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG106412	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:	
	AAAAATCATT TITATCACCA CICAAGATGC AGICTGATTG AAGIGIAAAG CIGCAGIAGA	60
	AGAGACAAGI AAGCCATCAT GAAGGIATGI TATAGGIGCT AAGIICCCGA TACNAGCACA	120
40	GTGGGCATGC TAGGGCTGCA GAGACAGGGC ATGGGCGTGT TAGGATAGCC GGAGACTCCG	180
	ATTOCCOGO: TACCOCCAGE TTACCOCCGC CTTCAAACGA TAATCOCTICC CACCACCCCG	240
	GCCACGGCGG CACTGATGCT TGTATTGTTT GGCATGAATC TGATACTAAC ATTCCTGTAG	300
45	TIGAACATTI CITACCCAGI TAATIGGIACG CNAAAGACCA TIGAGGICGA TGACGAACAC	360
	CGIGICCGIG TCTTCTACGA CAAGAGAATT 0000	394
	(2) INFORMATION FOR SEQ ID NO:166:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 559 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: INA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1064RP

5	(xi) SEQUENCE DESCRIPTION: SEO ID NO:166:	
	TAGTIGGATICE AGCATICOCGT CTCGACCAGT CCTGAGTITICE GCCGGCTCTA TCCTAGACCG	60
	CCAAACCCCA CCTTGAAGAC GTACTGCGAG ATCGTGAAGG AACCAAACCT CACTATATGT	120
10	TCCCTGAGCA CAGCGCTAAT GTTCGCCCACC TACTATGGGT TCAGCGTCAC GTTCGCCCAC	180
	TACTIGAAAC TIGACTATGG CTICAGTAAC CTIGOGATCG GCGCGTGCTA TGCCTGTCCA	240
15	GEOGRESCOC TAATCATEGG CTCCCCTCTIG GEOGGICACA TTTCCCGACCG CTTCCCCACG	300
15	AAGTOOGTAG CCAAGAACCC COGNAAGACC TTCCCCGAGCT ACAACCGCCT CATCTCGCAG	360
	GIGITTOSCA TOTOCGICAG CATOCCOGO TGTATOCGGT ACCGCTOGGG AATTCAATTT	420
20	CACTATCACA TOSCTATOSC SCTATTCTTT TCTTTCCTAA TOSCGTTOSG TATCACCTOS	<b>4</b> 80
20	TOCTCTAACT CCACCATGAC CTTCCTTACG GAGTCCAACC CAAAAAGAGC TOCCGGTACC	540
	ATTGCGTAAG CAACAGCTT	559
25	(2) INFORMATION FOR SEQ ID NO:167:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 611 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1064UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:	
	GATCIGITCT COCCCCCTA TOOCCCCTOC CTOCCOCCAC ACCCACATICG TCCTOCTCCC	60
40	CCTAGGCTAG GCACGGCCCT AGGCGGAGCT TGTCCTGCGG AGGCGGGGCC GGCTGAGCCC	120
	COCTOCOCAE GOGOCAGOC COTGAGACOG TAGOCOCCC COTAATGOCT COTACOCAGO	180
	GACCGCGCAG CGGACCTGCA CGTTAGTAAA AAATCATTTT TATCACCACT CAAGATGCAG	240
45	TCTGATTGAA GTGTAAAGCT GCAGTAGAAG AGACAAGTAA GCCATCATGA AGGTATTTTA	300
	TAGGIGCTAA GITCCCGATA CAAAGCACAG GTGGGCATIC TAGGGCTGCA GAGACAGGCC	360
	ATGGGCGTTT TACGGATAGC CCGGAGACTC CCCATTGGGC GGGCTTAGCG GGAGGGTTAG	420
50	COCOGNETTY GEARACEART ARTOCONTOC CANGACOCOG GCCACOGNOG GACTIGATOCT	480
	TGTTTTGTT TGGGAAINAA TCTTNATACT AACAATCCCN GINGGNNGGA CAATTCTTAC	540
	CCCNGTTAAT NOGTACOCAA AAGACCATIGN AGGTCOGNIG ANGACAACCN NIVICCCNNIVI	600
<i>55</i>	TICIINCGAN A	611

	(2) INFORMATION FOR SEQ ID NO:168;	
5	(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 615 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1065RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:	
	GATCTGTAGT TTCGCAGTCC CTGATGCGGT CCGCCAGAGC AGGCAGCGCC GGCCAGGGTC	60
	TOCGCAAGOC AGGCGITGTG TCACCGCGGA GCCACTCTCT GGGCAGGCAG TTCCACGCCT	120
20	CCTGAACGAG COCOOCATG ATGCCCCCA GAATGCTCCC ATACCCATCC AGAATGTCGA	180
	ACAGOSTOGT CTTTATOGOC AGACOCCTCT TATTATGTGG GGGTTCCATG TAAAGOGTGT	240
	CCTTCGAAGC ATCAAAGTAG AGGGACAGGT CGTTGCTCAT GTGGTACAGA ACAAAGACTG	300
25	ATGACATTOG AGTAGGTCTG GGATTCCOCA CAGACCCTGA CACTTOOOOG GCAAAATTICT	360
	TIGICTIGIC GAGGGNITIT CCCNICANIC CCCNGGCAGG TGGGGGCAGN CTICCCCNGG	420
	GCAAAAAAGG CIMTTOOOCA CONAGATNAA COCCTGGGAA ANCCCGAAGG IGNCANNAAT	480
30	TRIAGNOGAAG TRINCCTIVACC NCTCCACCINA ATCOGGAAAAA TTGOOGGANNA ANGOCCCANC	540
	CCAACNCCCA AANITTTCTT GGAAAAAAAA AGGGGNGCCC CACCCNGGNG GANTNANTIT	600
	INTECCCCCC NATEC	615
35	(2) INFORMATION FOR SEQ ID NO:169:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 604 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1065UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:	
50	GATCTCTTCC CTTCGATCAT CCCTCAGTTG GGTTCTGAGT CCATCGATGC GTTGACGCAG	60
	TTOSCCACAC AGTTOCAGAA COCACAGOCT OCAGCTCCAG CAACCGAGOG CCATGAGOCA	120
	GOCGAGAGA AGGACAACGA CATCCCAGAG TTGATTGAGG GCCAGTCTTT CGACGCGGAT	180
55	GITICAATAAG TOCOCTOTOC CAGGACTOTO TICTCOCCOC CCATCTCAGA ATTIGICIAT	240

	TICIOCAGG ANIATACATA TATIONGIOC ACATATOCAT ATTATGTATA TATATGTACA	300
	TACACTATAC CCGCCCCGTC TTAGTCGGAC CACATAAACC TACGGGTCGG CGCCCCTATA	360
5	TOGITITACA ATAAACOOOC COINCTIOCG OCINVINCTIC GANAATCICN TICOCOCCC	420
	CNCCNVCCNT TANNAGGINC TTCTNCCGGG TNGGAAGTNA AAAAGCNNNN GTTCNGTTGN	480
	NAGNETCCCC GGGGAAANC CNICCCCGNG GNGGATTTIC NCCCAAACCG NAGAANACNN	540
10	CNITGONCCA ACTIGOCCCT GOGAGAAAAA AANCONATGN NGAAGNAAAA TIGOCCCCTG	600
	CCCN	604
	(2) INFORMATION FOR SEQ ID NO:170:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 653 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1066RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:	
	GATCCTGAGG CCTCACTAAG CCATTCAATC GGTACTAGCG ACGGGCGGTG TGTACAAAGG	60
30	OCAGGGACGT AATCAACOCA AOCTGATGAC TTGCOCTTAC TAGGAATTCC TCGTTGAAGA	120
	GCAATAATTG CAATGCTCTA TCCCCAGCAC GACGGAGTTT CACAAGATTA CCCAGACCTC	180
	TOGGCCAAGG TTATACTOGC TOGCTCCOTIC AGTGTAGCGC GCGTCCGGCC CAGAACGTCT	240
35	AAGGCATCA CAGACCIGIT ATTOCCICAA ACTICCATCG GCITGAAACC GATAGTCCCT	300
	CTANGANGTIG COCANCCAGE ANATOCTINGE AGENCETATIT AGTINGGTTAN OGTICTCGTTC	360
	GITATOSCAA TTAAGCAGAC AAATCACTOO ACCAACTAAG AACGCCATG CACCACCACC	<b>4</b> 20
40	CACAAAATCA AGAAAGAGCT CTCAATCTGT CAATCCTTAT TGTGTCTGGA CCTGGTGAGT	480
	TTCCCCGTGT TGAGTCAAAT TAAGCCGCAG GCTCCACTCC TGGTGGTGCC CTTCCGTCAA	540
	TICCTITAAG TITICAGCCIT GCGAACATAC TCCCCCCAGA ACCCAAAGAC TITIGATTICT	600
45	CGTAAGGTGC CGAGTGGGTC ATAAGAAAAC ACCACCCGAT CCCTAATCGG CAT	653
	(2) INFORMATION FOR SEQ ID NO:171:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 669 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
55	(vi) Original Source: (A) Organism: Pag1066UP	

	(XI) SECURICE DESCRIPTION: SEC ID NO:171:	
5	GATCTOGAGG ACCTATATAT ACCATTTCOC TOCACCTTTC TTTTTGTOCC TGATGTTTTA	€0
	TAAGTAGACG ATCTCTGATT ATTATCOCGA OGTCGTTAAA GTCCCATGCG AGCACACTGT	120
	TTOCAATGAT GOCCATCOCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTOCATGTGA	180
10	OCCATACTAG GGTGACCTGT GTTGGCGGCC AGCTTGCAGG AGGAGGAAAA AAAAAAGATT	240
	OCAOCACCTG AGTITICOCGT ATOGTCACCC ACTACACTAC TCOGTCAGGC TCTTACCAGC	300
	TTAACTACAG TTGATCOGAC GOGAAACOGT OCTTTCTOGT AGATATOGCC OCAACCGAAA	360
15	TATATACCCT AGAGCAGACA TGATATCAGA TOGTOGATOC ACGTGAGGGC GTAGACATGT	420
	AATAACGATA TCGAGTACAT TTGGTGCCAG ATGGCTGGGG CTATGGCGCA GATGTGTGGT	480
	AATTOOCACA TCOCOCTAAC TCACOCOCTA ACAACACTIT CTCCCCATTC CACTOCCATT	540
20	CCCTACCGAA TCTCACCTAG TGATCTGAAA ACTGATATOC TATCTGAACT OCAAACTATG	600
	GCAACTICTOG CTOCOCTITAR GAAGAAGATC TCRACTOCAA COCAACOCAA CGTCOGARCA	660
	ATGCTTTGA	669
25	(2) INFORMATION FOR SEQ ID NO:172:	
30 35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 652 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1067RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:	
40	GATCCCCTAA CTITCGTTCT TGATTAATGA AAACGTCCTT GOCAAATGCT TTCGCAGTAG	60
	TTAGTCTTCA ATAAATCCAA GAATTTCACC TCTGACAATT GAATACTGAT GCCCCCGACC	120
	GICCCIATTA ATCATTACGA TOGTCCTAGA AACCAACAAA ATAGAACCAA ACGTCCTATT	180
45	CCATTATICC ATOCTAATAT ATTCGAGCIT GCGCCTGCTT TGAACACTCT AATTTTTTCA	240
	AAGTAAAAGT CCTGGTTCGC CTAGAGTACA AGTACCCTAG GTTAGCCAGA AGGAAAGGTT	300
	COSTITUGATO COSTACACISA AGAAAATOOS ACOSOSCAAC CAAACOCAAA STITCAACTIAC	360
50	GAGCTITITIA ACTOCAACAA CTITAATATA COCTATIOGA OCTOGAATTA CCOCCOCTOC	420
	TOSCACCAGA CTIOCCCTCC AATTGITICCT COTTAAGGTA TITTACATTGI ACTCATTCCA	480
	ATTACAAGAC COGTATOGOC COTGTATOGT TATTTATTGT CACTACOTCC CTGAATTAGG	540
5 <b>5</b>	ATTOOGTAAT TTOCGCOCCT OCTOCCTTCC TTOGATGTOG TAGCCGTTTC TCAGGCTCCC	600

	TCTCCGGAAT CGAACCITAT TCCCCGTTAC CCGTTGAAAC CATGGTAGGC CA	652
	(2) INFORMATION FOR SEQ ID NO:173:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 669 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1067UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:	
	GATCOGGIAG TGAGGGCCTT GGICAGAGGC GGCAAGIGIG CTIGIGGICT GICCICGGGG	60
20	GCTTGCTCCT GGGGACGGAC TGCTTGCGTG CTCTGTCGTA GACGGCCTTG GTAGACCATC	120
	TCTOGTCGTC OCTTOCTACA ATTAACGATC AACTTAGAAC TOGTACOGAC AAGGGGAATC	180
	TGACTGTCTA ATTAAAACAT AGCATTGCGA TGGTCAGAAA GTGATGTTGA CGCAATGTGA	240
25	TTTCTGCCCA GTGCTCTGAA TGTCAAAGTG AAGAAATTCA ACCAAGCGCG GGTAAACGGC	300
	GGGAGTAACT ATGACTCTCT TAAGGTAGCC AAATGCCTCG TCATCTAATT AGTGACGCGC	360
	ATGAATGGAT TAACGAGATT CCCACTGTCC CTATCTACTA TCTAGCGAAA CCACAGCCAA	420
30	GGGAACGGGC TTGGCAGAAT CAGCGGGGAA AGAAGACCTG TTGAGCTTGA CTCTAGTTTG	480
	ACATTGTGAA GAGACATAGA AGGTGTAGAA TAAGTGGGAG CTTCGGCGCC AGTGAAATAC	5 <b>4</b> 0
	CACTACCTTT ATACTTTCTT TACTTATTCA ATTAACCGGA GCTGGAATTC ATTITTCCACC	600
35	TICTAGCATT TANASTOCTA TACOGOCTICA TOCOGOTTICA ARACATTIGTO AGGTOCOGAG	660
	TITIGGCTGG	669
	(2) INFORMATION FOR SEQ ID NO:174:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 596 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1068RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:	
	GATCCACCNC TNNCCCATTC AATCCCTACN ACTCCACCCC CCCNVIGINN AANCCCACCC	60
55	GACCTAATCA ACGANAGCTG ATGACTAGAC GCTTACTAGG AATNOGTCCT TCAAGANCAA	120

	TGATTTOCTC TGTNTCTATC CCCAGTCATT ACNONCTANC AGACATGATC CTCCATGATC	180
	TETCOSTOCT CTCTOSTATN CCOCACGACN CCCNCNCTGT ACCOCCCGTG COCCCAGAA	240
5	NVICTANGG CCICCCAGAC NIGITATINGC CICTAACITN CATCGGNICN ANACCGANAN	300
	TOCTIVETAAG ANGTOCOGNA CCAOCANNIG CNINCCINGONC TATITIACTAG GITAAOGTCT	360
	CGITCGITAT CNCCNITANT CAGACAAATC ACTCCANCIN CTAANAACGG CINTOCCCCN	420
10	NONNOCINGAA INVININGAAA CANCTOTOAT CIGICAATOC TIATOGTGTC TOGACOCOCT	480
	GAGTITICCCG TGITGAATCT AANTAANCCG CAGGCTICNAC TCCTINNIGGT GCCTTCCGTC	540
15	NATIOCITTA AGITTCAACC CIGOGACATA NICCCOCAGA ACTCANAGAC INTGAT	596
13	(2) INFORMATION FOR SEQ ID NO:175:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 641 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1068UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:	
30	CATCTOCAGG ACCTATATAT ACCATTTCOC TOCACCTTTC TTTTTGTGCC TGATGTTTTA	60
	TAAGTAGACG ATCTCTGATT ATTATCOCCA OGTCGTTAAA GTCCCATGOG AGCACACTGT	120
25	TTGCAATGAT GGCCATCGCC CACCAGACCA GTCAGAAGTA GATATCTGAA TTGCATGTGA	180
35	COCATACTAG GETGACCTET GITGOCOGCC ACCTTGCAGG AGGAGGAAAA AAAAAAGATT	240
	GCAGCACCIG AGTITICOCGI ATGGTCACCC ACTACACTAC TCGGTCAGGC TCTTACCAGC	300
40	TTAACTACAG TIGATCOGAC GOGAAACOGT OCTITICTOGT AGATATOGOC GCAACOGAAA	360
-	TATATAGCCT AGAGCAGACA TGATATCAGA TOGTGGATOC ACGTGAGGGC GTAGACATGT	420
	AATAACGATA TCGAGTACAT TIGGTGCCAG ATGGCTGGGG CTATGGCGCA GATGTGTGGT	480
45	AGTTOOCACA TCCCCCTAAG TCACCCCCTA RGAAGARGTT TCTCCCCATT CCACTCCCAT	540
	TCCGTACCGA ATGTCACGTA GTGATCTGAA AAGTGATATG CTATGTGAAG TGCAAAGTAT	600
	COCAACTOTG OCTOOOCTTA ACAACARCAT CTCACTOCAA C	641
50	(2) INFORMATION FOR SEQ ID NO:176:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 654 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIG:	INAL SOURCE	Ξ:
	(A)	ORGANISM:	PAG1069RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:	
	GATOGACCCC GCTCCCGCTC GCATCAGCGA GCTGCCCGTG CCGATCAGCA GCCCGGTCCCC	60
10	TAGCCACCCC CCCATGOCTA TCATCCACAC ATGACCTGCC TGCACCTCCT TCTTGACCCC	120
	GATGCCCTCG TGCTTGCCAT CGTAGTTCCA GTCTACGGAC TGCGCCTCCT GGTCTGTGCT	180
	OCTIGIOGGIA TOCCOCAGAC COCOGCCCTC ACCAGCOGGG GCCAGCTTGG GGCCTTTCAA	240
15	CICGICCACC GIGGACCCCI CICATCCCIC TGCGAACTIC TCTTCCCCCA TAAGTGCCGA	300
	GCTGTTATCT ATGCTACTCA AGCTCCCGCC GTATAGCCTT GCTATATATA CTTACGCTGC	360
	GACCCCTAT TCCGGACACA GCTATATATT GGCCCGCCGT CTCGCGCGCT GCTTGGGGAG	420
20	COGACTGACC CCACCCTGAT AGTGCCGTTG CACTTCTGCT GGGCCGCCTC AGCCCGTTCA	480
	GOGTCOGACT GTGACATCGG GCTGCGCGAG CGCGATTAAT CACCCGACTG GGCTGCATGC	540
	COCACTAAAC CTCCCCTCOC GOCGCAGGGC GCCCTTATCG CCTCCGTGAT GACGTACGTA	600
25	TGTTTATCAA AGATCCGGAG AMCTGTTCCA GGCTCCTACG TTGCGATAAG AGGC	654
	(2) INFORMATION FOR SEQ ID NO:177:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 708 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1069UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:	
40	GATCTTTCTG CCCTTATCAG GGATGOCACC ACCGGTCTTC ACCTCGTTTG ACTTGTAGCC	60
	ACAGTOCTOG CAGACOGTOG ACATGATGAT GACCTCTTTG AAGTGTOOGA TGTTGACOGG	120
	CTTCATATGC GTGTCACATG GGTGAACACA TGATGGGCAC GTGGCAGTGA AGGTCTGCAC	180
45	CICGITIGIGG AAGTICICGA TATCCGIAGC GICAGATAAG AGACCGGCCT GIGCCCCTIG	240
	CGATTIGITG CGCTCGCGCT GCGACAGCTC CGCGCGCTTC TCTTGACGCC GTTGCTCCAA	300
	TIGGICGCCC CTAATGATGC CCACCIGGAC GITTIGCTCA TCIGAACGCA GGTACICGGT	360
50	TITICGACCAT TITICCCCAG CITICOCCICG CITICIATICG ATCCAGGAAT TOCCAGCAGG	420
	GICGICCAGC GIAAAAGICA GCGGIAGAGI GCCCGGCICG CACGACAGCG CAGCGGCGAC	480
	CTTGGCAATG AACTGCGCAA TCTGATCGTA CAGGTTCTCG TCCACTTCCT TCCGCGCCCC	540

600

CTGGTCGGCG TCCAAGTCCT CGATCATCTC GGTCAGCAGG CCCTCCACAG TCGTCAGCTG

55

GCCGCCCTTG GGAAGAATCT CCAGGTCCAA TTCAACGAAG CGGGAAGCCG CAGTTTCCCC 660

5	CTTGATGACT GCCTGTCAAA ATCGCCCTTC TCCTCAACCT TCAGCTGA	708
	(2) INFORMATION FOR SEQ ID NO:178:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 703 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1070RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:	
20	GATCCCGTAC ACGAAGAAAA TCGGACGGC CAACCAAACC CAAAGTTCAA CTACGAGCTT	60
	TTTAACTOCA ACAACTITAA TATACOCTAT TOGAGCTOGA ATTACCOCOG CTOCTOGCAC	120
	CAGACTIGCC CTCCAATIGT TCCTCGTTAA GGIATTTACA TIGIACTCAT TCCAATIACA	180
25	AGMCCCGTAT GGGCCCTGTA TCGTTATTTA TTGTCACTAC CTCCCTGAAT TAGGWTTGGG	240
	TAATTTGCCC CCCTCCTCCC TICCTTCCAT GTCGTAGCCG TITCTCAGCC TCCCTCTCCG	300
	GAATOGAACC CITATICCCC GITACCCGIT GAAACCATGG TAGGCCACTA TCCTACCATC	360
30	GAAAGTTGAT ACCCAGAAA TITGAATGAA CCATCOCCAG CACAACCCCA TOCCATTOGA	420
	AAAGITATTA TGAATCATCA AAGAGTCCGA AGACATTGAT TITTTATCTA ATAAATACAT	480
	CTCTTCCAAA AGGTCGAGAT TTTAAGCATG TATTAGCTCT AGAATTACCA CAGATATCCA	540
35	TGTAGTAAAG GAACTATCAA ATAAACGATA ACTGATTTAA TGAGCCATTC GCAGTTTCAC	600
	TGIATAAATT GCTTATACTT AGACATGCAT GGCTTAATCT TIGAGACAAG CATATGACTA	660
	CTGGCAGGAT CAACCAGATA ACTATCTTAA AGAACAACCC GAA	703
40	(2) INFORMATION FOR SEQ ID NO:179:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 675 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1070UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:	
55	CATCCTTTAG TTCCTCOGAG TTTCACCCTA GAGGTCOCAG AAAAGTTACC ACAGGGATAA	60

	CIGGCIAGE GENGICANGE GITCAINGES ACATIGCTIT TIGATICTIC GAIGIGGGT	120
	CITICCTATCA TACCGAAGCA GAATTOGGTA AGOGTTOGAT TGTTCACCCA CTAATAGGGA	180
5	ACCTGAGCTG GCTTTAGACC GTCGTGAGAC ACCTTAGTTT TACCCTACTG ATGAATGTTA	240
	TOOCAATAGT AATTGAACTT AGTACGAGAG GAACAGTTCA TTCOGATAAT TOGTTTTTOC	300
	GOCTIGTICCGA CCGGGCATTG CCGCGAAGCT ACCATCCGCT GGATTATGGC TGAACGCCTC	360
10	TAAGTCAGAA TCCATGCTAG AACGCGATGA TICTTTTTCT COCACATTAT AGATGGATAC	420
	GAATAAGGTG CTTTTAGCAT COCTGAACCA TAGCAGGCCG GCAACTGGTG TTCANIACGGA	480
	AAGGTCTGGG CGCGTGCCGG CGCATTGCAA TGTCATACTG CGCGAGAGTA AATCATTTGT	540
15	ACACGACITA RATGIACAAC AGGGIATIGI AAGCAGIARA GIAGCCTIGI IGITACGATC	600
	TOCTGAGATT AACCCTTOGT TGTCTGATTT GTTTTCTATT TGGAAGTCTG CAGGAGCAGG	<b>6</b> 60
	CTTTGAAATA RAGTT	<b>67</b> 5
20	(2) INFORMATION FOR SEQ ID NO:180:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 498 base pairs  (B) TYPE: mucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1071RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:	
35	GATCTONOGO GCAAACNCAG CATTCACCGT TGTGCAAAAA GATTTGACTG GTAACATCAC	60
	CAAGCTTCGC AACAGACAAT TGTCGCACCC COGTGAGTCT GCAACCCTGC AGGAGCTTGT	120
	GATTICCAÇÃO COTOCACADO OCACCAAGAC TOCTTCOGAA COOCTOCTOT COCTCACCAG	180
40	AGGCCTGCAA TTCACCGCGC AAGCTCTTAG AGAAACGCTA GACCATCCAG AGCTCGAATT	240
	GTCTAAGACA TTCACAGATG CGTATTGGAA GACGTTGACG AAGCACCATG GTATGCTTGT	300
	ACGICCGGIT TICAAAGCIG GCCATGAAAG CTIGCCCCTA CAGGAAGGAC TITITITICCAG	360
45	AAACTAGGCA GCGACCAAGA GAAGGTTGAC ACGCAACTTT AAGCAGTGGC TGGCTGCACT	420
	TGAAAAGATC GTAGAGATTC TGCTTCAAAT CCCTTGGGGG AAACGTGCAA AGGATTTATG	480
	AGTATTATTA TAGAAGCC	498
50	(2) INFORMATION FOR SEQ ID NO:181:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 625 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1071UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:	
10	GATCGACAGC CTCGAAGAAG TAGCCTCCAC AGCTTCAAAC ACAGCGCACA GGTCTGCATA	60
	CATCACOCTE GIOCTTOCTE CACOCTIVAC COGAGAACIT TGTOCOCGTE GCACOCCCT	120
	OSCAGACTOT GOCAGCACCC CCCCCGCCC GGGCTTATCT GCAGCTCGG GGAGCATGTT	180
15	CITCACCTCG GOGTCCTGTT CATGGGCTGC CGGTGCCGCT ACGCACTCGG GAGACTCTAC	240
	CTICGATTIC TIGACCCTCG CTGTTGACGT CGCTCCATCT TGAGGCCTCT TCAGCGCAGC	300
	GAAGAATOGG ACCAATGTGG CCTGCTTCTT TGGAGTAGAC ATTGGCCTGA AGTAAAACCC	360
20	TACTGACCTG CCAAATAGCT CCACTTTGGT CTCGCGACAG GAGCTTCCNA AGANTGACAT	420
	TINIVIGINEN NAAGGCCININ NIVIINICAAA GACGAANCIN NIATCAACCIN CCTNIVIINCC	480
	CCAGNONIA NAAGIAANAA NUMATININ OGNATINININ AAATTANOGI TUMUNAININ	540
25	NCTINGNAAA TINNINNGN TINNINATIC CONNOGNIT TONNIINOC NONCNOCINN	600
	GENTITTIIN NAMMINAAN MINCC	625
	(2) INFORMATION FOR SEQ ID NO:182:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 491 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1072RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:	
	GAGCAACTAT TATTAGGCGC CCCCCACCCC AGTCTGCAGC ATTCGAAAGC CTTCCTAGCC	60
	TTTGTGCGAT GTCCCAAGGT ACAATTTTCT CGCAGNIGAA AATACGAAAG AAGCGCCAAG	120
45	AAGTIGOCCTT CTTTGAATCC AACGCCGACG CCAATGATGT CGAGGCGGGC GAACATTTTIA	180
	TAACAGAGCT CGATAAGGGC GATAAGCGCC TCGGCCTGTT TTCTTCGATC GGCTTGATAT	240
	OCAATAGAAT OCTOOOGACA OGTATCTTTG TOOGTOCCOC GAAGATCTTC CAGTOCGACT	300
50	GGCTCAGTAT ACTITICCOCT AGGGTTATICG GTACTAGGAG CTITTAATTICC TCTAGCAGGT	360
	CITTATGTTT ACATGGAATT TOGTAACTOC AATACCGCCG AACGGTGGCG AGAAGAACTA	420
	CCTTGAGTGC ATCTCCAATG AAACCGAACT TCTTCACTTA CAGTCAAGTG TACTCAGCAT	480
55	ATGATCATCT T	491

	(2) INFORMATION FOR SEQ ID NO:183:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 726 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1072UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:	
	GATCCOCAGC TTCOOCAAGC OCCOCTTCTC CTCCGTGTAC TCCTCGTCGT CGTCGTACTC	60
20	COOCACCATC GACOCCICCG OCTOCICCIC ATCCCCCGIC GCGTCCTTCT CCTCGTCCAC	120
20	CGTCTCCGGC AGAAGAGAGT CGGCCTTCGC CCCCGTCTCG TCGTCGTCGC GCTCCAGCAG	180
	AGCGCCCGGA AGCGGCTGCT CGTCCGGGGAG CGGCCCGAGG TACGGGTACT TCACCGGACC	240
25	CATCTCCCCC TCAATCCCCCC GCATCAACAC CTCCCCCCACG TACCGGTCCA TGATCTGCCC	300
	ATAGTOGTAA GATTACCTAA TICATACGTG TAGATCATCC CATGCTTACC ATGTTGAACC	360
	GICACCATGI AAATTICCAA TAATTCTCTA GICTCTCATT TGTAGANATT AGNANCTTTC	420
30	CPITATATTA ATNOTPITAC TNAATAATTN ATNNANNITT TNNITTGANC ANITCICCAT	480
	ATTGTATTAA ANINATATAT AATATTATIN TCTACTAATC TAACAAATTA NNNTCINTAT	540
	TATATATTA NINANCATAT NATNATATTA AATTATTTAT AATNATINCIN TCCTCTINTA	600
35	ATMITTAAAT MINAMMINIT TMINCMIANN CIAATMNATT TITMGATATT TIMITINMIA	660
	MINIMIAAA AAATATININ TITATONANI ATOTTOOATT TATNAATONI MITTITATOA	720
	AACCCC	726
40	(2) INFORMATION FOR SEQ ID NO:184:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 641 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1073RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:	
55	GATCAATTAA TAAATOGIIT AACTAATAAA GITAATAATA AATCTATTAA TTATATAAAA	60
	CTACCIGATT TTATIGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120

ATTGAGITTA TATTAAATTC ACCACCICIT ATTCATTCAT TTAATACTCC TCTAATTCAA 180

	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTOGATAT AGTTTAATTG	240
5	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
	GGIGIGIACC TIACCICTCT AATTAAAGIT ATAAAATTAT CITAACTAAT AAAAATAATT	420
10	TATAATAAA ATAAATAAA TTTAAATTAA TTTAAATTAA TAAATAAATAA	480
	GITATATITA AATAGATCAA AATITCAACA ATTICCATTI CATTIAGTAC TACCATCACC	540
	ATGACCAATT GITACATCAT TIAGITTATT AGGITTACTA TIAACITTAG CTITTACTAT	600
15	ACATOGIATI ATTOGIAATA TITATCCTTT ATTATTATCT T	641
	(2) INFORMATION FOR SEQ ID NO:185:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 662 base pairs  (B) TYPE: mucleic acid  (C) STRANDFINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
<b>2</b> 5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1073UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:	
	GATCITAATT TAAAATTITTA ATTAACTAIT TATAATTITAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
35	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITIG TOQCATCITA	180
	ATITITATIA TITAATIGAT TATTATCTAT TIAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTTA TIAAATAGTA TITAATTTAA TITTAATATT	300
40	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GIGATATATA	360
	ATITAATITA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITICATAATA TITATITITA TIAGICTAGI AATATITCTA TITAATAGIC TACCCTITAA	480
45	TTGGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
	TAATAATITA TTATCTAAAG TATATAAATT AATTAAATCN TITITITATTA TTATITAAAT	600
	TATTATTAAT TAGTAAATTA TATTTATTTA TITTATTAAC ATAATTITTT GNATAATAAT	660
50	AT	662
	(2) INFORMATION FOR SEQ ID NO:186:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 615 base pairs	
55	(B) TYPE: nucleic acid (C) STRANDEINESS: single	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1074RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:	
	GATCTAAATA TATATAATTT AATITATAAA GATTAATATA AACTTTTTTA TTATAATATT	60
	TAAGTATTAA ATTATTTAAA CTATTATTAT CATTATTTAA TAAATTAATT	120
15	TAATACTTAT TATATAATTA TIATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
7.5	AATTATAAAA ATAATATTTA ATATGAATAC TATTTAGICT ATGITCAAAT TITAAATTAG	240
	TTATTAAAAT AITATTAGAT ATTATTATTIT TCTTTAATAA AITATTAAAT AGATTATCAA	300
20	TAATTAATAT ATTATTTATT AATTGITTAT TAAAATAATA TATTTTATTA TTATAAACAT	360
20	TTAATTTATT TAAATATTGT AAATTATTAT TTTTATTATA ATATCTATTT TTATAAATAT	420
	TATGITGATI TATATIATIT AACTITITAT AAGAATIATI ATTAAAATTA ATTITAACTI	480
05	TAATTICTTA TIATTAATIT TTATATTAIT TAATAAATTA TAITCAITTI ATTIATTIAT	540
25	TTACTTAATT ATTAATTTA TTAATTAATTA TAATTAAT	600
	TATTATAAAG AATGT	615
	(2) INFORMATION FOR SEQ ID NO:187:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 663 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1074UP	
40		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:187:	
	GATCTIGATA CTAGAGCTIA TITTACTICA GCTACTATAA TIATTCITAT TOCTACTAGI	60
45	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATOGTOGTT CATTAAGATT ACTAACACCA	120
	ATATTATATC TATTATCATT TTTATTTTTA TTTACTGTAG GIGGITTAAC TGGIGIAGIA	180
	TTACCTAATC TATCATTAGA TGTACCATTC CATGATACTT ATTATGTAGT ACTACATTTC	240
50	CATTATGTAT TAAGITTAGG TOCKGRATIC TCTATGTTIG CROGITATIA TTATIGAAGI	300
	CCTCTTGTTT TAGGTTTAAA TTATAATGAA AAATTATCAC AAATTCAATT CTGATTAATT	360
	TICTTAGGIC TIMATATTAT TITCTTCCCT ATGCATTICT TAGGIATTAA TGGIATACCA	420
55	AGAAGAATIC CIGATTATICC TGATCTATIC CTAGGITGAA ATTTAGTATC TICATTITGGT	480

	TCTATAATAA CTATTATATC ATTAATGITA TTCCTITTATA TTATTTATCA TCAATTAATA	540
5	AATOGITTAA CIAATAAAGI TAATAATAAA TCTATTAATT ATATAAAACT ACCTGATTIT	600
	ATTGAATCAA ATAATATTIT CITAATGAAT ACTACTAAAT CATCATCTAT TGAGTITATA	660
	TTA	663
10	(2) INFORMATION FOR SPQ ID NO:188:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 639 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
20	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1075RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:	
	GATCTATCTA ATTACAGTAA AGCTGCAAAG GGTCTTTTCG TCTTTCTACA AATACTTAGC	60
25	ATCTTCACTA AGATTICAAT TICACTTAGA TIAAAGGAGA GACAGTIGIT GTATCATTAC	120
	GTCATTCATG CAGGACCATA ATTAGTGGAC AATGAATTTC GCTACATTAT AACCCTCATA	180
	ATAAGCCTCC TATTTATAA AATTTATTAT TATTATCTTT ATTAAAATAT TAATTTTTAT	240
30	ATTITATCAT GGAGCAGAGI TCACACITTA TACTITAACT TACGITICIG CAAAGIGITIG	300
	TGTTTTTAGT AAACAGTTGT ACAACTTTGT TCTTATTATT AATTATTATT TTAATTAATA	360
35	TOTOTTTATT GACTAACGTC AGAGCTATTT TIGCCGAGTT COTTTCCTTT AATTATCTAA	420
33	TICACCTICA TATACTCTAC TAACATACCT GAGTCGGTCT ACATTACGGT ATTITTATACA	480
	TAAATATITC TIGAACTTAA TAAATTTATA AAGACATTAT TIAAGITAAT TTATATATTA	540
40	GATTATTTCT ATCATATTAT ATTTTTTAAT ATATTACTTA AGAACCOCTT TTATTGTTAA	600
	ACCITATOCT TRACGICATA ACCATTATAC CITATTITIC	639
	(2) ENFORMATION FOR SEQ ID NO:189:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 663 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1075UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:	

	GATCCAGTTA CTTAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGTTAA	60
	CAATAAATT CAATAATTTA TTTAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
5	TATAATGAGA TATATATTTT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTTG	180
	TOCCASCASC TOCOGTAAGA CAANSSSSET TAGOGTTAAT COTAATOSCT TANAGOGTTC	240
	GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
10	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
	TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC CCCAGTAGTT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
15	AATTAAAGTA TTCCCCCTGA TGACTACGTT ACCAATAATA AAAATCAAAA CAATAGACCG	540
	TTACAGACTT AAGCAGTOGA ACATGITATT TAATTCCGAT AATCCTCCGA TAAATCTTAC	600
	CATTITTICA ATATITAATT ATAATAATTT ATAATTAATT ACAGOGGITA CATAGITGIC	660
20	TTC	663
	(2) INFORMATION FOR SEQ ID NO:190:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 650 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1076RP	
35		
	(A) ORGANISM: PAG1076RP	60
	(A) ORGANISM: PAG1076RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:	60 120
	(A) ORGANISM: PAG1076RP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGTGIT	
35	(A) ORGANISM: PAG1076RP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTGGTGTT  ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGTGIT  ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT  ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCITT AAAAATAAAA	120 180
35	(A) ORGANISM: PAG1076RP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGTGIT  ACTAAACGAT TACCTOGAAT ATAATTATCA CGATGTCCTA AAGTATTAGG TGAAAAGAAT  ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTTT AAAAATAAAA  TAACCATCCA TIGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA	120 180 240
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATTCAG GTACAATAGA TOCTOGTGIT  ACTAAAOGAT TACCTOGAAT ATAATTATCA OGATGTCCTA AAGTATTAGG TGAAAAGAAT  ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCITT AAAAATAAAA  TAACCATGCA TTGGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA  TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTOCTG CAATAATAAA TGGTACTAAA	120 180 240 300
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GIACAATAGA TOCTGGTGIT  ACTAAAOGAT TACCTOGAAT ATAATTATCA OGATGTCCTA AAGTATTAGG TGAAAAGAAT  ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTITT AAAAATAAAA  TAACCATOCA TIOGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA  TGTACATGTA ATACCATTAA ATGCATAATT ACTATTOCTG CAATAATAAA TOGTACTAAA  TAATGAAACA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT	120 180 240 300 360
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGTGIT  ACTAAAOGAT TACCTOGAAT ATAATTATCA GGATGICCTA AAGTATTAGG TGAAAAGAAT  ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCITT AAAAATAAAA  TAACCATGCA TICGTAATCT ATCTAAATTA CCTGTAATAC CTAATGCATT TGATGAACCA  TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TOGTACTAAA  TAATGAAACA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT  CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	120 180 240 300 360 420
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GIACAATAGA TOCTOGTGIT ACTAAAGGAT TACCIGGAAT ATAATTATCA GGATGICCTA AAGTAITAGG TGAAAAGAAT ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCITT AAAAATAAAA TAACCATGCA TIGGTAATCT ATCTAAATTA CCIGTAATAC CTAATGGATT TGATGAACCA TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TOGTACTAAA TAATGAAACA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA CCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TOCTGCTATA	120 180 240 300 360 420 480
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:190:  GATCITAAAA TAAGATAGAA TOGTAATAAA TATCATICAG GTACAATAGA TOCTOGTGIT ACTAAAOGAT TACCTOGAAT ATAATTATCA OGATGICCTA AAGTATTAGG TGAAAAGAAT ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTIT AAAAATAAAA TAACCATOCA TIOGTAATCT ATCTAAATTA CCTGTAATAC CTAATGGATT TGATGAACCA TGTACATGTA ATAGCATTAA ATGCATAATT ACTATTGCTG CAATAATAAA TOGTACTAAA TAATGAAACA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TCCTCATAAT CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TOCTGCTATA GTTAAAATAA AGATAATAAC ACCAACTGTT CATACAATAA CTCTAGGTGA TTTATAAGAA	120 180 240 300 360 420 480 540

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 663 base pairs (B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1076UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:	
15	GATCTAGAAT TATTAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATTA	60
	AAATCATTAA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
	TAATAAATAAA TAATAATAATTAATTAATTAATAAATA	180
20	AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGTATTCTT	240
	AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTARR GGGTAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
25	TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
	ATTAATAAAC TTAATAATCI ATTTATTAAT AAAAATGGIA TATTTAATAT TAAAATTAAA	<b>4</b> 80
	TTAAATACTA TITAATAAAT ATTCTATAAG TAATTTCTTA TITATTTTAT AACATTTTAA	540
30	AATGITTTAT GITAAATAGA TAATAATCAA TTAAATAATA AAAATTAAGA TOCCACAAAT	600
	AATCCATTIT CCTTTATGAA TCAATTAACT TATGGTTTNC TATTTATTITT ACTAATTTTA	660
	TCT	663
35	(2) INFORMATION FOR SEQ ID NO:192:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 642 base pairs (B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1077RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:	
	GATCCAGITA CITAGUAGAA IGATAAAATT AATAAATATT ATTTAITAAT ATTIGGITAA	60
50	CAATAAAATT CAATAATTTA TTTAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
	TATAATGAGA TATATATTIT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTIG	180
	TOCCAGCAGC TOCCGTAAGA CAAAGCCCGT TAGCGTTAAT CGTAATCCCT TAAAGCGTTC	240
55	GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300

	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
5	TTAATTGACA TTGAGGAACG AAGOCTAAAG TAGCAAATCG GATTCGATAC COGAGTAGTT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
	AATTAAAGTA TTCCCCCTGA TGACTACGTT ACCAATAATA AAAATCAAAA CAATAGACCG	540
10	TTACAGACTT AAGCAGTOGA ACATGTTATT TAATTOGATA ATCCTCGATA AATCTTACCA	600
	TTTTTTGAAT ATTTAATTAT AATAATTTAT AATTAATT	642
	(2) INFORMATION FOR SEQ ID NO:193:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 658 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1077UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:  GATCCGTGTA TITTITATITT ACATTATITA ATTAAAAATA ATGATTTAAA TAAATATTITT	60
	TTATAAAAA TAATTAGTOC ATTGTTACAT GTTCATTAAA GAATGATTAT TATCAAAACC	60
30	ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTCAC TTAATTAAGA ATTAGGAACT	120 180
	TIATCIATIA GICTOGOCIG TITOCCITIT GAITATTAAC CITATCOCIA ATAATCIGAA	240
	ATATTTAATT TTAGATTAAT AATATATTCT GAGATTTAAT ATTTTTAATA AAATAAATAA	300
35	TTATTCCCTA AATAATATTA ATAACTATAC CATATATAT	360
	TAACATATGT TTCGTAGAAA ACCAGCTATT TOCAAATCAG ATTTGACTTT CTCTACTTAC	420
40	CATTATTCAT CAGATAATAT TOCTACATTA ACCTGTTCAA TOGTTTTTAT ATTITATTAT	480
40	ATTITAAATA TAATAAATAT ATATTITAAT CATTIGATAA TAGTAAGATC ATCTGCTTTC	540
	COCTTAATTA ATATTAACTA AATITAATTT ATTTTAATTA ATTITAACAT TCTTAAATAT	600
45	TTATATTATT TTTAATATCA TTTTTTATTT TAATATTATG CTAATATTAA TTACTTGC	658
	(2) INFORMATION FOR SEQ ID NO:194:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 445 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG107811	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:	
5	GATCTAGTTC GTTAACTTCC GCAAAACACC TGTCAAGCGC TTCAACAAAC GTCTGGATCA	60
3	GATCCAAGAT GOCCAGTTCT GACTCCTGGT CGTCGACAAT GAAAGTAAAA TAGAGTGTTG	120
	CATAGITCIT GIAGATIATI TOGATAICIT COITAATOGI TICACIACCA CICGATAGIA	180
10	OCCIACIOCO COTAATTAAG AATGAAGACT GAATTGAACT GTTOCOCTOG CTGATCACCT	240
70	CGIAAACCTG CTCCAGIAGT ACCTTCTCCT TCCCGCAGATC GACACGAGTA TAGTACTTTA	300
	CAAGCCTAGG TTGGCACTTC TTGTTAACTT CATGTGTTAG TAGGATAATT TAAGTACTGC	360
15	COCTOCOCCO TOCCAAAGOG CITICACCCAT ATCACGACCG CONCONNTCA TCCNCINGTCC	420
15	CCACCACGGN TACINGGCCNC NCCCA	445
	(2) INFORMATION FOR SEQ ID NO:195:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 443 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG107812	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:	
	GATCIAATAT TCAATTOOCA AACTCITGAG AGTGTCITGG AGGAAATTAT TCAAGGGGGT	60
25	ATGGTAATTG AAACGAACGT GAAGAAAATT GTGGAGACCG TCGACGAGCT CAATAGAACT	120
35	TCTAACCAGG AAGCCAGGIT TGGGAATGGA CTAGGAAACG CTTTTCAGGC CATCACCATG	180
	OGTOOCTTTT CAAATTOOOG TOOGCOOCAG TGAATATTAG CACACACTGT CTTGAAACCC	240
10	CATAATAAAT GAAATAAATA CTCCTTOCTA GTGTCTAAGT ACGAAACAAC GCCAAGGCTT	300
40	TTGGATCATC TATGTACGCA TTCAGTTCGG CAGCACTCAC CATGGGCACC AACTCTTCTT	360
	ACTIOCTATE TOCHGIGICE TOATTIGGGC TICGGCTGCC TGATGGTCTC AAAGCTCCTC	420
45	CCTAATCCTC TGTAATTCTC CTG	443
<b>4</b> 5	(2) INFORMATION FOR SEQ ID NO:196:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 451 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1078RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:	
5	CATCAGGATG CCGATGAGAT ACTACCTTGA ACCAGCAGCC TTGACCTCAG CTAACTCCGC	60
3	AAATTOCTTT CATTTTTCGA AAGCAGATTA TAATTGCTTC TAAGCCATTC AATTGCTTTA	120
	CTTTTCCGTT AATCAATCCT CTATTTTACC ATCATTCGAA GTAAGAGTAT GTCGATATGT	180
10	CTGACCTAAG CTACAGATTA TCTAATCACA TAGTTATGTA CGAACCAATA AGATTATCGA	240
	ATTICCTICA AAAACTCAGG CGAACGGCAC AGGGTIGCTT GCGCCTATTA GATGCTTTGG	300
	CCATAGCATA TCACGAAGTG ACCTCACAGT TTTTAAGTAA CCGGAATAGT CTGTAGATAT	360
15	GGTATTGTGA AAAGITTATT NOCTGGTTTC ACCCCCTGGG AATCTNGGNG CTGGNCTGGG	420
	TTCTTAGGIG GGGAATCCGG NCCCCCCNNT C	451
	(2) INFORMATION FOR SEQ ID NO:197:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 480 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1078UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:	
	GATCTCCTTC CTTTCTGGTG TCTTGCCAAG CCCTTATTTG TTGACCAAAG TATTCTTCAC	60
35	CGITICCCCIG TACTICIGITIC TCATAAATITI CCGCGGITAGG ACACCTICIGG GCTTTCTCTT	120
	GOCCATCTAT CAGGGCTTTG CAATCATCTT CACCGCCGCT AAAGTTTTCA CACCATTTTT	180
	GTATGAGCAG CTACTICAGT AAGCCCCCGT ATTAGGATTG TIAAAAGAAG TAGGATCGAT	240
40	ACCCTICAAT TCCAGATGAT CGTTGCGGTG GGCTATTAAT TTGTTAGCCA CCTAATACTG	300
	AAATTTACAT ATTATTGCAC TAGITAATTA ATATTTATGA TGCAATGGGA ATCTATATCG	360
	GTTCTCCGTT CCATCTTCTC GTAATTAGAT CACGTCCGAT ATNGTNGCCC CGTACCGAGG	420
45	AGOGACCOGA TIGOGIVITAT CITTATOGIC COGAGAANIN ATAGAGNOCO NIVAANATAGA	480
	(2) INFORMATION FOR SEQ ID NO:198:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 703 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(V1) ORIGINAL SOURCE:
(A) ORGANISM: PAGIC79RP

_		
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:	
	GATCOCTCAT TATTITICGT COGAGOCTICG GCCCTCTTCT CCTTCTTCTC AAATACCTTC	60
10	AAATITTOGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC	120
,,,	TOSTIGAAAT ACTOCACOSC CICTOCACTC ATGCGATICA CCATTGAATT GCGCTCTTGT	180
	ATCTCTTGCT GGAACTGTTC TIGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA	240
15	CTGGTTGTAT CAGACTOGTC CACTTCATCT TOCACGTOCA GTGGATCCAT COCTGCAGCT	300
,-	AGTCTAGGTG CAGTGGTCTA TGTACAGTGC TGCTGTGGGT GTTAGCGGCC TCACCTTCTG	360
	CGACTIGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG	420
20	CACOCGAGCC TAATTTTGTC AGCTTOCOGA TTTAGCTCAG TTOOGGAGAGC GCCAGACTGA	480
	AGAGAAACTT COGTCAATOG TAATCTOGAA GTCCTGTGTT CGATCCACAG AATTCGCATA	540
	TITITITICCTC ACCITCACCCA CCOCCITANCA ACTOCCATTG CCTACCTAAT CCCCACCACT	600
25	GGAAAGCOCT CTTGTGATAT ATATATATCA AGTAACACAT CTATGTAACC TTTTGACACA	660
	GICCCAAGGI GAATCITGCC TCGGAICTGC CTCATCIGAR TCC	703
	(2) INFORMATION FOR SEQ ID NO:199:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 673 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1079UP	
40	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:199:	
	GATCAGOGAG CTAGGTACCO GGACGAACAT GCCGTTGCCGC AGCTTCCCAT ACTTCAGCGA	60
	COGTIGTICT ACCOCAGAGE TICCOGTCCTG GAATAGCGAC TOCACCTCTG CGTTCAGCAG	120
45	ATCOCCCTCT TTCAGAAAGC TOCOCATCTG CAGCTCATCG CTCTCAGACT TCCGCCGCAG	180
	CACGCCGCCG GGCAGGTTCA CAGAACCCAG CATGAGCACT GCGTGCTGCT TTCCGCCAAT	240
	ATCCACCTTC CATCGTTTGT TOCCCGACCTC CACGATCCTG CCGACAATGT GGTCGCCCGT	300
50	CTCTGGCGTG TACCGCCCGC GCCAAGGAAT CACCGACAGG AGTCGGTTCA CCCTGGAAAAC	360
	GETGCCCGCC ACCGACCAGT ACGTTTTGTT CTCCAGGAAG TATGTGCCGT GOCCTCGCAT	420

CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCACCGACG AATCCGCTCC

TICCATCTCC ACCTCCAAAT CAAACTCTTC TTCCTCATCG TCCACCTACT COCTCCCATG

480

540

55

	GAACTGAAAC CCACOCCOCT TOCOGATOGT TATTACCTCG CTCATTACTG CTGAGACGAC	600
	ACCITICARA ACTICACAGO CICOCIAGOC CAGOCGAAAC ACTOTIGARG ATACOCTITIC	660
5	TTACTTCTTG AAG	673
	(2) INFORMATION FOR SEQ ID NO:200:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 441 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1080UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:	
	GATCCGGCCA CGCATGTATT CCACTATGTA CGCTATATCG CGGCCTCGCC TCCGTGCGGG	60
	GCACCGCCTT ACACCTCAAA GCCGCAGCCT TTCATGCAGC CCTTGTACTT TTGCACCAGT	120
25	TOOTGGCACT TGACCGCATC CACGCCGTTG AACAGCAGAC AGCTGTCTCT CGCTTCCTTC	180
	TOGGGCTTGC ACACACAGCA TGGCTTTGGC TTGTCGGTAC TACTACCTTG TGAAACACCT	240
	GOCACAGAAG AGGATTCAGG CATGATTAAT GCTACAGTTC TTGGAGATCT TCCAACACG	300
30	CCCCCTCCTT GOCSTTTTC TCACTTIATT TTTCCTTCAA CCCCCAAAAA TTGTTGTCCA	360
	ATTACAATAT ACAGAGGGC AGTAACCCCT TTAGTGGCTT TTTGGCTTCT TGGGCTGGAA	420
	ANTINGACCC CCCAACNINC C	441
35	(2) INFORMATION FOR SEQ ID NO:201:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 644 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1081RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:	
50	GATCTITICGC AGTGACTAGT GCATGCGGCT ATTTAAAAAG TATCGAGTTA CCCTTGGAAA	60
	TTTCAGCATT TATAGTACTG ACGGAGCCGC TACAAAGCCA AGGCTTTGAA GGTACTAGGA	120
	GACATATICA GOCGCATAAA TCACCGCAAG CIGGATIGAG CGATGITITG GGITGIGITT	180
55	ACAGGAGCCA GCGCGGTGGC ATGCGTTTTT GCGTATGGGA TGGTGGACCG ATATCTCTCC	240

	TTCAAGCTGC ACAGGCATAC GCACCCGTTT GTGTTGGTAA CACTTTTCGC AAATATGACA	300
	CIGITICCICT CGATCACATA CCTCCTTCCA CTCGATGTGT TTTACTCAAA CCAGACAACC	360
5	GGGCGGGAAG ACGAGCGGCC AGAGCTGCCG AACCTCGCGT TGTTCTGGGC GGTGATCTAC	420
	TOOOCOGAGE TIGICATATE CIEGITIEGIE TICCCOGIEC TEATITICGIA CETEGATCIC	480
	AAGTACTTGT ATCCCCCCA GCCACAGGAG CCCCCCCCCC	540
10	CGANCOCCC TTATATOCAA TCTCAAGTTC TATOCTCTTT GTCTACTGGG GGTGATCTGC	600
	NGOCTOGTIAT ATCTCAAGAC GACGACCGAT COCOGCGTC AGAC	644
15	(2) INFORMATION FOR SEQ ID NO:202:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 669 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1081UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:	
	GATCCAAGAC GAGCTGCGCC AGGGGAGAAA ACCCCCCCAC ATATGTCCAG CGATACGCTC	60
30	AGCATGGAAA ACCCAACCGT GGACTTGCGC TCGTAGTTGT GCTTGGCCTG TGCCATATAC	120
	TICAGCACAG ACATGATGAT TITITATAAAG TACAGCACAT GOCAGTAGAA CAGTGTCGAC	180
	TGATTGTTCA ACCCTGTTTG CGTAATGCTA ACCACATATT GCACTGTGCC AATGCAAAAA	240
35	AGCCCGATGA ACAACTGCAT CATCTTCCGG TGCGCTGTGC TCATCCTATT CGCCGGCTCT	300
	CCGGTGAAGC CCCATAGTCT GGTGCCCCAT AGCACCTGCG ACGCCAGCAG TCCGTTAAGA	360
	AGCCAGCTAT GCATGGCATA CCAGTAGTCC GACCACCCTA CCGACGGCCT CACCGCCTG	420
40	GACGIGICGC CITCATICTG CCAGAGCACG TCTGCACAAC CAGCGAGAGT ACTAGCGCTG	480
	TATACCCGAT GCAATTAAAC ACCACGTAGC CTTTCGACAA TGCTCTTGCG CTCTGCCGCT	540
45	TCCAGTTGAT CCATAGTGGC GGATACATCG ACACCGACCA ACATGTCGCG TACAAGTATC	600
45	CGAGCAACIG TCTCTTCCTC ATTCCAGCCT CGTTCCAAGT GCTTCTACGC CGGTCTTCTG	660
	GCGTCAGAT	669
50	(2) INFORMATION FOR SEQ ID NO:203:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 654 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

	(VI) ORIGINAL S (A) ORGAN	OURCE: ISM: PAG1082RP
5		
	(xi) SEQUENCE D	ESCRIPTION: SE

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5**5** 

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:	
GATCCACGAG CAAACTATTA TTAGOCOCCC CCCACCCCAG TCTOCAGCAT TCGAAAGCCT	60
TOCTAGOCTT TGTGCGATGT CCCAAGGTAC AATTITCTCG CAGCTGAAAA TACGAAAGAA	120
GCGCCAAGAA GTGGCCTTCT TTGAATCCAA CGCCGACGCC AATGATGTCG AGGCGGGGA	180
ACATTITATA ACAGAGCTOG ATAAGGGGCGA TAAGCGGCTC GGCCTGTTTT CTTCGATCGG	240
CITICATATOC AATANAATOC TCOOGACAOG TATCITTGIC GITCCCOOGA ANATCITCCA	300
GITGACTOCC TCAGIATACT TIGCOCTAGG GITATOGGIA CIAGGAGCIT TAATTOCTCI	360
ASCAGGICTT TATGITTIACA TOGAATTIGG AACTGCAATA CCGCGGAACG GTGGCGAGAA	420
GAACTACCTT GAGTICATCT TCAAGAAACC GAAATTCITC ATTACGTCAA TCTACTCAGC	480
ATATGTCATC TTTTTAGGCT GOGCCGCAGG TAACTCTGTG ATGGCAGCTG CAATGTTCCT	540
TOATOCTOCA AAGGTOGAAG CAACACGTTG GCGTTGAACG CCGTCTTGGA GTTGCGGTCA	600
TITICTICIG CITCCITGIC AACTOTOTOA GIGTCAAAGO TOOGTIGITA CITC	654
(2) INFORMATION FOR SEQ ID NO:204:	

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 680 base pairs

  - (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: PAG1082UP

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GATCCGCAGC TICCGCCAAGC GCCGCTICIC CICCGIGIAC TCCTCGTCGT CGTCGTACTC	60
COSCACCATC GACOCCTCCC OCTOCTCCTC ATCCCCCCTC GCGTCCTTCT CCTCGTCCAC	120
COTOTICOSO ASCASOGAGT OSTOCTICOC COCCOTICTOS TOSTOCTICOS OCTICOASCAS	180
TOCOCCOGA ACCOCTOCT COTOCOGAG COCCCCAGO TACOGOTACT TCACCOGCCC	240
CATCTCCCGC TCAATCCGCG GGATCACCAC CTCCCGCACG TACCGGTCCA TGATCTGCGC	300
ATAGTOGIAG ATTICCGACT CCTTCGTGTT GTACATCCGC GCGTTCCACG TGATCCGCAC	360
CAAGICGITC ACGAACICCT GOOCCCCCTT GIAGICGITG ACCTICITIT TCACCGICGC	420
CACCCTGACC COCTTCTTCA TCATCCCGTA GTAGTCCCGCA TAATCCTTCC TCACCCCCAA	480
AGTGTAGAAA ATCGCCAAAA TCTCAATACC ATTTTCCTCC TTTAAGTCAA ACACGCCATC	540
CAACAAAACT TIGAGCIGGI CCCGIAGCAA CATCGITIAGC CCTCGCCACC TGAAAAGCTG	600

	AAGACTITOG TAGTGTACTA TGTGTTCCGA AACAACATCC CACGCGTCGT TTCTGCCCGT	660
_	TCACAGCCTT GCTTCAAGTT	680
5	(2) INFORMATION FOR SEQ ID NO:205:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 613 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1083RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:	
20	GATCATCAAT TICTTITIGG CIGITTICIT ATTIACAGCC ICIATTICIG AGCGAACATG	60
	CGACGCCACA GCAGTOCTAA TGAGCTCATC TGTTAGTTCG GTTGCAACCG CGTTACGCAG	120
	TTCATTCCCT TCTATTGCTT TGGAGCCAGA ATCTCTAGCT TCATCTTGAG CGCTAGCTTC	180
25	AGTITOGOCT CCCAGITTIA AAGCIGITIG GITAAAATGA AAAGIATTIT CCTCTTTTAG	240
	CTOOGAATTG CCAGCAAATG GITTITCTGTG CGATGACTCA AACGGTACAT CTTTTTTTAGT	300
	TTTTGTTCC TCTAAAATAT GCGGTGAGGT TGTAGAGCCG ACACTAGACA TAAATGGTGC	360
30	CGTAAACTGT TTCGTGGACT GCAGATCAGA CTGTTGCTGT GGCTTGAACT GCATGCTAGA	420
	TITCACTICA CITCCAGOGC GOGATIGOGT AGIGOGTICG GTAGICITAT AATCTCCACT	480
	ATCGAAGTIG AAAGTITITAG ATATATCCTG GTGTTCTCCG TGCAAGGAAG ACCCCTGCTC	540
35	AATGATGCTT TCCGAATATG TGGGTAGATT TGAATCATTG CTCCCTAGNA GCAGCATCAT	600
	CCTCCGAAAG AGA	613
	(2) INFORMATION FOR SEQ ID NO:206:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 656 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1083UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:	
	GATCCTCAGC GCTGCGGAGC AGGAGGAGCG CGAGGAGGAG CCGGAGGGGG TTGTGGGGGA	60
6.5	AACCGTGAGC COCAGCCGA COGGCGGGAC GAAGCGGCGC TITTGCGGATG AGGAGGCGGA	120
55	· - · · - · · · · · · · · · · · · · · ·	

	CAACGCCGAA CACCCCCCA CCCCCCCCCCC GGACGACGAG GAGGCCCCA AGAAGGCCCC	180
5	GAAGTAGCGT AGATAGAAGG ATATAACTGT ACAGTACCAT GCAAGACGAA TCTGAGGCCG	240
J	GCGCACGCGC GCTGGCGCGG CGCCGCGGTTA GCTGCGGAGG GCAGAAAAAA TCGCCGTTCGA	300
	CARTCTCTGC GTCATCATCC COOCCAGAGG ACAAGATGGC TGGCAAGAAG ATTIGCGGGTG	360
10	TOCTAGOCOC GACOOOCTICC GTOCOCCACC GGTTTATCCT OCTGTTOCCG GACCACCCTG	420
	ACTITICAGCT GAAGGTOCTT 0000CATCOC COCGATCCOC TCOCAAGCCG TATOCOGACG	480
	COCTGAATTG GAAGCAGACC GAGCTGATGC COGCGTTTGC CGAAGACATC GTGGTGAGCG	540
15	AGTOCAAGOC TGAAGCATTT TOCOGCTOCG ACGTTGTGTT CTCTGGGCTC GATGCGGACT	600
	ACOCAGOCCC CATCCAAGCG GGAATTIGCC GACGCCSGAC TGGCTGITGT CTCGAA	656
	(2) INFORMATION FOR SEQ ID NO:207:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 453 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1200RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:	
	GATCOCTCAT TATTITTOGT COGAOCCTOG OCCCICITICT OCTTCTTCTC AAATACCTTC	60
	AAATTITOGT CTATATAGGT CTGCAGCTCT TCCTTCTTCG AACATTCCGC CTTGTGAAGC	120
35	TOGTIGAAAT ACTOCAOOOC CICTOCACTC ATOCCATICA CCATIGAATT OCOCTCTIGT	180
	ATCTCTTGCT GGAACTGTTC TTGTTTGCGA ATGGCGTTTT GCCGCAGTTG AGCTTGCAAA	240
40	CIGGITGIAT CAGACTOGIC CACITCATCT TOCACGTOCA GTOGATOCAT COCTOCAGCT	300
40	AGICTAGGIG GAGIGGICIA TGIACAGIGC TGCIGIGCGI GITAGCGCGC TCACCITCIG	360
	CGACTGTTCA AAGATGTGCG TTTCCAGCAA GAAAAGAGAC AACCGGAAGT ATAAGTACAG	420
45	CACGCGAGCC TAATTITIGIC AGCTTGCGGA TTT	453
	(2) INFORMATION FOR SEQ ID NO:208:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 590 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:	
	GATCAGCGAG CTAGGTACCC GGACGAACAT GCCGTTGSGC AGCTTCCCCAT ACTTCAGCGA	60
5	COGNETETET ASCOCAGASC TICOGNICITE GAATASCGAC TOCACCTICIE CETTCASCAG	120
	ATCRCCCTCT TTCAGAAAGC TGCGCATCTG CARCTCATCG CTCTCAGACT TCCGCCGCAG	180
	CACGCCCCC GOCAGGTTCA CAGAACCCAG CATGAGCACT GYGTGCTGCT TYCCGYCAAT	240
10	ATCCACCTIC CATCGYTIGT TOGCGACCTC CACGATCCTG COGACAATGT OGTCGCCCGT	300
	CTCT0900TG TACC0CCC9C GCCAAGGAAT CACCGACAGG AGTCGGTTCA CCCTGGAAAAC	360
	GGIGYCCOCC ACCCACGAGT ACGITITGIT CTCCAGGAAG TATGTOCCGT GOCCICGCAT	420
15	CCACACAGGA TCATCTGTAA TCAGCTCTCC TGGCGTCATA ATCACCGACG AATCCGCTCC	<b>4</b> 80
	TICCATCICC ACCICCAAAT CAAACICIIC TICCICATOG TOCAGGIACT GOCTOCGATG	540
	GAACTGAAAC CCACOCCOCT TOGOGGATCGT TTTTACCTCG CTCATTACTG	590
20	(2) INFORMATION FOR SEQ ID NO:209:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 754 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1201RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:	
35	GATCTTOCAG ATGAACCCAA TATGGAACAC GGGCTTCGGC AGCTCGATGT GCCCGAAGTG	60
	CCCCCCCCCACA CGTCTCACAC TTCAAGTTCC CGTCCAATGCA	120
	GCCCAGCCGG GGGTCGTTCA GCCCTCCCAC CTTTGCGCGC ATCTGCGTCT CGTCCATCGT	180
40	CTCTGGAAAC TCAATCTTGG CCACGGAAAT CGCCCGCACC TCCTCGGGGG AGAACAGCCC	240
	AAACTGCACC TCCTTGATGG TCCGCAGAGG CGCGCTCGAA TACGGAAAGT CCACCATCGC	300
	TGTGTCGTAC TACCGCTCCC GGAGATACAC CCGTTTGCAA GTTCGTGTGT GCACCTGACG	360
45	CCCAGCCOCC ACTCOCAATC CTCGTTTACG CCGACCGCTT TGTTTCOCTC CCTTGCCGCA	420
	ACAACGAAGC TCTGTTATAT GTGCCCGCTC GAGACCCTAA GCCTGCTCCT GTCGAACACA	480
	COCTCACOCC CAGAAACTCG TGTCTTTACC TTOCACCTCT GGAATTOGTN COCOCCAAAC	540
50	CNOCTIATIG CITOCOCCAA CNCCTATOCT CCCTCTINATC TCACCTOCAA TNCACCANAA	600
	ACNGACCCCC CACCTACCCC NCAACTCTGG TTATTGGATT TTGCCGGGAA TAAACNCANT	660
	GTINCCAATC CHINCACCCC CAACIGHIGI NICCNCIGH CNGINCNCIN TIACICNINA	720
55	COCTOCNACN CCAATTITTT TINCCOGTIG COCT	754

	(2) INFORMATION FOR SEQ ID NO:210:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 643 base pairs  (B) TYPE: mucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1201UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:	
	GATOCTOCGA TTAGOCTOGT CTTAAAACTC AACCAAGCTG CTCTGAAACA AACAACACGT	60
	ACCACTRCTG TGFTGTTCCT CTGCGCTTGT TGACCGTCCC GCAACTACTA TGTCGTTACG	120
20	TGTGTTTTTT COOGAAACTT GCCACCGTCT CAGAATCAGA GOCTGTGAGA TICTTCTGTC	180
	GAATATOGOT CTOGACGTTC GOTTACGTGC GCCCCGCCAG TGCTCTTAAC CGGCGCCGTA	240
	GCCCCCGGCC CTGGCCGGTA CCAACAAGCA TGGCAGGAGA CACAGAGTAC TACAAGCAGG	300
25	COGTOCADGA GTACGCCCCC CTCAAGCAGG ACACGGACCC GGAGGAGTGG GACAGCCGGA	360
	TOCCOCAGAC COCCTGATA GICGAGAATA TOCCOCTGCA CCTGTGCCAC CCGGAGACCG	420
	GOCACTOROG GOCGTOCOCG GCGGACATGG CGCGGTTCAA GOCGTGCTGG GCGGCGCACG	480
30	CAACCOCCAG COCCTGACOC ACCCTGGACG GTGAGCTOCG GOCTGTAAAT AGGTGTATCT	540
	GCACCCGIGT CACGITICACA CTGCACACGI TACGAANCAT TNICNGGNIN GCCCNCCGCA	600
	ATGGCCANCC CCNATCINAN NACCCAAACN GGGGIATGAT NIN	643
35	(2) INFORMATION FOR SEQ ID NO:211:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 735 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1202RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:	
50	GATCGAAAAC GCTGCCACCG AAAGCTTGAC ACTGAAGGGA TTTGAGTATT CTCTTGCATT	60
	TTCCAAGOCG AATACCAGCT TGTCCCAGGC TGCCGATCCA ACCTTCCCCCT CCTTCAGGCC	120
	CTOCTTGTAC CTGTCGTCTA TCTGCAGCTG AGGTAGCAGC TCTGTGATCA GCATGACGAC	180
55	GOCCAGCOCA GAGGTAAAAC CTTTCAGAAA GOCCTTTGAG ATTGCATTGT CGATGAAACC	240

	GAGCCTGAAG ATGCCCATGG CGAACACCAG GACCCCTGAT ATGCATCCGA TAACCGCAAC	300
	OCTUATURAC OCTITURADOS ACTITUTOSOS CURTOCATUS CARCTUSTOSC CURCUACAGA	360
5	OGACOCAACC GTCTOCOOCC CTACAACCAT CGTCOOGAACG CTOCCGAAGA CTGCATATAT	420
	CASTOSSOS ATCACCASTS CSTACASCCC TOCSTATOST GACACATGTS CCATAGTOST	480
	CASCGARATG OCCASCGGTA TCTGGARTGA CGTCAGCGTC ASCCCAGCAA OCATGTCCTT	540
10	COCATTITOCO CAGAATACTO TOOCAGOCAG OGTATAATOG OCOGTAGTAA GACNCATAAA	600
	ATTINITICC INCCTACOGT IGIONNITTA INGNOTGIAC COCNTACGAC TIGICANAAG	660
	CAGVINOCOC CCCCCCCGAG ACTICCANCC CNICCCIACI CCCAATITICG ACCANGACCC	720
15	CONTROL CONTROL	735
	(2) INFORMATION FOR SEQ ID NO:212:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 777 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1202UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:	
	CATCOCCOCC OCOCCCAGE ACTACOTOGA CTTTCTCTCG CTCACACACG TACTOGACGA	60
	CCCGCAGCAG CCCGAAGCGG ACTGCGTGGA GCACAGCTAC ACGCCCGATC CGCTGCAGCT	120
35	COCCUTATAC OCOCACOCCC AATGAGAGCT CATCOCTCCC GCOCAGTGCG ATTTTTTTTGC	180
	COCCOCCO OLOCOMOCO CAMOCOCCO LOCOLLOCO CLOCOLMOLO LOCOLLOCO	
	COCCOCCCC CACCOCTCCC CCTGCCCGTC ACCGAAGCCC CAGCGATGAC AGCCAGCGTC	240
	CAGGATATOG TOGTOCCCAC COCCOGOGAC AGCOCCOGG GOCGCGACGG GCGCCCCAAC	2 <b>4</b> 0 3 <b>0</b> 0
49		
49	CAGGATIATOG TOGTTOCCCAC OGCOGGOCGAC AGCOCCGGGG GGCGCGACGG GCGCCCCAAC	300
40	CAGGATATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGGOG GGCGCGACGG GCGCCCCAAC CAGGCGGTCA CCCTCCCCGT GGCGCTCGAC AGCGCGACGG GCGAGGTGCT GGTGGGCAAG	300 360
<b>45</b>	CAGGATIATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGGOG GGCGCGACGG GCGCCCCAAC CAGGCGGTCA CCCTCCCCGT GGCGCTGGAC AGCGCGACGG GCGAGGTGCT GGTGGGGAAG GCCACCGGCA AGACCCGCGT GCGCAAGGGC CAGACAGAAG AGCAGTIACTG CGAGCAGGTG	300 360 420
	CAGGATIATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGGOG GGCGCGACGG GCGCCCCAAC CAGGCGGTCA CCCTCCCCGT GGCGCTGGAC AGCGGCGACGG GCGAGGTGCT GGTGCGCAAG GCCACCGGCA AGACCCGCGT GCGCAAGGGC CAGACAGAAG AGCAGTIACTG CGAGCAGCTG CAGCAGTACT TCGAGCGTGA CGGCGGTCCC GAGTGCACGG ACGAGGGCTG GCTCGACCGC	300 360 420 480
	CAGGATATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGACG GCCGACGG GCCCCCCAAC CAGGCGGTCA CCCTICCCCGT CGCGCTCGAC AGCGGCGACG GCCGAGGTGCT GGTGCGCAAG GCCACCGGCA AGACCCGCGT GCGCAAGGGC CAGACAGAAG AGCAGTACTG CGAGCAGCTG CAGCAGTACT TOGAGCGTGA CGCCGGTCCC GAGTGCACGG ACGAGGGCTG GCTCGACCGC GCGGCGCCCG CGGCCGCCCC GCCCACCAAG CAGGAGCCCC AGCGCCTTCGC CCGCCGTCTA	300 360 420 480 540
	CAGGATATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGACG GCCACGAGG GCCACCCCAAC CAGGCGGTCA COCTICCCCGT CGCGCTCGAC AGCGCGACG GCCAAGGTGCT GGTGCGCAAG GCCACCGGCA AGACCCGCGT GCGCAAGGGC CAGACAGAAG AGCAGTACTG CGAGCAGCTG CAGCAGTACT TOGAGCGTGA CGGCGGTCCC GAGTOCACGG ACGAGGGCTG GCTCGACCGC GCGGCGCCCG CGGCCGCCGC GCCCACCAAG CAGGAGCGCC AGCGCCTTCGC CCGCCGTCTA CCAACGCCTC TACTTCCTCG GCCGCCGTCG CGAANCCGCC GCNNTCGCCC GCCACTGCTG	300 360 420 480 540 600
45	CAGGATATOG TOGTOCCCAC OGCOGGOGAC ASCOCCGAGG GOCGCGAGG GOCGCCCAAC CAGGCGGTCA COCTOCCGT OGCGCTOGAC AGCGCGACG GOCGAGGTGCT GGTGGGCAAG GOCGACCGGCA AGACCCGCGT GOCGCAAGGGC CAGACAGAAG AGCAGTACTG CGAGCAGCTG CAGCAGTACT TOGAGCGTGA CGGCGGTTCCC GAGTTGCACGG ACGAGGGGTTG GCTTGGACCGC GCGGGGGCCG CGGCCGCCGC GCGCACCAAG CAGGAGCGCC AGCGCCTTGC CCGCCGTCTA CCAACGCCTC TACTTCCTCG GCCGCCGTCG CGAANCCGCC GCNNTCGCCC GCCACTGCTG TATACGTTCC CNGNTCNGGG CNCCTNCCNA TINGCGCCCG AANINCTCNA NCTCNNNNCT	300 360 420 480 540 600
45	CAGGATATOG TOGTOCCCAC OGCOGGOGAC AGCOCCGGOG GGCOCGACG GCGCCCCCAAC CAGGCGGTCA COCTCCCCGT GGCGCTGGAC AGCGGCACGG GCGAGGTGCT GGTGCGCAAG GCCACCGGCA AGACCCGCGT GCGCAAGGGC CAGACAGAAG AGCAGTACTG CCAGCAGCTG CAGCAGTACT TCGAGCGTGA CGGCGGTGCC GAGTOCACGG ACGAGGGCTTGG CCTCGACCGC GCGGCGCCGC GGGCCGCCGC GCGCACCAAG CAGGAGCGCC AGCGCCTTGG CCGCCGTCTA CCAACGCCTC TACTTCCTCG GCCGCCGTCG CGAANCCGCC GCNNTCGCCC GCCACTGCTG TATACGTTCC CNGNTCNGGG CNCCTNCCNA TTNGCGCCCG AANTNCTCNA NCTCNNNNCT NNTNCTNNCN GACCCNNNNN CCCTTAATTT TTCNTTTNNN NNTTTNTCTTT TTCCCCTCCC	300 360 420 480 540 600 660 720

5	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1203RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:	
	GATCAAACAG CTOCAGTTGT TGAAAAAGGTT OCTTGAATCC AAACCAAGGA AGGACGTATT	60
	TICGITICIA GOCCIGGATA ACTAATOTOT TOTOCACTOT AGCTGGGGAT AACACCTGCA	120
15	OGACGTGAAC TAACAAGTTG ACTACTATAC AOCAAAATAA CTOGAACAAG TTATACAGAA	180
	TTTTGTAAAT ATATTATAGC AGCCCTATTA CTATAATTCC ATCATTTGTT AACGCTTTAG	240
	CCTTCGTTCT CAGACTCGTC GTCATTTTCT TCATGATAGT TGATATTTTT GCGTTGCCTT	300
20	GASCITITICO TIACIOSSOC ISCATIGASS CICCIACICI TIGSOCISTA SICACCISCA	360
	GASCITICGIC TATCITICGIC CTCCCTTCCC TCATCCACAA CTTTCCCCTT CTTCTTAGTT	<b>4</b> 20
	TTAGATGAGG CTGATGATGG CCGTTGCGCT TCTTGAATTC TCTTCCTCTG CCCTTGGCCA	480
25	TGTTGAATTG GCGCGATTAG AGAAGCGCGA TACTTTGGCC CTTATATTTA CTGTCAGTGT	540
	TTCAACATGC TOGTCTGATA TATAGCTCAT GAACGCGTTT CTTTGCGCCT CTTCCCATAT	600
	TOGGGAATOG CTGATAAAGT TCAGAAGGCA GATTAGCTCC CAGGTAGACT GGTAGATTCC	660
30	ACCCCCCTTG GTTTTACCTC AAANATNATC AATTGGCAAC CNGCTAGANA TAATNINTGA	720
	ACATATOCTC COTOTINOGAT CCCRVIGCOGAT CTCCCCC	756
35	(2) INFORMATION FOR SEQ ID NO:214:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 781 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1203UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:	
	GATCATIGOC TOGOTIGOTOG GOGAGACCAT CTCOGAATGC GACACTGTGT CGATGTCTGT	60
50	OCTOCOGAAG ATCTTCAACA AGITTCTGAC ACACCATTIT GOCCCGCTGC GCTCCCTGCA	120
	GOCCICCOCC COCCACCOC CCITICATIT TICICICACC ATCIOCCACT CGIACAGIAA	180
	COGACTORGE CORCANTICA CGAAGITCIA CICCGAGAIC CIGIACOGGA TIACGAACOC	240
55	TOOCTCOOCC GOCTCAGOGG ACACCOCOGG CCTOCAGTCG ACACTTGACT COGAGTTCAA	300

(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear

	GACTICTTICTG AAACTGCATA AACTTACGGC CAACATATGG GAGCATGTGC CGGAACTGCT	360
	PROCTECTIC GICCGATTIG TOCATCAGGA GITATOCTICA GACAATGIGC COCTOCGAAT	420
5	TOOOCTACG CGACTTGTAG GTGATTTGTT AOCCGCACCC TCCGCTGCCA ACTTCGTCAC	480
	GATOCATACG GACACATATA ATOCCTOGAT GTCGAAGATA OCOGACATAG ACOCCACOGT	540
	GAGOCOCGAA TOOGTGAAAG CCATACCTAA GATACTOGAT AACAGTCTGA TTTOOCAACA	600
10	GATATOTOCA AAGOOTOAAC AAGACACTAA TOGATACOGA CGATGTOGTT AGACTATOCA	660
	OCTTAGAAGC OCCTGAAAGA ACTACAGTOC CCACGATTCT GOGANATCTC AAAATTCCAC	720
	TIMPICCIVA ITGITGCGCC TACCCAAANA AAACNAANCT TAGGAACTIT TCATTIGTAC	780
15	С	781
	(2) INFORMATION FOR SEQ ID NO:215:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 765 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1204RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:	
	GATCCGCTTG GCTAGGTCCT CAGCCGGCAT GTCGTCACGG TATAGGGCCT CGGAGCCAAC	60
	TAGGAAGCCG CGCACCGIGT CCCACTIGAT CCATGGCAAG TAGGICTIGA GCGCATCCIT	120
35	CTCCATCGAA AAGTGAGCGT CGTCGTCTGG CCAGACACCG ACCCATAGCT TGAAGCCAGC	180
	ACGGTCCGCA GCAGGACCCCA AGAACTGCAA CGTGTTGCAG TCAGAGGTAG AGTAGACTTT	240
	CACCETETICE CTCTAGGGGC CCAAGGCCTC CAAGTCCTCC AGGTAGTCCT CAGTGTACTT	300
40	GCAGGTACCG TOGTGCTTICT TCACACCTAG GTTGAAGGCC AAATOGCCCA TAGCGTGTAC	360
	AGACGAGGCA CCAAGCAGAG CTGCGGAAAC AGTGCCAGAG AAACGCATAG CTAACGAATT	420
	CATGGTGAGT TAGTCTGGCT AAAGTGGCTT GTACTGGAGA AACGACAGAG AGGGACAAAT	480
45	ATATOTTAAT ACCAGGICAG COCCATOTOC COCGAGGAAAA AGAAATGTOC COCGTGTTCC	540
	COOCACCTIC CITAATITIAG AAGCATEATC TATCACGIGA ATATCACGIG AAACACGITA	600
	AGCCTACAGA GAGCTATTGA COGTGOCTCG GAACACGITTA OCACTGAGIT ATGTACTAAG	660
50	GTGGCCACGC ACCATGCAGC TGTCCTCGAT GCAATATAAC CCCCCGGGCCC CCGGCAGTCA	720
	ACCOCCATCA AAAGINCTON CCCCGAGNNC CCTCAAATGT CCNTG	765
	(2) INFORMATION FOR SEO ID NO:216:	
55	(2) INFORMATION FOR SEQ ID NO:210.	

5	(A) LENGTH: 776 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1024UP	
10	(21) Constitution Production	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:	
	GATCAGGAAG CAATAGGTAC TCAATTGCGG AAGATTCAGA GACAGCAAAG GTCAAGTGCA	60
15	GTTCAGCAAC ATCGAATCCA CACAAGTTAT GTCGTACAGA GGCCATAACT ACAACGCAAT	120
	GGCACCCGGG GGGCAGACGT TCTCCAACAG TCCATATACG AGCAATATGG GGTCCACGGG	180
	GGCTCGCCGG CGCAGCTCAG AGCTGTTCCA GAAGTTCGAG CGATTTCGA AGCGCATAGA	240
20	GCACCTICACC GACCACCCOC TOCTOCACCG CITCCTOCCC TACACACCCC TGATTGCCCC	300
	GTTTTTTATT GTGGCCACGT TCTACGAAGA CTCGATCCGG ATTCTGTCGC AATGGCCGGA	360
05	GCAGGTGTGG TITICTATCCT ACTACCGGCG CTACCCCCCA GTTTTCGTAG TGCTGTTTTT	420
25	GATOGTOGTIC OCOGTOCTICA TICATOGTOGG OGCCALCIATIC ATICCTOCTICC OCAAGCAGCA	480
	GCTGTATGCG ACTGCGATCC TATGCGCGTG TATCATCTCC CAGGATTTGT GTACGGCCTG	540
30	TICICCOOCA CTCCTTCGTG TTTGCGGAAT TICAGCGTAA TCGGCGGTTG CTGATTACTT	600
30	COGTIGACTICC ATCCCTTOCAG AAGCCCATCA CATTCCGCCAT GCTGCCCGCAG CTAACAGCAG	660
	GAAGGCCCAC CAAGGCTACA TCCTGCTTGC GGCCGCATAT CATAGTCTTA GTTTGTGACT	720
35	TTACCTCCCC AAACTGGTGA CGNITCCTCN CCTCGCCQNAC GGTNCTCCCC TCGGTN	776
	(2) INFORMATION FOR SEQ ID NO:217:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 747 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1205RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:	
50	GATCOCACTT CAACCCATTC AAGAAGACOC ACOOCAGTCC OGAOGACGAG AACCOTCACG	60
	TODOCCACAT GOCCAACCTC CTCGCGCACG CAAACGGCGT GGCCGTAGGA TCCGCCGAAGG	120
	ACCCTCTAAT CAAGATTITT OCTOCTACGT CGATTCTGGG CCGTACGGTC GTTGTCCACG	180
55	CCCCCCAACGA CGACTTAGGC CGCCGCCGCA ACGAGGACTC GCTAAAGACG GGCAATGCCG	240

	CCCCCAGACC TGCTTGCGGC GTGATTGGCA TTGCCAACTG ACCTGGCTGC TGCCGCGTGC	300
	COCAACCTCT OCAACCTTCC CAACTACAAG CTCTCATCAC TATGTTACCA GAATAAACGT	360
5	TYTATGGITC GCTGTGTTGG CGCTGTATGT TACAATTGCA GCAATTAGAA GTCTGCTCTC	420
	OCCCCCACC CCACCCTCCC CACCCACTAC CTTCCTTACCA TCTTTCCCCC CCCCACCAAC	480
	AAGCCGAGGA AGGCTOCGA AGGCTTCTAG CACCTTGGAC ATGTTACTCT GGTTGGTACT	540
10	OCCIOGOGAC GITAGIAGOG TIOGICGACG AGCIOGAGAA TCICOCACCG GIOCCGICIC	600
	GICTOTOCCC CONTACTICAG CCAGONOCCG ATTICTOCONC ACTITOGITG ATCCONTACN	660
• 6	ATGAAATNIT CONCCCAAAG AGOCTOCOGT TATTTCTNAN ATGACATOGG TTCCCCCGAA	720
15	AAGIGICIAA ACATCCCTGT CCCCCCN	747
	(2) INFORMATION FOR SEQ ID NO:218:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 777 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
05	(ii) MOLECULE TYPE: DNA (genomic)	
25	(ví) ORIGINAL SOURCE: (A) ORGANISM: PAG1205UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:	
	GATCITCAGG TTCCGCGACA TGATTATCAG CGAGATGGGG TGGCTGCGCC GGCGCCCCGG	60
	CTCCTGCACA CGCTGCGTGA ACTGCTCCGG CTCCGGCAGG TCCTGGGGCA GCACCGCAGA	120
35	GATCATCTTG TOCAGCAGGA TGTCAATGAA GTGCTCCTGC TCCTGTIACCT GAGACACCGC	180
	GCGCAACTIG GCCGCGCCCT GCTCCTCCGT ATCCTCCTCG TCCGACATAC CGGCGCCATT	240
	GTCGCTGGTC TCCTCCTGCC AGAAGCTGTC CGCGCTGCTC TCCAGCTGGT GCCGCAACGC	300
40	GAACTOGTOG AAGTOGTOGT OGATTGTTTT GOGCTOCTOG TCTTTOCCOG TCCGCAGCOG	360
	CTCCCATGTC GCGTCGAACA GTGAGCACGC GATGTTGGTC ACCAGCTCCC GGTTGGTGAC	420
	GCACGGCCGC GCCTTTTCAT CGTCTGCCAC CCTCTCCTCT	480
45	CITIGOGOGOC AGGAATITOCO COAGCAGOGA ACGCOGOTTIC TITGOTIGOCAA TITGOAACGOT	540
	CTCAAGCGCC TIGGTCTATC GTCCTCCTTC ATCGGTCCTC CGCCCCCACG TCATATAGAT	600
	TOCGOCTICOC GOTIAGCACAC TOCCGAAGOC TOCCTTOGITI ATATOCCOCT AGAAGCAGTIC	660
50	TCOCCOCTCA GITACTCCTT TCGTCATCAT CACGTGTTCA CCATCACTCG CATATACAAC	720
	AGTCATCTAT CGATTGAGAA CATACCTATA TAGAAATGAT TTACTGTAAT ATATCGA	777
	(2) INFORMATION FOR SEQ ID NO:219:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 751 base pairs	

(B) TYPE: nucleic acid (C) STRANDETNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1206RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:	
	GATCOCCRICC GICCRCGICG OCTOCTOCRIC CRCGITGAAC TCCCGICCACA OCTTGAACOG	60
45	CCGCGCCGAC AGGTCCACCT TCGCCACCGT CTCCGTCACC ACCTCGGTTC CGAACTTCAC	120
15	GCACTGCGCC TTCATCCGCT CCATGAGGTC GCTGCCCGTT AGCCCGTCGG GGAACCCGGG	180
	GAAGTICTCA ATCTCCGTCG TIGTCGTCAG TIGCCCCCCT GCAGCCACTC CGTTCGCGAA	240
	CATGCCCTCG TACAGCGTCG OCTTGATCTC COCOCOCCCT AGGTAAATOG CCOCAGTGTG	300
20	TOCOGCAGOG CCOGAGOCCAA TGATCGIAAC TITGIGATOC ACCATTCGIG TCTGCAAAGC	360
	TIGICCCAAC COSTATCTIG TIGCIGCIGC TAGCATCAAC TGTGCACCGC TAAGTTICGC	420
	TOSOGCTIGO TOGITTTATA COTOTOGOCT TCACCATOGG TGAACCTIGA TCOCCGITAC	480
25	TATTICCGAC GCITATGICC GCACCIGACA AATTCGGCTT CGCGGGIGCG CGACTGCGGT	540
	CAGTIGGGGG TGCAGTIACAA GATIACGCACC GCGGGCCTIVIT NGNNIVICNINC GGCCCTCTCN	600
	GNEGOCCOCC GNECCTICNE AGGATENTIN CETEANCIAN AACNNEGOCC GENENNTET	660
30	TITTITIGIN CNOCNAACGA AGOCAATINNA ATNITINNIN GONCNINNGT INGAANIGIC	720
	CNNCNGTGGG CATCGCNGCT TATNAACACN C	751
	(2) INFORMATION FOR SEQ ID NO:220:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 778 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1206UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:	
	GATCCGCTGC TCGTGCACCA CCTGCTGCAG GTAGGTTGCT ACTCCACGCG CGAGATATGG	60
50	GIVCTGGTCA ACATCCTACA GCTGACCTGC TTTAACCAGA CAACCAAGGA CAAGTACGAC	120
	COCCOCATCA TCACTICOCG COGAACOGIT TCGACOOCCC TGTCTOCAGA TAAGACCTTC	180
	OCTCAGGAGT TTAACTCCAA ATGTCTCAAC TTTACGACCT OGTGGCACCT CATGGCCCCC	240
55	CTAGACCACG CTGTTTTCAT GTOGTGTCTA GACATTATCG TGGCCGAGAA CTCACAACCC	300

	TTCAAAABCA ACCCCATCAT CCGCGATAAG CTCAACGGCA AGGACTGGGA CTACTACCGT	360
5	GATCTACACG TIGHTGTCAN CTATAGGATT ATCTGCGCCC TGACTCTTAC AGTGCTTCTC	420
	ASCTATCATT TIGGCTICAA TAATCTCTAC GACCTCTCTT TIGTCGACCC AGCCTTCCAG	480
	ATAATACCCC CCCAACAACC GACTTCCCCC ACCTTCCATCC AACCTTTATC AAGAAATCCC	540
10	ATCACAACTA TAAAAAGITC TAGITOCTCG ACTIGIAATC TCATCICTAA ACATAATATT	600
	CTITITATAIG CITGIATIAC TIANOCICAA CAIGAINACN TATOCCIGGA AGAITITOCNC	660
	CNIGOCCGIN AGAACNGATT TGTGTCAACT TNTATAAAAC TGACCCGTGC GCCCCTCCCG	720
15	TAACCCGANA TITICCTGATN CNIGATCCTA TGANGATGCC GOCNCATTINI CANTATTC	778
	(2) INFORMATION FOR SEQ ID NO:221:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 756 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI207RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:	
30	GATCTGTTTC AAAAATTOGA AACOCTTACC ACCTCACCAA CACACCAGGA CTTTATTTCG	60
	TAGAAACAGG CGATCGGCCT GAACAACAGT CACTAGAAAC GGTGCACCAA GGCAGCTTGG	120
	CAACGAGGAG GCACCCTAGG GCTCAATGCG TTGATAGTAA AGCATGTACA CGAGCTTTGT	180
35	CTCCGAGAGA AGGAACGAGG TCTTGCACTC CGACAGGTAC GAGTCTGAGA TACAGCACCA	240
	COOSTICCGIA GIOGIOCCAC GIAAAGCCIT CAGTITICCOG CCACGCCCCT CCGGCACGCCC	300
10	GAGTIACCTTC GTGCCAGCCG AAGATIACCCC CGATGAGCTC GCAGAGCTGG CTCCGGAGCT	360
40	GTCCTGCTCC GCTGACGCGT CGGGCTTGCA GACGGGTTCT TCCGTTAGTA GTGACTGTTG	420
	ATGGAAGCTC CCCAGTAACG GTCTTGAGCA AGCGGCCATC GGCCCAGGCG GAAGGCTTCC	480
45	ASCTSSCSTA GSSCACAGSC ATTOCAGSGG CTGSCTGCGG GACGSCGTCC GACGAGATCA	540
70	CATCTGAGCG AATGATATCT COCCCGTCCT TOGTCCTTCC TAAGTCAGTT TGTTGGCCGAA	600
	CATGCGTTAT OCCCTGAGAA TGGTTGCCAT GTGCTTGATT CATGCGCCAA CAGCTTATAG	660
50	CGAATGCCAA ACCCCCACCA TTGTTIVICCC CNACACTGCT CNTGAGACAC CCCCCCCCGA	720
	AANINAATOC OGITTINITIG TTAAAACCCN TNAAAA	756
	(2) INFORMATION FOR SEQ ID NO:222:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 771 base pairs  (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1207UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:	
	GATCTAATGA GCGATAAGTC ACCOGITATA GAAAGTTCCC CGAATCCTAC AACTGACTCC	60
	AACTOGCCAC AGGAGATATO TOTATTAGAA AAGAATATOA AGGATGTOAT GOGTTCACTA	120
15	AAGGGCTTG ACACGCACTC ATGTGAACAG ATCATTAACG AAATTCTTGT GGTTGATTAC	180
	GATGITCGAT GGGAAGATAT AGCTGGTCTT ACAATAGCAA AGAAGTGTTT GAAGGAAACA	240
	GITGITTACC CATTITTGCG GCCAGACCIT TITICGGGGTC TCCCGGGAACC TATCTCCGGG	300
20	AUGITETTAT TIGGACCTCC AGGAACAGET AAAACGATGA TIGCCAGGGC CGTTGCGACT	360
	GAATCGAATT CAACTITCTT TTGCATCAGT GCTTCCTCTT TGTTATCGAA ATACTTGGGT	420
	CACTOGGAAA AACTTGTCAA GOCCTTATTT TACCTAGCCA AACGGCTTTC CCCCTCAATT	480
25	ATATICATIG ACGAAATOGA CICTOTACTA ACTACOGITO AGATAATGAG AACGAATCAT	540
	CCAGAAGATT AGACGAGCTC TTGGTCCAAT GTCCTCCCTA ACGAGCGCCA CGGCTAGGAA	600
	CAGAGAGGGG AAGAGGCCAG ACGCGTACTG TCTTGGCCGC AACCACTTAC CGTGGGCAAN	660
30	AANGANGCIG CNATAAACIT TTTCACOOGI CIATNATCCC TTOCCOGAAT ACAACNAAAT	720
	GITCTTIGAA AACTINIGOC CTCCAAAAAG AATTICGAAC INATTONNON T	771
35	(2) INFORMATION FOR SEQ ID NO:223:	
<i>35</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 740 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1208RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:	
	GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
50	CTACCIGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
	ATTGAGTITA TATTAAATTC ACCACCTCTT ATTCATTCAT TTAATACTCC TCTAATTCAA	180
	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGTTTAATTG	240
55	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300

	ATCATTAATA TAATAACTOT TTAATTAGAG TIGGIACCAC AAGAATOCTG AAAGCATTAG	360
	GOGTGTGTAC CTTAGCTCTC CTAATTAAAG TTTATAAAAT TATCCTTAAC TAATAAAAAT	420
5	TAAATAAADA AAAAATTTT DTAAAATTTA AATTAATT	480
	AATATGITTA TATTTAAATA GATTCAAATT TOCAACAATT COCATTCATT TAGTACTACC	540
	ATCACCATGA ACAATTGTTA CATCATTAGT TTATAGTTTA CTATACTTAG CTTACTAACA	600
10	TOGTATATOG TATAATANOC CTAATAAACC TTATANANIT TTIACCNAAC TINGATTAAA	660
	AAAAGGGCGA NCNNCTTTGG NGGACCCCTA CCCNTAAAAG GNGTAATGGT TCCCCAATTG	720
	CTCCCCGAAA TAANTTCCCC	740
15	(2) INFORMATION FOR SEQ ID NO:224:	
žθ	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 782 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1208UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:	
30	GATCTTAATT TAAAATTTTA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
	AATIKAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITIG TOOCATCITIA	180
35	ATTTTATTA TTTAATTGAT TATTATCTAT TTAACATAAA ACATTTTAAA ATGTTATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGTA TYTAATTTAA TTTTAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TIAATATTAA GIGATATATA	360
40	ATTTAATTTA TATAAATTAT TTAATTTACT TCCCCTGATA TATATAATTA TTAAATGITC	<b>4</b> 20
	CITICATAAT ATTIATIITT ATTAGICTAG TAATATITCT ATTIAATAGI CTACCCCITI	<b>4</b> 80
	AATIGGATAI TACTACCTAC TAAATATTTA CCCTAATAAT ATATTATTAA GAATACTTAA	540
45	TCCIAATAAT TTATIATCCT AAGITATATA AATTAATTAA TCCTTTTIAT TATTATTTAA	600
	ATTATTATA ATTAGTAATT ATATTTATTA TTTTATTAAC ATAATTTTTG ATAATATATA	660
	TCCATATAAT GGTATTTATT ATATACCNIN ATGAATTAAT GANAACCCTA TATATGANAT	720
50	TAGITATAGI GACTIAATOC CNATCICAAT ATATATAATT ATTATAGAAN ANATACITIT	780
	TC (2) Theorement on the training of training of the training of train	782
	(2) INFORMATION FOR SEQ ID NO: 225:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 533 base pairs	

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1209RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:	•
	GATCAGCCTA TGTAGCAACT CATCGGCGCT GGTCCGTGTC AAACGCCGAA AACACCCCAC	60
15	CAGATTACOC AGACACTOCC ATATTITGAC OGACTOGAAC TITIGTGTACA CAAAGCTATT	120
	CAGCITIGICA CIGGOCACOG TCAGOGOCAT GITGITCAGO OGAGICOCTA GOOCOGCACT	180
	OCTIGITICOCC TOCGOCAGOG AIGOCTCCTT AAGATCCTCC GITICOCATAT ATTGCGCAAA	240
20	CITOGATAGG TCTCGACTGA GOGAATTACC GACATGGTCC AGTAATAACA ACACCCCAGG	300
	GCAGCCCCCC CAGCTGTAAT TCACCGTTTT GACCAGCAGA AAGTGCAATT GTAAAAGAAT	360
	GTACCAGTAA TOOCAGTAAA ATGTOGAAAA CACCTOGTOG TTCTGAAGAT ACCAAATCAT	420
25	CACCIGAAGA TICIICAGIC TICICCGICC CGAACATCTI GGAAAAAATCI GCNGNICGIC	480
25	CCTTCTCTTC CACTCCAACC CCACCCCTTC CAACCACACT CCTTCCAATT CAA	533
	(2) INFORMATION FOR SEQ ID NO:226:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 534 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1209UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:	
	GGAGGATOGT CGAACTIGAT TATTITICTIC TGGIACGACG ACACCICGIC CGCGITCCGC	60
	TITIAACOCCA CCAGCACCAC GIACITICITC GACCOCAGCC CGACTGTGGC GCTCCCCTGC	120
45	TIGATOSCCT CTASCOCGIA CICCACCTOG AACAGTCTCC CAGTCOGGGA AAACGTCACA	180
	GTATCACCGT CGTAGTTATT TCTGAACATC ACTAACTCAC AGNOCCCCAA TTGNTCGTGC	240
	ACACCOCCCT CTTTACTOGT OCTAGTTAAC TOGACAGGAG CTGTGTTTGC CACCCGGCCG	300
50	CCCCAACTAC CICTOCTATT GICATTICAT ACCCACATTT CATATICCIC CAAACCTATA	360
	TAGATGATTC CGTCTCCCCG ATTGATTGGA GCCTCGGTCG CATACTGGAG TCGTCCGANG	420
	TETCENATOT TOTACATAAC CETTENAGEN CAGOGEAGAG ETTTENINGE GEAGTTETCE	480
55	COGAGTACCA TATTAGGCGA TGTGCGGTGA AGAGGTATCT ACTGGTGGTG TTAT	534

	(2) INFORMATION FOR SEQ ID NO:227:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 547 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1210RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:	
	GATCIAAAIT TATCAGCCCA TOGACGGATG GATTTACGGC AGCGTGTCGC CGCAGCACGG	60
	GGCACGCCAG ACTGCGAGGT GGCAAATAAT TCACATAGCA ACCTGCATTA TAAACATCCC	120
20	AAGICATTAA ACTTACTAAA TATTGTTGCG TAACCAAAAG CACCGTGTAT CATCATCTTC	180
	ATAGICITAG CIGAACCTAC TGICOCACCA OCCCITTACT ACGIATIGIA ICTCCCTTIT	240
	ACAATGCTTG CCCACTGCCA GTTTTCCGCA CGGGGGTTAG CATGAAGTCT TTGCCGCCTT	300
25	TGTACCACGG CTTGACGTCT GACTCTACGC GGACCAACGA GGTTAGACGG AGTGCACCGG	360
	GGACCGAGTC ATCCTCGCTC GCGTGTTCCC AGAGACAATT TGAGGTTCCA CGGAGCATCC	420
	ACGCCCATGC AATCCTGCCC GTAAAAGITT GCACANITCA TCCCACACTT GGGGGGTINI	480
30	TATCACNCCA NCCTGATCTG GTACGNAAAA MTTTCCNIN TTTGGTGAGG AAATCAGGTT	540
	CCCAATA	547
	(2) INFORMATION FOR SEQ ID NO:228:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 600 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1210UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:	
	GATOGAGAAG ATGCGGCGCC OCAACGAGGC CGCCACGCCC GAGGCGGGGC GCNACGAGCT	60
50	CCTGACGCCG GCGCAGCGCT ACGCGCTGCA GCAGGGGCAG GGCTTCCTGG CGCCTGTCGT	120
	CCCTGTGGGN GAGCGGGCNC GGCCCCTGGC GGTGCCCTGC AACGAGCTTC CCGATGAATA	180
	CTOCATCACC AAGACTGACT TCGACCOOCT COCTAOCCAC GOCATCCCOG TCGAGGACGT	240
55	CCACGAGGAC AGCAAGGACT GGTACTTCCA GTGCCCCTGT GGAGTAGAGG AGGTTAGCCC	300

360

GEGCCTAGAG AGCCCCGCGC TGCAGCAGGC CCTGGTCTGC TGCGACCAAT GCCTCCGCGT

	GOCAGCAGCT GOGACTOCCA GCACCCCGCA GCGATTGAGC TTOCTGGCCN GCGGGCAAGA	420
5	CTCCTCACTA TITTISCCCTC CIVIGCCCCCT TGGCCTOCCC CACGCGCCCG CGCCCTCACG	480
	GOCGGNENCG GOCGGNAAAC CCCTIACCAGA ACCAAANNAA CNACGCCNCC GCCGCCCNTC	540
10	GETGAAGCGA ACCCTITTIN NCTCCTGTCT TCCCNCCCTG AAAGACCTAN TTCTCCTTCA	600
70	(2) INFORMATION FOR SEQ ID NO:229:	•
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 539 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1211RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:	
25	GATCTCCTCC AGTAATGGCG TCAGAGCACA CTGGTAGCGG ACCCCTGCCA GGTAGCTCAT	60
	COCCAAAAAG ATACCACCCC TATGTACCCA CCACCGACCC CCCGTGATAAG GAAACTGGTA	120
30	COCCACCACC CATACCTCTG GTGCCCCTGG GTTCACCCCC TCCCACTTGT ATAAATTGAG	180
	CACGGAAAGC CACACTITIAC CCCAGTACGG CGAGCCAATA GCACCCCCCA TGCGCAGCAG	240
	GETCTTCCGC GCCCGCTGCA TCACGATGTG TTCGCGCTCC ATCCCTAAGA GCCGCAGCAG	300
35	AACGIAGITIC AGCGCGGTGC CCATCGACAG TCGACTTGTC CTCCGAATGC AATCCCCACC	360
	COCCGTOGAC AGGTGTOCCG TGTTCACCAC GTTAGCGCAC TAGCTCCCGC CGCTGAGGCT	420
	CAGGAATACC ACCCCCCCA CATGCATCGC CACCACATAC CCATATCATN ACATCNGGCC	480
40	CCCTGTTACA ACAGGAAANT GCCCNAACCT CCTCCTGCAG ANGGCCCAAA CCGCCCCCG	539
	(2) INFORMATION FOR SEQ ID NO:230:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 593 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1211UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:	
55	GATCTACATC ATGGGAGGCT AGGAAGAGCA AGGCACCGCG TGCATTTGTA GACTACACGC	60

	TATAATATOC AAATOOCCAA TACCTTTGCC CCGCATCCAA AGAAGGGCAC TGTCAAGCAT	120
	ATGGTTATCG AGACGAGCTT CAACCACTTG GCTCTAGGCA TGGTCAGCCA GATATTTCCG	180
5	CACTAAACAA COTCTAGAAA ATGACTTGAC CTATGACGTG CCGGGCTTGA CTCATCTTAC	240
	TATOCTOAGS COCCOCCTC TICTITOGOGA GCATGOCTCT AAACCCGTAA TAAGCCCTAC	300
	CAACCCTGAT ACAGGAAACA TOCTTACOCG CTGTTACACT TATAAGAAGA ATGTTATOCG	360
10	CACCCAATIT AATTOCCTTG COCCAGTITA AGAAGTTOCG CCAACACTAA GTCACCCGAA	420
	CTATCCGCGA AGOCTACCTA TCATTTACCC TGGAACTGGA TIGTTIGGCT ACTCANTCCC	480
	CACCIVIGADA ATTOCCCCINA ATTOCCCCCTC CAGADINOCOT ATCCCADOGA ACTACTOGAC	540
15	CAAATCIAAT TICCCCTATA ATGIGAATTA CACTGTNAAT TCAGAANIGA ACN	593
	(2) INFORMATION FOR SEQ ID NO:231:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 536 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1212RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:	
	GAGATCTCCC AGTACGTCTT CAAGCTGCCC TTTTGCCCGTC TAGGATAGAG CCCGCCGAAC	60
	TCAGGACTGG TCGAGACGGG ATGCTGGATC CCGAAGCTCT TCATAAGCAA CAACCGCGGT	120
35	TOCCOCCIUT ACTOATOCAA COGTOCCTOA GOGAATOCTG CGAGTOTOCA COTGACATOA	180
	CCATTGCCCA CGATGCACCG AAGCGTTTCT GGAAGGAACA CGCAAACTAG CAAGAAGCCG	240
	ATOCCOOCCA TGATOCTAGT GAAACCAAAC AACCATCTOC AACOGTCATT ATOGAATAGG	300
40	ATCAAGCCAG CAATAATIGGG COCCCAAAAT COGGCCCACN TITTAGCCCCC CAACATNAAT	360
	TACGCAATIG CCTIGCCGGG GTITTICGGN GGIGTIGATT TCNCTTACCG TACGGGCCCC	420
	TGACAAAAGG AGAACTONGA GGAAATGCTG CNCCCCTNIT AAAAAAAATAC NCCCATOGNG	480
45	CAGGNIGAAA GCANTIACNC ITGACTATAA ATCANCCCCC GANAANNITA NACTOG	536
	(2) INFORMATION FOR SEQ ID NO:232:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 586 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
50	(A) LENGTH: 586 base pairs (B) TYPE: nucleic acid (C) STRANDELNESS: single	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:	
5	GATCAGCAGT GTCTTCCGGG ACGTCAACGG CTTGACGGTC TTGCGTACCG TGGCCAGCGT	60
	CCGCACGCCA TGAAATGCCT GCACTGCCTG CCGCAGTCCA CAGTTGCCGCA GCGATGCCAG	120
	ACACGAAAAC ATCCTCGTTA ATGCAGCTTG GGTCCTTCCG TCGTCACTGT GCGTCTCGAT	180
10	TAAGCCCAGG TTATCAGTAA CATCAAAATT TTACATAACT GCCACGTGAT ATACACGTGA	240
	TAAAGATCTA CACCCATGCC CCCTGATTGT GTAAAAAAGC AACTTTTGAA AAATTTTCTA	300
	COGTICCATC CGATGAGATG AGCTTAGCCT AGTGCGAGTC CAATATCAGT GCACTAAGTT	360
15	TATOCAGIGA TACTIGITOT CGAGCITICA GCAACAGCAT CAGITTACAA ATOGCACCAG	420
	CAGITATOCC TOGAAAGAAA TOCTACOGTIC CGAACTOCCA TGATAGITTG ATACOGCOCT	480
	TACAGACOCC AGCGAAAATC CCACATCTCC NGGNGGCTTC AAATNINGTT CCGNGGTTCT	540
20	AAAOCTTAGG GGNATICCCA TOCANOGGIT TATNAAATIT GANAAT	586
	(2) INFORMATION FOR SEQ ID NO:233:	
25	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 535 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEINESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
	(ii) MOLECULE TYPE: INA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1213RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:	
	CATCHTHIT AGAGACTICA GIGICOCCAC CAACACOGIC OGAGOCCCTI CACCTACTIC	60
	CAGAAGGICG TAAAGAGICT CCAGTAGCCC CAGGGIGCGC TCGIGGICAT AACAGICCAT	120
40	CTGAGGTAGC GTGTTAATAA CCGCTTTCAG CATGCTCGTA GAGGACTTCT TTACTAGGGC	180
	AGAACITATA AACITAAATG TCTOGTCTAT GCATTCAGGG GTACGAAGAG CTGCCAGTGT	240
	COGAATGICA TCAGCOGATO TOCTOGITTI ACTITICCICA GAATOGOGOO ATAGTITAAC	300
45	TINCHGITICCC AAATTAACCC GGITTCCCNG GACCCTTTTIN AACAAAAAGG AAAAAAAATT	360
	CCGTTTCCCC CCCNCTNCCC NNNVTGCGCN AAAAATTTTT TNCCNCGGCN AAAATTTANC	<b>4</b> 20
	CCCCCCNCTT AAGNCCCATT AAAAAAAAN NNNNNTTT TTTTTTTTTTT NGGNGCCCNN	480
50	NAAAAANIN CCCCINITIN NAAAANNCIG NGCNITINING NIINANANIN NAINN	535
	(2) INFORMATION FOR SEQ ID NO:234:	
55	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 603 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	

(C) STRANDEINESS: single (D) TOPOLOGY: linear

(VI) ORIGINAL SCURCE: (A) ORIGINAL SCURCE: (A) ORIGINAL SCURCE: (A) ORIGINAL SCURCE: (A) ORIGINAL SEQUENCE DESCRIPTION: SEQ ID NO:234:  GATCOCCCAC TYCA-GAACT CO-ACCTOCOC AGGCGGGGG CCCTCCCCCC CTGCCTCCTC  GCCCGCTAC CCCCCCTTCA CATACACCTA GAACCCCCC CCCCCCCCCC	5	(ii) MOLECULE TYPE: DNA (genomic)	
GATCOCCCAC TICACGAACT CONSCITCOR ASSOCIAAAC GITGICGCCA GETCOCCCTC GCGCACGCC CCCACGITCA CATACACGTA GAACCGCCCC CCCTCCGCCC CTGCCTCCTC GCGCACGCC CCCACGITCA CATACACGTA GAACCGCCCC CCCTCCGCCC CTGCCTCCTC CAACCGCACG TICATCTCCG TIACGTATGT CACCGCTTC ACCTGGTACC CCACCGCCCG GCCAGGCAC TIGICCCACA CTTCCTCGTG CACCGCCTC ACCTGCTCC CCCCCACCGC GCCAGGCAC TIGICCCACA CTTCCTCGTG CACCGCCCC GCCCTCCACC GCACGCCCCG ATGCACGCAA ATCCCCTCTC GAATCCCTTT GCCCTGCCC GCCTTCCCGT GTCTGCGCCCC ATGCACGCAA ATCCCCTCTC GAATCCCTTT GCCCTGCCC GCCTTCCCGT GTCTGCGGTT GATTCCCACG AATCCTGAAC CAAACTCACA CATTITCCCA AAACAAACC CAATGTCTCT CTT  30  (2) INFORMATICN FOR SEQ ID NO:235:  (1) SEQUENCE GAARACTERISTICS: (A) LENGTH: 527 base pairs (B) Type nucleic acid (C) STANDEDRESS: single (C) STANDEDRESS: single (C) STANDEDRESS: single (D) TOCCCGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  46  GATCGTTCAC GTCAGCCAAT TCTGTGTGT ACCCACTAC ATTGTAGACT TRACAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CACCTTCTGT AGTCTCCCTA TRACAGATTA TTTCATCTC AACGGTATGT CTTGAACGCG GCTTTAAGGA ACCCTTCATC GAAGTACTGC ACTTCAACT CTTGTGGTG ACCGAATG TTAGCCGGGG GTTCTAGCA TAACCTCTCC ACTTCAACT CTTGTGGTG ACCGAATG TTAGCCGGG GTTCTAGCT TAACACTTCC TTACTGCCAG AACCTTGTGGTG ACCGAATGTTC TCCCAICTGG GTTAAAGTA AACCTCTCCCCACG GACCACGATG TTAGCCCGGG GTTCTAGCT TAACCACTTCC TTACTGCCAG AACCTTGTGGTG ACCGAATGTT TCCCAICTGG GTTAAAGTA AACCTCTCCCCACG GACCAACGAA ACTTTAACCTG GCCCTTCCAG TTTTTGTTTCT TTACTGCCAG AACCTTGTGGGG ACCGAACGAA ACTTTAACCTG GCCCTTCCAG TTTTTGTTTCT TTACTGCCAG AACCTTGTGGGG CCCCCAGTGCTAACGAACTTC TCCCAICTGG GTTAAAGTCA TTTACTGCCAG AACCTTGTGGGG ACCGAACGAA ACTTTAACCTG GCCCTTCAGG TTTTTTTTTT		·	
CCCCCCCTAC CCCACCTICA CATACACCTA GAAGCCCCC CCCCCCCCCC CCCCCCCCCC	10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:	
CCCCCCCTAC CCCCCCCCA GCCCCTCACT CACCCCCTTC ACCTGGTACC CCACCCCCCC  CAACCCCACC TICATCTCCC TTACGTATGT CCCCACTCT CCCCCGTGC CCCCACCCC  GCCCAGCAC TIGTOCCACCA CTTGCTGTG CACCCCCCCC CCCCCCCCCCC  GCCCAGCAC CCCCCGTCTAT CGTGCGGGT CGTCTGCGTC ATTGCTCCT TGCGCCCCCG  ATGCACGCAC CCCCGTCTAT CGTGCGGGT CGTCTGCGTC ATTGCTCTC TGCGCCCCG  ATGCACGCAC ACCCCCTCTC GAATCCTTT GCCCTGCCCC GCCTTGCGGT GTCTGGGGTT  GATTGCCACG AATCCTGAAC CAAACTGACA CATTTTGCCA AAACAAACGC CAATGTCTCT  CCAACGAATT TCNCANTCTC GTTGAACTAA CCCCCCCCC CAGTTGGGTG AAACCACCTGC  TGTTCCCACC TATCCGGTAG GGTTCAGCCT TCCTGTCNITT CCACTANTGG NAAACNCCTG  CTT  (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 527 base pairs  (B) TYPE: nucleic acid  (C) SERNDEDHESS: single  (D) TOROLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE:  (A) ORGANISM: PAGI214RP   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45  GATCGTTCAC GTCAGCCAAT TCTGTGTCGT AGCCACTAC ATTGTAGACC TTATAGATTA  AACCTCGAAT GCAATCATTG GGGTAAGCCA CACCTTCTGT AGTCTGCCTA TAGCAGAACT  TTTCATCTTC AAGGGTATGT CTTGAAGGCG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTGCGG GCCTTCAGG TTTTTGTTTCT  TTACTGCCAG AACTTGTGGG GCGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTC  TTACTGCCAG AACTTGTGGG GCGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTCC  TTACTGCCAG AACTTGTGGGG GCGGCATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTCC  TTACTGCCAG AACTTGTGGG GCGGCATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTCC  TTACTGCCAG AACTTGTGGGG GCGGATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTCC  TTACTGCCAG AACTTGTGGG GCGGATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTTCC  TTACTGCCAG AACTTGTGGGG GCGGATGGT AGGAATTTTC TCCCATCTGG GTTAAGCTGC  TTTTCTTCCATCTCCATCTCCCTCACGG GCTTAAGCACACCTCTCTCTCTCTCTCTCTCTCTCTCTCT		GATCGCCCAC TICACGAACT CCAGCTCCGC AGGCCGAAAAC GTCGTCGCCA GCTCCGCCTC	60
CALCOCAGE TICATOTICOS TRACSTATES CACACITET COCCAGENCE CACCOCAGO CACACOCAGO CACCAGO CAC		GCGCGACGCC CCCACGTTCA CATACACGTA GAAGGGCCGG CCCTGCGCGCGC CTGCCTGCTC	120
CACCAGGAC TOTOCCACCA CTTOCTOGITG CACCGCCCCC CCCCCCCCA GGATGCACTIG  CAGCAGCAC CGCCGTCTAT GGTGGGGGT GGTCTGGTC ATTOCTCTC TGGGCCCCG  ATGCAGCAA ATCCCGCTCT GAATCCCTTT GGCCTGCCC GGCTTGCGGT GTCTGGGGTT  GATTCCCACG AATCCTGAAC CAAACTGACA CATTTTGCCA AAAGAAACCC CAATGTCTCT  CCAACGAATT TGACGGTAG GGTTCAGCCT TCCTGTGNITT CCACTANIGG NAACCCCTGC  TGTTCCCACC TATCCGGTAG GGTTCAGCCT TCCTGTGNITT CCACTANIGG NAACCCCTGC  CTT  (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS:	15	CCCCGCGTAC CGCCGCCCA GCGCGTGAGT CACCCGGTTC ACCTGGTACC CCAGCCCCG	180
20 CASCAGCAC COCCRICTAT CRICGOGGET CRICTOCGIC ATTOCTCC TOCCCCCCCG ATGCACGAA ATCCCCTCT GAATGCCTT GACTGCCCC GCCTTGCGGT GICTGGGGTT  GATTGCCACG AATCCTGAAC CAAACTGACA CATTTTGCCA AAACAAACGC CAATGTCTCT  CCAACGAATT TCNCGNICTC GITGAACTAA CCGCCCGCC CAGITGGGTG AAGCCCTGC TGTTCCCACC TATCCCGTAG GGTTCAGCCT TCCTGTGNIT CCACTANIGG NAAACNCCTG  CTT  30  (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1214RP   (SG) SEQUENCE DESCRIPTION: SEQ ID NO:235:  46  GATCGTTCAC GTCAGCCAAT TCTGTGTCGT AGCCCACTAC ATTGTAGAGC TTATAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CACCTTCGT AGTCTGCCTA TAGCAGAACT TTTCATCTTC AACGCTATCT CTTGAAGCG CCTTTAAGGA ACCCTTCATC GAAGTACTGG  60  GICTTTCTAC CCCTCCCCCG GACCAGCAC ACTTTGCCGG CTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTGCCGG GTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTTGCCTG GGCCTTCAGG TTTTTGTTTCT TTACTGCCAG AACTTGTGGGG CCGTGTGGT AGGAATTTTC TCCCATCTGG GTTTAAGTTTC		CAACCGCACG TICATCTCCG TIACGTATGT CCCCAGCTCT CCCCCGTCGC CGCCCAGCGC	240
ATCACCCAA ATCCCCTCTC GAATCCCTTT GECCTGCCC GCCTTCCGGT GTCTGCGGTT  GATTGCCACG AATCCCGTAC CAAACTGACA CATTITTCCCA AAACAAAACC CAATGTCTCT  CGAACGAATT TCNCGNICTC GTTGAACTAA CCGCCGCCC CAGTTGGGTG AACCCCTCC  TGTTCCCACC TATCCGGTAG GGTTCAGCCT TCCTGTGNIT CCACTANTGG NAAACNCCTG  CIT  30  (2) INFORMATION FOR SEQ ID NO:235:  (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDERNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI214RF  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45  GATCGTTCAC GTCAGCCAAT TCTGTGTGGT AGCCCACTAC ATTGTAGACC TTATAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CACCTTCTGT AGTCTGCCTA TAGCAGAACT TTTCATCTC AAGCGTATGT CTTGAAGGG GCTTTAAAGA ACCCTTCATC GAAGTACTGG  50  GTCTTTCTAC CCCTCCGGG GACCAGGAT TTAGCCGGA CTCTCAATC AAACTCTTCC ACTTCAAACT CTTGTGGTGG ACCGAACGCA ACTTTAGCTG GTCTAAGGTTTCT		OCCAGOCAC TGTOCCAGCA CTTOCTCGTG CACCOCCCC CGCGCCCGCA GGATGCACTG	300
GATTOCCACG AATOCTGAAC CAAACTGACA CATTITGCCA AAAGAAACGC CAATGICTCT  CGAACGAATT TONCONICTC GITGAACTAA CCCCCCCCC CAGTTGGGTG AACCCCTCC  TGTTCCCCACC TATCCGGTAG GGTTCAGCCT TCCTGTGNIT CCACTANTGG NAAACNCCTG  CTT  (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 527 base pairs  (B) TYPE: nucleic acid  (C) STRANDERNESS: single  (D) TOROLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE:  (A) ORGANISM: PAG1214RP   (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGTTCAC GTCAGCCAAT TCTGTGTCGT ACCCCACTAC ATTGTAGACC TTATAGATTA  AACCTCGAAT GCAATCATTG GGGTAACCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT  TTTCATCTTC AAGGGTATGT CTTGAAGGGG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GTCTTTCTAC CCCTCCCCCG GAGCACCCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTTCT  TTACTGCCAG AACTTGTGGGG ACCGAACCCA ACTTTAGCTG GCCCTTCAGG TTTTTGTTTCT  TTACTGCCAG AACTTGTGGGG ACCGAACCCA ACTTTAGCTG GCCCTTCAGG TTTTTGTTTCT  TTACTGCCAG AACTTGTGGGG ACCGAACCCA ACTTTAGCTG GCCCTTCAGG TTTTTGTTTCT  TTACTGCCAG AACTTGTGGGG GGGGAACGCAA ACTTTAGCTGG GTTAAAGTTCC	20	CASCASCASC COCCGTCTAT CGTCCCCCCT CGTCTCCGTC ATTOCTCTCC TGCCCCCCCG	360
CGAACGAATT TONOGNICTO GITGAACTAA COGCOGGCC CAGITGGGIG AAGCCCCIGC TGITCCCACC TATCCGGIAG GGITCAGCCT TCCTGTGNIT CCACTANIGG NAAACNCCTG CTT  30 (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: mucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGTICAC GICAGCCAAT TCTGTGTCGT ACCCCACTAC ATTGTAGACC TTATAGATTA AACCTCGAAT GCAATCATTG GGGTAACCCA CACCTTCTGT AGTCTGCCTA TAGCAGAACT TTTCATCTTC AAGGCTATGT CTTGAAGGC GCTTTAAGGA ACCCTTCATC GAAGTACTGG 50 GICTITICTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG GCCCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG GCGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGGTCC		ATGCACGCAA ATCCGCTCTC GAATGCCTTT GCCCTGCCCC GGCTTGCGGT GTCTGGGGTT	420
CGAACGAATT TONCONTOTE GITGAACTAA CCGCCCCCC CASTIGGGIG AAACCCCTGC  TGITCCCACC TATCCGGTAG GGITCAGCCT TCCTGTGNIT CCACTANTGG NAAACNCCTG  CIT  (2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: INCleic acid (C) STRANDEDNESS: single (D) TOROLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGTTCAC GICAGCCAAT TCTGTGTCGT ACCCCACTAC ATTGTAGACC TTATAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CACCTTCTGT AGTCTGCCTA TACCAGAACT  TTTCATCTTC AACGGTATGT CTTGAAGGC GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GICTTTCTAC CCCTCCGCCG GACCAGGTG TTAGCCGAG CTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CCCCTTCAGG TITTGTTTCT TTACTGCCAG AACTTGTGGG CGGTCATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC		GATTOCCACG AATOCTGAAC CAAACTGACA CATTTTOCCA AAACAAACGC CAATGTCTCT	480
(2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRUBENESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGTTCAC GTCAGCCAAT TCTGTGTCGT ACCCCACTAC ATTGTAGACT TTATAGATTA AACCTCGAAT GCAATCATTE GGGTAAGCCA CACCTTCTGT AGTCTGCCTA TAGCAGAACT  TITICATCTIC AAGCGTATGT CTTGAAGGCG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GTCTTTCTAC CCCTCCCCGG GAGCAGGATG TTAGCCCGAG CTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG GGCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC	25	CGAACGAATT TCNCGNICIC GITGAACTAA CCGCCGCGCC CAGITGGGIG AAGCCGCIGC	540
(2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGITCAC GICAGCCAAT TOTGIGITGIT ACCOCACTAC ATTIGIAGACC TIATAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT TITCATCTTC AACGGTATGT CTTGAAGACG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GICTITCTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTCC ACCTTCAACT CTTGTGGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT TTACTGCCGG AACCTTCTGG GGGTAAGGTTCC TTTACTGCCGA AACTTGTGTGG CGGTTAAGTTCC		TOTTCCCACC TATCCGGTAG GGTTCAGCCT TCCTGTGNIT CCACTANTGG NAAACNCCTG	600
(2) INFORMATION FOR SEQ ID NO:235:  (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAGI214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATCGTTCAC GTCACCCAAT TOTGTGTCGT ACCCACTAC ATTGTAGACC TTATAGATTA AACCTCGAAT GCAATCATTE GGGTAAGCCA CACCTTCTGT AGTCTGCCTA TAGCAGACT  TTTCATCTTC AAGCGTATGT CTTGAAGGG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GTCTTTCTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTCC ACTTCAAACT CTTGTCGTGG ACCGAACCCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT  TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC		CTT	603
(A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  45 GATOGITCAC GICAGCCAAT TOTGIGICGT ACCCCACTAC ATTGIAGACC TIATAGATTA AACCTCGAAT GCAATCATTG GGGTAACCCA CACCTICTGT AGICTGCCTA TACCAGAACT  TITICATCTIC AACCGTATGT CITIGAAGGC GCTTTAAGGA ACCCTICATC GAAGTACTGG  50 GICTITCTAC CCCTCCGCGG GAGCAGGATG TTACCCGGAG CTTCTGAATC AAACTCTTCC ACTTCAAACT CTTGICGIGG ACCGAACGCA ACTTTACCTG CGCCTTCAGG TITTGITTCT TTACTGCCAG AACTTGIGGG CGGTGATGGT ACGAATTTTC TCCCATCTGG GITAAGTTCC	30	(2) INFORMATION FOR SEQ ID NO:235:	
(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1214RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:  GATOGTICAC GICAGOCAAT TOTGTGTOGT ACCOCACTAC ATTGTAGAC TITATAGATTA AACCTOGAAT GOAATCATTG GOGTAAGOCA CACCTICIGT AGTGTGCCTA TAGCAGAACT TITCATCTIC AAGGGTATGT CTTGAAGGG GOTTTAAGGA ACCCTICATC GAAGTACTGG  GTCTTTCTAC CCCTCCCCCG GAGCAGGATG TTAGCCGGAG CTTGTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC	35	(A) LENGTH: 527 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
(Xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:  45 GATCGITCAC GICAGCCAAT TCTGIGTCGT AGCCCACTAC ATTGIAGAGC TTATAGATTA AACCTCGAAT GCAATCATTG GGGTAAGCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT TTTCATCTTC AAGGGTATGT CTTGAAGGGG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GICTTTCTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTCC ACCTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC		(ii) MOLECULE TYPE: DNA (genomic)	
GATOGITCAC GICAGOCAAT TOTGIGIOGI AGOCCACTAC ATTGIAGAGO TITATAGATTA AACCTOGAAT GCAATCATTG GOGTAAGOCA CAGOTITCIGT AGICTGOCTA TAGCAGAACT TITCATCITC AACGGTATGT CITGAAGGOG GCTITAAGGA ACCCTICATC GAAGTACTGG  GICTITICTAC COCTCOGCGG GAGCAGGATG TITAGCCGGAG CTICTGAATC AAACTCTTGC ACTTCAAACT CITGICGTGG ACCGAACGCA ACTITAGCTG CGCCTTCAGG TITTIGITTICT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC	40	·	
AACCTOGAAT GCAATCATTE GGGTAAGCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT TITCATCTTC AAGGGTATGT CTTGAAGGCG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  50 GTCTTTCTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTGC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:	
TTTCATCTTC AAGGGTATGT CTTGAAGGG GCTTTAAGGA ACCCTTCATC GAAGTACTGG  GICTTTCTAC CCCTCCGCGG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTGC  ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT  TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC	45	GATOGITCAC GICAGOCAAT ICIGIGIOGI AGOCCACTAC ATIGIAGAGO TIATAGATTA	60
GICTITICTAC COCTCOGCOG GAGCAGGATG TTAGCCOGAG CTTCTGAATC AAACTCTTCC ACTTCAAACT CTTGTCGTGG ACCGAACGCA ACTTTAGCTG CGCCTTCAGG TTTTGTTTCT TTACTGCCAG AACTTGTGGG CGGTGATGGT AGGAATTTTC TCCCATCTGG GTTAAGTTCC		AACCTCGAAT GCAATCATTG GGGTAAGCCA CAGCTTCTGT AGTCTGCCTA TAGCAGAACT	120
ACTICABACT CITIGIOGIGG ACCGAACGCA ACTITAGCIG COCCITCAGG TITIGITTICT TITACIGCCAG AACTIGIGGG COGIGATGGT AGGAATITTIC TOCCATCIGG GITAAGITCC		TITCATCTIC AAGGCTATGT CITIGAAGGCG GCTTTAAGGA ACCCTTCATC GAAGTACTGG	180
TTACTOCCAG AACTIGIOGG COGIGATOGT AGGAATTTIC TOCCATCIOG GTTAAGTICC	50	GICTITICTAC CCCTCCGCCG GAGCAGGATG TTAGCCGGAG CTTCTGAATC AAACTCTTGC	240
		ACTICAAACT CTIGICGIGG ACCGAACGCA ACTITAGCIG CGCCTICAGG TITIGITICT	300
55 TICCATATON ATTGACACTG CACGCCCCAA CATTONAATT TOCANANCCC CTACCCCCCC		TTACTOCCAG AACTIGIOGG COGIGATOGT AGGAATTTIC TCCCATCTOG GITAAGTTCC	360
	55	TTCCATATON ATTGACACTG CACGCCCCAA CATTONAATT TOCANANOCC CTACCCCCCC	420

	MANATELLAA IIII CAGGI ILAMAGGACI TAICMACCI MICAATITI CIIMAATMAA	480
	CICCATITGI CCCNAACNAA CAATINAATI CCCCTGITCC TICCCNA	527
5	(2) INFORMATION FOR SEQ ID NO:236:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 597 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1214UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:	
20	GATCAAGACC TGACGGCTTC CTAAAATCGC TAAGTTTAGT ACATAAATTG CGGCAAGAAT	60
20	TACCCAAATC ACCTRCTGTG GAGATACGAG GCAAGCTGAG CROGTRGGATG TRCCCCATTRCC	120
	ACACCAGTAA CTCTTTOGTG TGTGGCTGTC ATGGTACTGC TCGCTACCGC CGTGTTCACG	180
25	OCCUTICATORA ACCOCIAAACCA ACCOCIAA ACCOCAAATCA TOTAACACCO ACCOATAACT	240
25	CCACGAGCAG ATOCTICAGAG OCTICGACCAG AACGACGTCG CATGGGTGAT GCTACAGATG	300
	CCTATOCGIG TGACAGGICG AAGCAACIGI GITCTGCITC AAGTAATAGC CAAACTTGGC	360
20	COCCTAGAGA ATGACACTOC CETETCTGTG CATATGTTGG CACTATGCAA GGTTACAGAT	420
30	TOSCAASCTG COCGAATGIT GSCCCAAATT CGAACAACCA GCCAGCTATT GGTATGGAAT	480
	TATATACAAC TTGGINGGGG AGGAATTCCG GIGAAAAACG GCGCACCAGG NAACTTTACT	540
0.5	CCAACGGCAA NCGGGNAATT TCCCCCCCNC CCCGGGTTTT TGCAACCGGC CCCNTTG	597
35	(2) INFORMATION FOR SEQ ID NO:237:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 754 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1215RP	
	(xi) SPQUENCE DESCRIPTION: SEQ ID NO:237:	
50	CATCAGAGCA AAGTGATTCA AAGCGATTTT GGACGACGCG TAAGCTGCCA CCGCAGGATG	60
	OCCCATCTGA CTGAGCCCCG AGGTTACGGC AATGAAAGCG CCCTOCGACT TACGTAGCAG	120
	TOGAAGCOCC TTGCTGCCCA GATTCACGAC GCTAAACAGA TTAATCTCGA ATAGGCGTCT	180
55	CCATTCCTTG ATGTCCGCCT CCGCGATGCG TTGTTGGTAC GAGACACCCG CGTTCGCTAC	240

	GACAGOGTOT AGCOGOCCAT ACTOCGAGGA CACCTTATOG ATCAGGGCOT GCACCACACG	300
	CTCGTCAGTG ACGTCTCCGA CAACATAGTC GAATTTCTTG CCATGTCTCG CCTTCAGCTC	360
5	CTGCAATTIG GITTCCGCCC GTGCAACCCC TACTACAACC ACGICGGGGG TTGAGCACAA	<b>4</b> 20
	TOTGTCAACG GTT0CC0CCC CAATOCCACG CGAT0CACCT GTCACAATTA TAACCTTCAT	480
	TOTTGOTTGG TACTTTATOT TOAATGGGCC ACGAACGCTC CCGCTGTTAG TITTATATATG	540
10	ACTICAGGG CIGITGGCAC AGCICACTAG CACACTACCC TICACATGIC ACACCAGTIC	600
	GAGAATGAAT GGCACAGTTC CATTTGTAAT CATGATTATC AATACAATAT GTGTTGTAAT	660
	TATTGATTTG TAATATOCAT AATATAGATG GITATGATTT GTAATACAGT AAATATACOG	720
15	TAAATATAAA GIATTTTAAG GAATATTTAT AATT	754
	(2) INFORMATION FOR SEQ ID NO:238:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 776 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1215UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:	
	GATCGCCCGG GGCCTACGTC ACTGCAGATT GGCGCAAGCC AGGAACAAGA CGGACACTAA	60
	GICATTCTGT TTATGTAGAT TOOGTOCOCA OCAGCOCCAGG COOCGCCGCT GATCTAGCCG	120
35	TACCIGCACCA ACCICCICAC GCATCCCCCC CCCCCCCCT AAACCACCAC CCTCCTICCCC	180
	GETGCCAATG GACCGCGGG TCATCCACCC CGCTCAGCGG GAATGTAGAC CAAAAAAAAGA	240
40	GIGIGGITCC ASCICTCAAA TIGGGCTGGT CTCAAGGGGT CGCGGCCCCG CAATCGCCTA	300
40	TATAAACOGA CAGOGAGAC AGTCCGTGCA CTGTCGAGGA CAGOCACACC GATGGTGAGG	360
	GITATCATTC TCACAGGCCC GTCGCGCGGC ATCGGTCAGC CAACCGTTCA AAAGTTGTGC	420
45	ACAGCCCCC ACCTIGICGT CGTCCCACTT CCCCCCCCCCC AAAAGACTIC AACGTCCTCA	480
<del>7</del> 0	AAGAGAGATA TOOCAGTAAA TIOGACTACG TIOCIOGAGA CGICACOGAT GAAAGOGTOG	540
	TOCAGOCOGT OCTOGACAAG GTGTCCTCOG ATTATOGOGG OCTAGACOCC ATCATAGOGA	600
50	ACGCAGGCGT CTCGCGCTTC GAACGCATCG CCGAGGCAGA CATCCAGCAG TGGAAGCGCA	660
	CGITTGAGAT CAATTGTTTA GCGCGGTAAG CCTGGTGAGC AAGGCGCTCC GATGCTAANG	720
	collianii amialiy ococompo cologiano woocociec aniociwika	
	AATCCCAGGG TTACOGTGAN TGTGGTTACC TCNNGANTCA ACNAGGTAGN TANCCG	776
5 <i>5</i>		776

5	(A) LENGTH: 546 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: UNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:	•
15	GATCAAGTCT TITTATCACTA CAAATGAGCA GCGCTTAAAT TTCCAGAATC GTTTACAGCT	60
	GGGTACGCTT GCAAGCAAAT TIGGCCTTTT TGAGCTAGGG GAGGAACAGT TCGCTCACGC	120
	CAAGOOCCTC ATOCOOCCTA CAGAOCOCCG CGAGCTTTAC ATGTATTACA AATCTCTCAG	180
20	COCCUTATA TOCTTAGOCA AAATOCCGAC CTGCTTAATA GATACTCTGC GTGCCTTTAA	240
	TAACGAGCCG CACTOGTCCC TCCGTAACAC ACTACTGGCT GCGCTCTATC CGAACACATA	300
	TCCACTGGCT CCGCCGCAAT AATGCAGAAG AAGAGGTCCA TAGATGAGCT GAACCAGCCA	360
25	GOGOCANCAG AATGTACTOC CACTTATGCG AACTCCNANA NTGGAAGGCC CTGCATACAT	420
2.5	TICCOGTICCC ACCIVACITET OCCITECTIC OCTIVACCACT CITCICAACC CAAINGIOCG	480
	GCATGCCTIG CCCAAAAACC CCTGGAAATC CATAAATACC TCNCGGGGGT TANCTGCGCT	540
30	ccacac	546
	(2) INFORMATION FOR SEQ ID NO:240:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 593 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
35	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:	
	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP	60
40	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:	60 120
40	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  GATCHGICAA TATATECTIG GOGICGATIG GITTGCCAGT GCTATAGAGA GCGGTCACCG	
40	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  GATCHGIGAA TATATOCTIG GOGICGATIG GITTGCCAGT GCTATAGAGA GCGGTCACCG  GCGTACGCAC GCCAACTCIT CGAGTTGICA GCCCAAGTAG CCTGATCATA TACAGGTGAT	120
40	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  GATCTGTGAA TATATCCTTG GOGTCGATTG GTTTGCCAGT GCTATAGAGA GCGGTCACCG GCGTACGCAC GGCAACTCTT CGAGTTGTCA GCCCAAGTAG CCTGATCATA TACAGGTGAT GGATGGCTCC TGTATACCTT CCCACACTGC AAGCCCCTCA GTTGCTCAGG TGTTACTGCG	120 180
40	(A) LENGTH: 593 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1216UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:  GATCHGICAA TATATOCTIG GOGICCATIG GITTGCCAGT GCTATAGAGA GCGGTCACCG  GCGTACGCAC GGCAACTCIT CGAGTTGTCA GCCCAAGTAG CCTGATCATA TACAGGTGAT  GGATGGCTCC TGTATACCTT CCCACACTCC AAGCCCCTGA GTTGCTCAGG TGTTACTGCG  GCAGATGGTC ACATCCCTTC GGAGTATATA GTCTGCGCTT TGAGCCACTT AAAAGGCGCT	120 180 240

	CUIGCCACGG AACCCGCAGC CIGCAANCCT CCCTAATIGC CCATGGIGAA TIGAACTCNC	480
	AASCTTATAT CTCCTTGCCT GATCCCCCAT NATGCATTTG AAGTTCNCCA NAGGACAAGA	540
5	AACANACNCA AAAAACNAAA TOGITAAGTA AAATTGATTT OGTGTTOCCN OCT	593
	(2) INFORMATION FOR SEQ ID NO:241:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 592 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1217UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:	
	GATCTOGTTT CTGGGGATTT TTATTGGGTT GGAAGAGGAC CTTGGGCCTA CACCACTGAA	60
	GETGTGCGAG TTCTCCAGTT GAGGCCTATT GAAGTGCATA TCTGATGATA GAGCGCTCAA	120
25	ATGITCTGAT CCTGACATCG AATACAGCGC ATTITTCTGT ATGGTAGCCG CTGGGTTCTC	180
	OCCIOSCATA TETTICATOT TIGGACIOGI GITGIOCATE ATGIACACCA TATTICATOT	240
	AATCOGTIGA ATACCATGAG GAAGTOGACT CATTIGATIG OCTOGTOOCT GCOGATGTGT	300
30	TACCATIGOC GTAGAGGTTA GAAAATIGGT GAGTITGCCA AAGGAAGAGC TGGCTGGCTA	360
	GCACAATGAT GCACTGGCGT TCAAGCGCCA TGTTTCATCC TTTCCAGGTT AAAAATTAGG	420
	AAGGGACAA GGACTCCCCT GAATCCTACT ANCCCCTTCT AAAACTTGGC AATATTGGTC	480
35	CCCTGAACAG ATGCNCCCNC CACATCCCCC TATTAAATTT TTTAACAACC ATATTTGTGG	540
	ANACCINGAA MITGAACITG CONGCNAANN GATICCCCIN CCTCCCCAGA IN	592
	(2) INFORMATION FOR SEQ ID NO:242:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 558 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1218RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:	
	GATCTITICTIC GOCCACCACC ACCACCIGGAG TACCOCCCGT GOCTTGGACG TACCACTGAA	60
	AAATGITCTG CATGAATCCC ACCTTGATAA TACCCATGGA CCACTGGAAG TTCTGCGACC	120
55	ארוסיבאס בארוסיבאס אראוסיבאס לותודאמראה אראוסיבאר פוואסיבאר אראוסיבאר אראיסיבאר אראיסיבאר אראוסיבאר אראיסיבאר אווסיבאר אראיסיבאר אראיסיבאר אראיסיבאר אראיסיבאר אראיסיבאר אראיסיב	1 20

	OCAACTACCA GAAAAGAGAG ATCGACTTOG AAGCCATGTG COCCOCAGTG GTTGAGTGCC	240
5	CCATCACAGA CACAAACCCG GAAGTCCAGG ACACCCACAC CAGCTATCGC GGCGAATCGG	300
	CCACGAATGC ATACTTCGTC TGCACCGTCT TGCCGTGCCG	360
	CAGOCCCATT GGATGCTCCG TACTGGTGTT TCAGCTTTCC GCNAAGGCCT TTACACCATC	420
10	CGTOCTTCCC AGTTCCCNOG AAAATATACC CONCCTTOGT ATCTTCCCNT GAAAAATCAC	<b>4</b> 80
	COCCGAAATT TCCCAGTTGA ANCCTCTTTG ATTCCCCCCC CNIGCCCTCC CCCAGNNCGG	540
	GANATICACA ACNAATINO	558
15	(2) INFORMATION FOR SEQ ID NO:243:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 604 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1218UP	
25	(ii) Gazilaii II-2121612	
	(xai) SEQUENCE DESCRIPTION: SEQ ID NO:243:	
	GATCCACAGT TTCCGCACTG AACTTACTAT CCCTCAGCAA CCGCAGGTCA TCGTCAAGCG	60
30	THETEACATE ACCETTCACE COSTAGCTEA TAATGCCTGG GACGGATGCC THOSTAGAGT	120
	AACAACCAAA AAGGCATGIT GGATCAGCTG CATAAGCTAG TAAAAAAAGAG CAGACGCCGC	180
	CTGAGCCACT AAAGGCAACG ACCCGCCAAT ATATGATAAA TAGAGAATAT AGAATGTTGC	240
35	CACTAGOCCA AGATGACCTG CATTGAGATC CAGGGACAAA GTGCCAGGAA TTAAGOGATC	300
	TICAACAITC CIGAICATAT GAGAAGAGCA ATACAGGGIT AAAACGGCGG CGTTTAAAAT	360
	TICACAGACT CAATCAAATG TITCACAATA CCTGGTTTGG ACAAGTCCGA GACATCCCCC	420
40	TAACTGATCT GOCTOCCCCA GCCAAGGATT TIGOGCCATA TACGGGCCAT ATTTTGCCTG	480
	ACCATICTT TOCATTCCTC CCCCAACCAC AAANACCTTA GOGOCACNAA CGGCCCCATT	540
45	CCCUNANCAA AAAAAAATA GGTOCTTTGN ATMACCCGNA CCCCCCCCC CCCCTMITTC	600
45	CONG	604
	(2) INFORMATION FOR SEQ ID NO:244:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 550 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1219RP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:	
	GATOCTGATA TIGIACOGOC TCATAAATAC TITOGATATC TICOGACAAT GIATOGTACC	60
	CGATACCTTT CAGCACATGG ATCAGTATAT CATGCTTCTT CCTAAATGCA GCAACAGTAT	120
10	TGAGGACTIC CTICAGACTG TCCGTCTGAG TATCTATCTT CATAAAGATG AACTTTCGG	180
	ACCTOTTOCT CATCAGOTOT CTGATGAGTG ACGTTGAATT CTTTTAATAG COCTTCCCAC	240
	TOGITTGATA ATCTTGATAC AGTOGTCCAT AGTCCTCCCT OGAAAGAAAT GAAGTCOGAA	300
15	GAAATCAGIT TIGGCAGCAC TCTCTCAGIT TCTGATTCAA CTCCCGTTAG ATATTTCCTC	360
	CCACAAATGT TTACOOCCCT ACAGTTOGTT TCTTTTGANA CCTTCACTTC CNTCCNAAGC	420
	CATGAAAATG ANICCATONC CNCCCCCCCA CITTGINAAA MITCCCATTC GCAAATINCN	480
20	CAGTIGAATT CCCCCANCCG GGTGTTCCCCC GGGTTCCCCCC NAAAAAANAC NGAGGGGGGGT	540
	TTTAAAAAAN	550
	(2) INFORMATION FOR SEQ ID NO:245:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 598 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1219UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:	
	CATCOCOCCC CTGCCCCCCCC CGTCGCACTC GCCCCACGTC GCCCCCCT TTTGCCCAAA	60
40	TOCCASCOGI GGGCGGGTIT CGAGCIGCTI GACCTTCCGC GGCATGICAA AGTGCGGCGT	120
	TAGITTOGTC CTGTAGOOGA ACTGTAGOOG CGATGCGACC GTCTCGCCGA CGGTGGGGAG	180
	CAGOCCCTCG GCCAGCAGCT GGGGAGCAAA GAACTTGAAC GCATTTGACA CGGTTCGCTG	240
45	TITIGAGCTICC AGCTICCTICGT CATACGTCAG GAACTGATAC TIGGCAACCIGG AGCACTTICCC	300
	GAAGTACTIG CAGTICATCA GGTCGTCGTG GCGCATTTCA GCAGAGGTCT GCACCTCCAG	360
	CAGAGACOCT TOOSCOTAGT GOGGTGTGTC TTGTGCACTT GGATGGTGAC CACGTGGCCC	420
50	TOSCCAGOOC AAATTOGCAC CCAGCACTAC TGTTTCCTTG TTTGCTATCC TCCCGGGCTG	480
	TOCAACAANA COCATOCCTC COCATOCACT TTACNTOCAC ACATCACTITI CATCAGCNCC	540
	GGTTGTTCTT CTGCTGCATC GCCCCCGAA TTINITICAGA ATGATTACTC CTCCNCNG	598
55	(2) INFORMATION FOR SEQ ID NO:246:	

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 747 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220RP	
	(xí) SEQUENCE DESCRIPTION: SEQ ID NO:246:	
15	GATCOCOCAG TTGTCCCCCT CAGCCAGCCG CTTTTTGCGC ACCCCCCGAGA GCGTGTCCAT	60
,,,	GTACCOGTOG GOCACGCCCC CGTGGCCCTC GCCGATCAGC TGCAAGTGCT GCTGTAGCTC	120
	CTCCGGCATC AGTCTCACGA TCACATTIAG TAGCGCGGTG CTGTGCGCAT CTGCCTCCTG	180
20	CAACATGTCA OCCAGCTOCC TOCGAAAGTTC GGACCGTGTC CCCTGGTCGT CTGTGACAGT	240
	TAGTATICIT GOCCGCAGIC GGICGCACAT TGOCATCACT TACTATIGIC GCTGGGCATT	300
	CACCTCCCTG GATCACTGGT GCTCCCGGTG GCGGTAAGGG GCAACAGACA GGCTTTTTTT	360
25	ATTITICCTOT ATAATACOOT GOTOTATGIA GOGTATACTA TACAAGIOTT AACTAAGGIG	420
	AAGTGAGAAG TCATTATTTA GCTGCGTTTC GGCCGGTCAT GCAGCCGGCT ACCATATTTAG	480
	CATCCCCCTC CCCTTCACCC CTTTCCACCT CCCCCAATTC TTCATCCCCA ACCACCTTAT	540
30	GEAGTICAAC CICACGGAGA GGITTICCGAG ATCGAAAATG TCACTTICGG CAAATTIGCGA	600
	CACACCETAA TACTCEBECAA ACGAGTTCTC GACACCECTG ACCTCGTCGT CGACGTCGTC	660
	CACATAGGAC AGAAGAGGCT TOGTTOGGGC TGGCGGGGCGC GCGCGCGCAA CCGGAAGNGC	720
35	COCCCANAG CTGGGGGCCC	747
	(2) INFORMATION FOR SEQ ID NO:247:	
40 ·	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 777 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:	
50	GATCCAGAAT ACTCGTCGCA CCACTTCTTG AACCGCGGGT ACAGCGCGGG GTCCGTGCGC	60
	TCCAGCGGG CCTTGTGCGC CGCGTGGAAC AGCCGGCGT CCTCCTGGTA CAGGTAGCTT	120
	GECCLICAGEL CCCAGCCGCC GCCCAACCAC CACCLICICCE GCLICCCCCC CECCLICCCAC	180
5 <i>5</i>	GICICAAAGT AGCGGTAGIT GAGGTGCACG GTCGGCGCGT GCGGGTTCAC GGGGTGCATC	240

	ACCAGAGAAA TOCCOCAGOC GAAGAAGAGC ACGCCOGOCG CCGCCTGCCC GGTCAGGGG	300
	TOOGTIGGGGA GETIGCAGETTI TITTETIGCTOOG GCCCGCATTGG CACTGACGGC TIGCCGGCCGAC	360
5	ACCTCCCCCT CGACTACCGA GACGITAACG CCCCCCTTTT CGAACGTCGT CCCGTCCTCC	<b>4</b> 20
	AGCACGCACG ACGTGCCGCC GCCACCCTCC TTGCGCTCCC AGGAGTCGGC CTTGAACTTG	480
	ACCOTOTICGA TOSCOTOGAA COCCOCTOTIA ATCTCCCCCT SCITTCCCCCC CACGASCTCT	<b>54</b> 0
10	TOCATOCOCT COCCCATICTIC COCCCTICTICS COCCCATCOCCA TTICCTCCCCCC COCCCCAACAG	600
	GOGAAATNAN CNGTGCGCCC GOCGGCTTAT ATAAAAGCGT GGCACGGGTG TTTTGCCCAC	660
	GNCACCANGE OCTOCNAACE TOOGCOCCAA NANANCCAGG GTOOCGOCCA NAACACNTOG	720
15	GCGGGCGCC NAACGCCGCC NCNCACAATC ACNCCGACAA TCGCGCNCNG GGATTCC	777
	(2) INFORMATION FOR SEQ ID NO:248:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 537 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
05	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1221RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:	
	GATCTCTGCT GTTTGGGCTT GCAAGCATCT TCCTCGCTAA CTCGTTCGGC GTTTACGTTT	
		60
	GAGGITIGCOG OGACGITATIOC TANACCGAGG OCATTICCOGG GITIGAGOOGA AGAGGITIGAG	60 120
35	GAGGITICOCO OGACGITATOC TANACOGAGO GCATTICOCOC GITIGACOCCA AGAGGITIGAG ATTATICAATIC ATTATIACTIC TITATACOCOC TOCCOGGICOC TIGICOCCGIC ATCACCACGO	
35		120
	ATTATGAATG ATATATACTG TTATACCCCC TGCCGGGTGC TGTCCCCGTC ATCACCACGG	120 180
35	ATTATCAATC ATATATACTC TTATACCOOC TOCOOCTICO TGTGCCCCTC ATCACCAGGC ACTTACAACT TCAAAAGGTC TTCATCCATA TTTACCAACT TGTAATAACG CTCTTGTGAG TCTGAGTTGG AGGAGCCGGG CTGGTCGCCA TACTCCATCA ACGTGTTTAC CATTGCGCGT GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG	120 180 240 300 360
	ATTATGAATG ATATATACTG TTATACCGGC TGCGGGGTGGC TGTGCGCGTC ATCACGAGGG ACTTACAAGT TCAAAAGGTC TTCATCGATA TTTACCAACT TGTAATAACG CTCTTGTGAG TCTGAGTTGG AGGAGCCGGG CTGGTCGCCA TACTCCATCA ACGTGTTTAC CATTGCGGGT	120 180 240 300
40	ATTATGAATG ATATATACTIG TTATACCOOC TOCOGGIGGC TGIGCOCGIC ATCACGAGGG ACTTACAAGT TCAAAAGGIC TTCATCGATA TTTACCAACT TGIAATAACG CTCTTGTGAG TCTGAGTTGG AGGAGCOGGG CTGGTCGCCA TACTCCATCA ACGIGITTIAC CATTGCGCGT GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG GTGGTGTTCC ACAANCNGGA AAACCTATCC TGTTAGTINNA GAAGGGTTGA GAACACCGCT AATCCCTTAG GCACTCCACC ATGGTTTTAT CCGTACCCCA TTACCCAAAT TTCCCCCAAG	120 180 240 300 360 420 480
	ATTATGAATG ATATATACTG TTATACCGGC TGCGGGGTGGC TGTGCGCGTC ATCACGAGGG ACTTACAAGT TCAAAAGGTC TTCATCGATA TTTACCAACT TGTAATAACG CTCTTGTGAG TCTGAGTTGG AGGAGCCGGG CTGGTCGCCA TACTCCATCA ACGTGTTTAC CATTGCGGGT GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG GTGGTGTTCC ACAANCNGGA AAACCTATCC TGTTAGTINNA GAAGGGTTGA GAACACCGCT	120 180 240 300 360 420
40	ATTATGAATG ATATATACTIG TTATACCOOC TOCOGGIGGC TGIGCOCGIC ATCACGAGGG ACTTACAAGT TCAAAAGGIC TTCATCGATA TTTACCAACT TGIAATAACG CTCTTGTGAG TCTGAGTTGG AGGAGCOGGG CTGGTCGCCA TACTCCATCA ACGIGITTIAC CATTGCGCGT GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG GTGGTGTTCC ACAANCNGGA AAACCTATCC TGTTAGTINNA GAAGGGTTGA GAACACCGCT AATCCCTTAG GCACTCCACC ATGGTTTTAT CCGTACCCCA TTACCCAAAT TTCCCCCAAG	120 180 240 300 360 420 480
40	ATTATGAATG ATATATACTIG TTATACCOOC TOCOGGIGGC TGIGCOCGIC ATCACGAGGG ACTTACAAATG TCAAAAAGGIC TTCATCGATA TTTACCAACT TGIAATAACG CTCTTGIGAG TCTGAGTTGG AGGAGCOGGG CTGGTCGCCA TACTCCATCA ACGIGITTIAC CATTGCGCGT GTATAGCTGA TCAGGTTTTC GAGGGATGAC TCGCTCTCCT CCTTTAGGAA CATCAAAATG GTGGTGTTCC ACAANCNGGA AAACCTATCC TGTTAGTINNA GAAGGGTTGA GAACACCGCT AATCCCTTAG GCACTCCACC ATGGTTTTAT CCGTACCCCA TTACCCAAAT TTCCCCCAAG TGCCCTTNAA CTTTGNCGAA CCCCCGCNAA ATNCCCGTTT TTAAAAACCCN AAAAANG	120 180 240 300 360 420 480
40 45	ATTATEAATE ATATATACTE TTATACCOCC TOCOGGIGGO TGIOCOCGIC ATCACGAGGG  ACTTACAAGT TCAAAAGGIC TTCATCGATA TTTACCAACT TGIAATAACG CTCTTGIGAG  TCTGAGTTOG AGGAGCCOGG CTGGTCGCCA TACTCCATCA ACGIGITTAC CATTGCGCGT  GTATAGCTGA TCAGGITTTIC GAGGGATGAC TCCCTCTCCT CCTTTAGGAA CATCAAAATG  GTGGTGTTCC ACAANCNGGA AAACCTATCC TGTTAGINNA GAAGGGTTGA GAACACCGCT  AATCCCTTAG GCACTCCACC ATGGTTTTAT CCGTACCCCA TTACCCAAAT TTCCCCCAAG  TGCCCTTNAA CTTTGNCGAA CCCCCGCNAA ATNCCCGTTT TTAAAAACCCN AAAAANG  (2) INFORMATION FOR SEQ ID NO:249:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 584 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	120 180 240 300 360 420 480

### (A) ORGANISM: PAG1221UP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249;	
	GATCGACCCT ATCAACGCCT TGCAGGCTGC TATGGAGGGC TATCAGGTCA CCACTATGGA	60
	CCAGTGCGCC AGCTACGGCC AGGTTTTTGT CACCACCACC GGCTGCAGAN ACATCATCAA	120
10	GANGGAGCAC TTCTTGGCCA TGCCTGAGGA CGCCATTGTG TGCAACATCG GCCACTTCGA	180
	CATCGAGATIC GACGTCGCCT GGCTAAAGGC CAACGCCGTIC GANGCCGTICA ACATTAAGCC	240
	ACAAGTOGAC COCTACTTOC TITICCTCCOG CAGACACGTC ATCCTOCTTG CCGATOGTTA	300
15	GACTAGTCAA CCTAACCTGT GCCACTGCCC ACTCCTCCGT TTGTCATGTC TTGCTCTTTC	360
	TOCANCOAGT CITTOGCACA GATGGTCTON TTCANGGGCA ATMANANAGGC CITCANAMAN	<b>4</b> 20
	ATIMITIMIT TECCCAAAAA ACGGCCNICA AANCGGCNIT CATITCINNC CNAAAATIGN	480
20	AAAGGCGCNC CCATTICCCC CTAAATTIGG GITTINITTT AAAACATICC CCCCCCCCA	540
	TTICCGGGTT CCCAAAAGGG INTTINGGGG NCCCTTAAAT NITA	584
	(2) INFORMATION FOR SEQ ID NO:250:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 535 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1222RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:	
	GATCGAATAA TAAAAGTGOC TAATACITOG TAATAATATA ATAGAAAGOG AAATAGAAGA	60
40	GAAGTCAAAT GOGAAATAGT CAACOOCGTA CTAGGTGAGT GTTCAGTTGC ATGGAATOGT	120
	AGICAGAGAG GITTATICAAA AACOOCAGIC GICTGATGAT AOCAGTATICA CGAAGTOCTIC	180
	ATGCGCCCTG CATACAATGG CAGGCTCAGC GCAGGATCAA ATGGATAGCA GCGGGCGTAC	240
45	COSCEARCOG ACTICAGTOSG TOGRACTOSCC CCGGTOGTAC TTICAGOCCGT TGAGGTTCTT	300
	GTAACGTTTG CCACAGACCT COCACCOGTA AGOCTTGTCC TTCTCGAACC CATGCCCGTC	360
	TOGATAGOOC TOGITOGACT CCGOGTOCAT GATOCTAAAA GTOCCCGTCT GGGTTTTCAT	420
50	GAAGCTTTIG ATTCTOGTOG CCGTOGTTTT ATOGTACTTG AGTCCCGTTT GATCCTOGTT	480
	AGTOTTATOG CASCOCATGA GOGACINNITG AAGOCTINTO COCINCOTTGT CONON	535
	(2) INFORMATION FOR SEQ ID NO:251:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 581 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1222UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:	
	GATCTCCCTC AGACCGTCAC CCACGITGTC TGCAAGGCCC TCCGCCGCTT TANCTGCCTG	60
15	CCACGOCTITE GAGCACGCTA GCTGCACGCC AAACGCGGGC AGCTCCGAGC AGTGCGCCTT	120
	GGGCAGCGCC CACTCCGAGT TGGTGCCCTG GATCAGCGGC ACAGCGAGCG CCATCTCACT	180
	GTACGTCACG TCGGCGCCCA ATTGGCGCAT CAGGCGCCGG AACGGCAGGT TCCCCGACGGT	240
20	GGTCAGCOGA GAAACGATCT TCTTGTGATG CAGGTCCAGC GGCTTCTTCT CCTGTGCAAA	300
	GTAGCCTGTC TCGTGATACT GGGCGTACAG CTCGCGCTGC CGGGCGCGCT TGTTGCTCAA	360
	TICCTCCTCC COCTOCTCCA CCTCCCCCAC CTCTCCCACC CCCCCTCCCC CCCCCCCC	420
25	GCCCCCTGCA TCTCGTCGCC GCAACTCCTG CTGCATGOCG TCAAAATTCC ACNATTTICTC	480
25	CCTGCNCNGG AAGGGCCCCAA NTTTTCCCCCA ATNANCNCCA ATGAACCATT GWINCCCCCN	540
	TOGITINCAAA ACNAATTTIG CCCCCCCCCG AGATTNICCC A	581
	(2) INFORMATION FOR SEQ ID NO:252:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 544 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1223RP	
±0		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:	
	CATCOGTTTT CACCTCAATT COTTTCTOCT COCCAGTTG GTCATOCTCC TGATGCTCAA	60
45	OCTOTANTIC CTGTTTCTOC TGAGCAAACT GCTGCTGCTG TTTCATCCAG GGATTCTCCG	120
	GAGGAGCTGA GTCCGGTTTG CGCCGTCTCT GCTTGTCGTT CAACAAGTTG TTATATAGCT	180
	OGITICATACC TITOGGAGGIC AGGAACTGAC TGACATICOC GICOCCCTOC GOGIGGICIA	240
50	OCANACOGAG CATOOCCTCT CTCTCCTGTA GAGTTTTCTT TOCCCCCATC TCANACTTCC	300
	TAGATTCCAT TATCAGCOCT TCTTCCTCAG CAATCTCAGC CGCCGACCTC GAAAGCAGCC	360
	TOOGICAAAT ACTICITICOG CIGIATITICO CIGGICTITIG GAATACOCTA OGATOGIAGI	420
55	AGCOGITICC CCGGGICTIT CGCCCTGAAA TIATTITTGG CATACGNGGT TAAAAATCTC	480

	CCCGTANTIC CICCAACGGT CCINNANNCG NCNTAAANAN ACNGGTCNGT AAATNATAGC	540
5	NNCC	544
J	(2) INFORMATION FOR SEQ ID NO:253:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 608 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1223UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:	
20	CATCOCCCC TICAACATGC ACCTGCACAC COCCGAACTGC COCTGCACCC COCCCACCCC	60
	TOCGTOCTOC ACCTCTGTG GTGCCATGGT CCCCTCTGTC TTGAGCTGCC GCACAACCCC	120
25	GOCGGATATG COCTGGACCC TACTGGCGGC GAGGACATCT CGTAGCGCGG CCGCCTGCTC	180
	GCACTICACC ACGACACIGG OCACGCGCAC CTIGGIGGIC GGCGCCGIGA ACGCCGIGIT	240
	CACTOCAAAC TOGTCCCACG CCCCCATOCT CCCCGGCACGC ACGCCTTTTC CTCACCATOC	300
30	GTGTGCCCCG CGCGACGCCG AGCGACATGA GCTGGCCCTG CAGCTCGGCA TCTGGATTGC	360
	OGTICAGGTICC TIGAATICTICCT COGTIGGTICAG TTICTOCGTAG TCTCCOGGAAA AACAGGAAAA	420
	ATGGTTGGCG GCATNGTTCA ACATCCTTGG CNCCCTGGGT TAAAAATGGC CGAACTGGNN	480
35	GCCGATTTCC CCCAGAACCC ATTITICITAT CCCCCTTCCT TCTGCNINCC GATTTTTTTG	540
	CAAAANINAA AACCCCCCCT AAGAAGANNN C999GNNOCC CCNCG9CGGN TITTITITITC	600
	CNCCCCCA	608
40	(2) INFORMATION FOR SEQ ID NO:254:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 731 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1224RP	
	(asi) CONTRACT DESCRIPTION, CTO TO NO 25 4	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:	60
55	GATCAGTAAC AACCATAOCA GCCGCACCTA CGAAAGCATT CGATACATTT TTAATAAATT	120
	CGACAGCAGG TAGTAGTCTT CTTCCGGATT GCTTTACAGG CTCGCTAAAG ATGTGTTCGT	120

	AGCTOTTOCA AAGAGAAATT TGTGTAACTT CAGAGTCAGC AGGGGACTCA AAACAGCACC	180
	TCAACCAAGC GGTTGACCGC ATAGGTTCAT TCAAGCCCAA TAGTTTTTTGG AATAGATCAG	240
5	COCCAACACT TOCAACATOC CTACCOCCTC TCCCTTTTAC TCCCCTAACT ACTITITATCT	300
	CTACTITIGA AAGATAGICG TAGICOOGAA OCTCAACATT GTAAGICAAC AAGCTAGOCA	360
	AAACTGTAGT CAAGATTGAG TTCCCCTCAG CGTTTTGACA ACAGAGTAGT TATTCTCTCA	420
10	CTCCCCAGGC AAGATGTACT GCTATAGAAA ATCCAGTTGA AGCCATAACC AGCTCGTTGT	480
	CACAGTOCAC CAGAAGATAG GANACATCAG GTTGAAGAAT TOCTCATCTA GGTTATCTGC	540
	TOCCTTTCCT GITCTGCTTT GGACCAACCC ACAACCCNAA AACCAACGCN AAATCAAANA	600
15	CONSCITOCT TOOTHEWICE COCCNAATGA AANAGETTIT GAAANSETTIN TOOCTOTTOC	660
	COOCCCAANT AAAAAAAAACC CCCNCAGGNT CNACNATATT ANCANTCCCCC NAAAAAACCCC	720
	TICIGNICIA A	731
20	(2) INFORMATION FOR SEQ ID NO:255:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 762 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1224UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:	
35	GATCOGGICC GGCACATGCC TCATCGGGCA GGTGGGGTGG CGGAGGCATA AACCCACCCC	60
	TOGTTGTTOC AGTGAATAOG TATGGGTACA GCCTTGGCGG CCACGAATGT GCCGAGACGT	120
_	TTCAGCTOCC AGAGGGACCC GACCGCACCG GTGGACTGTT GGCTTGGTTG GACGCTCCAG  GGTTACGAGC CGGCGCCCTG CGGAGCACAT GATGTCGAGC TGTGCATTGG TCCAGGTGCG	180 240
40	CACTAACCAT COCAACCCA TOCGCCAAC COCCATGCC CTGCACCCC CCACCCCCC	300
	ACGACTATCA CTAAGAAATC ATCGATTAAA ATATAAACTA CATAAACTAA ACCCCCCAT	360
45	GAGTICCACTC TCACCCCACT ACCACCGAGT ACCCGTAGTT GAACCACTTG CNTCCCGATCC	420
, -	GTGGCACGAA GCGGAAGTAA CCGGAACTCC GATAGTTCAG AACGAAGAAC CGAAAAAAACCC	480
	TIBABANTOC TICACNOCTA GETCCCCCAA CNEGTOCTICC TETTTIGGAAT TAGGETGGGC	540
50	GGAAACCCAA ACTGCCCANT TGTTNICCAA TTCCCCGGNG GCCCCAATTT NAATTTCCAA	600
	ACCIVATORION ATOTOGOCTIG NATIOCOCCOC NITIGOCOCCO TOAATGGCCC CGAACCTTTT	660
	NICHOCOCCC CCCAAGGCC CTICNENATT TITTICCCNG CCCNCCCGVI INICITAAAA	720

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	(2) INFORMATION FOR SEQ ID NO:256:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 710 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1225RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:	
	GATCCTTTC TTTCTTCTTC CCTCCTCCGA GGATTCCCTT TTTGAGCTTG CCCACTGCGC	60
	CCAACCCACC GCCTATGACA CTAGTACCGG CGGACAGACC AGCGGATAAG CCCTTATTGG	120
20	CAAAATCOCC AACCITTGTC TCCACCITGG TAACAGAGAC AGTGTACCTA GGAGAAAATT	180
	TGAAGITCAA GTAAAGAATA CCACCGTCCT CCCCGTTAGG ACCAGTTAGC TCGACTTCCA	240
	THOOGETTIC ACTIGICTOCC TOCACCICAG CHAGAGOGAT GETTIOCOGTIC CCAATICAGAT	300
25	OGICACIGIT TOOGGCATOC CAGTOCATGA COTTGATGOG CAGGTAGTTG TTAATCCOGT	360
	TATTCAACTG CAGGGATGTG TTCTCGTTCC AAACAGGTTC AAGCGTCTTC TTCTGGGTTC	420
	TIGGICTIGI ATATTACCIC ATCIGAATIG TCGAGGTTAG AATTIGACAT AAGGTCGGAC	480
30	THEOCETTICC GETCAGCAGE TAGASCCTGA CTOCATTTAG AACCTCCAGT GTTAGGTCGC	540
	AGTOTTOGTA TCAGTTTOCT TOTNOCATCT CNAACCCAAA AAGGAACCAC AACCGTTANN	600
	TOCTTTIGNG ACCOMACCIT NITTACAMN AGGITTMANT TACAMITTON ATTIMITION	560
35	TOGAANGAAC COCNAAGNOT CONCCIGITT TACTGANONI NIVICCONAAT	710
	(2) INFORMATION FOR SEQ ID NO:257:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 750 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1225UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:	
50	GATCCTACTG GAACCACCCA CTCAGGAGCA GGTTAAAAAA CCAGCCAAAG TAAAGACAGA	60
	GACAAACGTA AGCATCCCAA AGCAGACCCC TACTCCAAAG TCTAAGTCGG CTTCAGCTTC	120
	GTCTTCTAAA GTOCCTACAC CCCTGTCAAA GCAGGAGCCC GAAGCCCCGT CTACCATTTT	180
55	TGACOCTOCT TCTTCTTCCT CCTCCACTCC OGTGCCTGGG CACTTGGATA TCTTTAGCAA	240

	ATTTACEAAA GCATCCAGIG ACITIGACAA GCCCITIGIG GCCGAGICGA AIGAAGITGC	300
	CGAGAAGCCG TCCGGGAAGGG CCAAAACGGCCA AACTACTCCC GCTGCCAGCA AATTAAAGCC	360
5	COCTOCAAAG AAAATAAAGA COCCCOCOCT CGATGAAAGC GAATCTGATT TTGACCTTGA	420
	CCTCAGCGAC TCCCAGCCCG CCATCGCCCC TAGAAGTAGA GCCTCGCGAG CTGTCGCCAA	480
	AAAGCCAACC TACGTAGTTG ACCTTTCCGA TGACAGTTTT GTTGATGGAG ACGCCCAGAG	540
10	ATGITICAGGA ACCGATACTG ACGAATCCTT CCAGCTCTGA CTAGCACTCT AGCTCGCCCA	600
	TTGACAGINC NCTACCITAT GGAGGNITCC GAAATCCNIT GAATACCCCC CGITTITITAC	660
	TAAAACCCCC NCTTTCCTTT TCACCCCCCA ACCCCCAGGG GACGAATACT TTTTTCTTTA	720
15	CITICIATCA NOCOCITOGI CNOCONOCONI	750
	(2) INFORMATION FOR SEQ ID NO:258:	
20	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 729 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genamic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1226RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:	
	GATOGICCTC GCATGOGAGC ATCAGATGTC ATATCOGOGA AGCCTTTCCA TATGOCOGCT	60
	ACCAACCATA CCACTICCOC TCCTGCTTGC GCTGTTGGGG TCTGTGAGCG TGCTGCTATT	120
35	GCTGTCGCTG ACGCCACACA TGTGGCCTGG ATGGCCATCT CCGGCAGCAC GGGAGGTCCC	180
	GGCTTCACCA GAGTCACAGG CCCCGGCTTC ACCAGAGTTA CAGGCCCCGG CTTCAACACA	240
	OCCACAGTOC CCAGCAGOGT CTAAGACOCT ACTGCAAGAC TTACTGCTAG ATAGCAAAAA	300
40	ACCOGAGOGO OCCTICTACOC CACAGATOCA GTOCAAGCOC TACTITIGAGG GCACATATCT	360
	CCGGGAGCCT TCCTGGGCAA ATAGCGTGTT GCGCATGGCA GACGACTTTC TTACGGCTAC	420
	GCAATACACA GCGAGGCTGT TGGAGCGGTG GCGCATATTT GCTGATTGTT TCGTTATTCA	480
45	GATTICCGAT TITCAAATAC NCTATCCAAA CAAAAAAAAC TGCCCAANIT CCATCAGCGA	540
	ANTICCCCTT TCMINGOCAA AAAAAAAAN MGAGGANATT TIGCCTNICC CCNGAATTIC	600
<b>50</b>	NCCCGGGAAA ATITTTAAGG NGGNITTTT GNAAANGGGC CCCACCAAAA NANAAAAGGN	660
50	GOCTITITIG GAAAACOOOC CCTITICCCC OCNCAGAACA AATINNINNN GOOGACOCCC	720
	NGAATTTIC	729
55	(2) INFORMATION FOR SEQ ID NO:259:	
J	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 742 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1226UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:	
15	GATCCCTTCA AATTICCAGC CGTIGATATT CAAAGAGTGG TCACGTTCCG AAAGATGGTC	60
,3	CTTCTGTTCG TCTGTACGTT TOGAGOOCCG OCCTACCOGG OCGTTCGGCC TTGTCTCCAC	120
	GGTGCGGTGC TGTCCTATGG GGACATCCTG GATGTTGTTC TGCAACGCAT TAGCAAATGA	180
20	GITTITIGIAG TOGIACITAG CAAGITTATA ATTIAGOCIC AGITCIATAC TOCCOCIAAT	240
	ACTITICACCI OGAACAATCA TOOTTATIGIG CICACCICIG OOGIGITICIC TAGOGIATIC	300
	COGCOGNOCT TOAGCATTIG GITGITICCIG GATCGITIGGG TATGGATCCT COCACTICIG	360
25	TAGCCAGTIG GTATCCAGCT TCTCACCCTG CTGATGCCAT TCTGGACGCG GGGGTTTCAG	420
	CAGGOGTTAG CAATGAAGTT GOOGTTGOOG GTTCAAAAAA AAANACOGGN GOOGGCNTOG	480
	TAANCCCCINC CCTTTAAGGG CGGCCCCATA TICNCNATNA CCNNNACCGC NCCCCCCATN	540
30	ACGCCCCCAA AANAINITIG AAAAAATIGC CNIACCITIT TGNGGGAGCC CACNCNCTTA	600
	NATAACCCAT TITTIGAAAN ANGCCNNICI TITNITIAAC NCCNCOGITC NCNANTATGC	660
	NGGOGCAAAA TIAAACCNCC CCCCCIVAAAT GNAATCNVIT TCCCCTCIVAA NACAAAAAAT	720
35	ATTINNITI NOOCCNOCCA AT	742
	(2) INFORMATION FOR SEQ ID NO:260:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 744 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1227RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:	
30	GATOCATGAA CAGACTOGAG AACAGAGAAA GGTGGTGCCC CTCGAACTCG AACGGTTTTT	60
	CCCGCTCGAT TITGATGAGA TATTACTCCG GGATACGATG CAGAGGAACG CAGCTATGGA	120
	AGAGGAGGAC TACAGGGAGC TGGGGAAAAG AGATATTGAG GTGGCGTTCC AGAACACCGG	180
55	COTGACCOTTO CATGACAGOC TOCAGTOCTT OCCOGOCCATA TOCCTOTTOG GGACGTATGT	240

	ACGGGATATC GACGGGATGT CGGAAGCGCT TGCGGACGGG GACAGGCACA TCATGGTGTT	300
	TOCOCCGACA AATGACOCCA TTACOCCGAT OCCCAAGAAG CCCTOCGAGT ATCCACOGAA	360
5	CATCGACAAG TIGGAGCAGG CAGGCGGGTC TGCGAGCGAA ATCCACGAGG CCATCCAGGC	420
	GAATGIGAGA COCTITIGIOC TAACCCACGI OGITTCOGAC ATCGACCICT CTAAGGIOGI	480
	TCGCGAAGAT TGCTCCAGCC GTGTTTGACA AGCGACTTCA TCCCAAGAGC ATGCAGGGGA	540
10	TATTCTTTTG COCCCAGGAT GOCAANDGTT TTACAGTNIC NICCAANANN GOGCOGACCT	500
	TOCCOTTNAG ANGITIACCOC COOCTCTAAC OGITTATTIT OGITINICACN COCCCTTOGN	660
	TOOGAATING AAAACCCTCC NOCTONCCON NOCCAATNAN TONCTIGAAT COCCUNITING	720
15	GAACONION TINCCCCCAN CNCC	744
	(2) INFORMATION FOR SEQ ID NO:261:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 768 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1227UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:	
	GATCATTTOC COGACCAAGA AATATTTTCA CTCCTCGAAG ACCTGGCCAC TAAACTTCGT	60
	GICTOGITAG GITCCOCTCC AGCIGAIGIG CTAGATATCG AGGIGAGAGG TAAGCITAIT	120
35	GAATACTICA TGAATACTIC ACTITIATTIC GGTGGGAAAA TAGAACATCC TACATCGACG	180
	ACTITICATICA CICACCATICA TICAACACICAA TICTICAAAGCT CICATITICOGA ATAGTICCAGG	240
	CAAGITAATA CCCAATOCTC GOCTTTAGCC TCAAGGGAGA TATCGGTAAC AGCTCTATCT	300
40	ATOCTOCCAG CACGTACCAG TETETACTAA ATTIOGCATA CAGITCATOG TATTIGACAT	360
	AACCTTAATG TITICATTOOC AACACAAGOC TITOCOGATGT GTAAAGTGOG COGCGTCTCT	420
	GCATTCAAGA CAGCATACAT GAACTITCAG TITTIATACOC CGATCATGTT GATTICTAAT	480
45	AGGGCTAGTC CATGGCCCCT ACCTATAATA TACTACCATC CAGCCCNCCG AACCGNAACN	540
	NNATITITIA TITTAATNAA ATTITGGGGG NATNOCACAC NNNCCCTANC NNGGANITCC	600
	AATGITTATT TAANINAAAA ANCAGITIGA AGGGIATICC NNCNCCCCNC CCCACCNGNI	660
50	TCAAAACCAA ACNANACCET GAACCINTEIN NTCCCCCNCA ACGAGNOCCC CCCCGCTTCN	720
	AAAAACGGIN NCCTTINCON CCCTTGCNCA ANATTCCCCC CGCTGCCC	768
	(2) INFORMATION FOR SEQ ID NO:262:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 738 base pairs	

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1228RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:	
	GATCCATTGG GCCCAACGAT GCTAATGAAG TICTTGCCTC CAAAACCCAC ACTGTGCACA	60
15	CCCTIGTACG ACTIGAAGIT CITCACCTCT AAGCCAATCA GCCTCCCCAT CTTTTTIGAGA	120
	CACTGAAGCT CAGTCTAACT GCTCTCGATG TTGTTAGTGC GCTGTTAATA TGTCCAAACA	180
	AACGCGATCA TGGTTGTGAA GAACTGCGGG TTCGCATACA GCGTCAGCAC GTAGCCCAGC	240
20	GOCCCGGGG GCCCGAACAT CACTGAGATC GCCAGGAACA GCGGCGTCCA CAACAGCACC	300
	AGAAATACCA AAATCGCCCC AAACCTTATG ATGTACAGGA TCACCAGAGT CACCGCCTGA	360
	ACCCAGATET OCCCGTOSCC CATCCCGACC ACCATCGACT OCCTGAATTA GTATATTCCG	420
25	TCCCACCTOC TGTTTCATAC ATACCACCCC AGGGCACACC AGGCGGTAAC AACCCCAAAG	480
	GNGTCCCTAG GCAGCGCATG CAAAATATCC ACNCTCCGCA TGGCATCTCC CNNTTGGAAA	540
	GGGGNCCCCC NAAATITGGG CCNAAANCCC TIAAAAGGNC CCTGTGNCCN CAANNACTIC	600
30	NAATTTCCCC NITNOGCCCC CCCCCCCCTC CAACGGGATT TAAAACAGGN GGGNGNGGGA	660
50	AAAACCCNCC AGGGGAVITIT TITINGCCCCT TTCCGAAANA ANCCNCCCCC CCNGGGAAAA	720
	AAATATTTTT TTTTNOOG	738
35	(2) INFORMATION FOR SEQ ID NO:263:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 748 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1228UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:	
	GATCATGCCA TICTTACGCT TTGCCCACAT GGACGCCCAA ATGAATTICT GTGTATGCGA	60
50	CENTICATE GATICACTE ANCACENCA CENCACCENT ETENCOCCTE CITICTATENC	120
	OCCIACIATI TOACCIGIGA ATACTIGITO TIGGOCCICI GIAGACATAA ICTIGITAAG	180
	GACAAACCTC CTOCTGTCGG TGTGTATCAG GTCAAGTAAA GTAACCCCCT TAAATCCCAA	240
55	TITIGGAGATA COGAAGATTA AGCATGOCAA ATOGITIAGOC GOOCTAAACT GOCATGOCTG	300

	ATGCTGGGAA CAGGTAAATA TGGCCTGAGG TGCTGTGTAC TTACCTGATA TAAAAGTATG	360
	CAGTATOCOG GOCOCTTCGT ACCTTCTOCT GTAGTCTATC GGATCCTOGA TAGATGTTAG	420
5	TICATCOGTA AATOGTTOGA GATAATTTTC GICCTOCGAG CCCTGTATAG TAGTTTCCTG	<b>4</b> 80
	TGTTTGAATA TICATGAAAT GGTTGGGCTA GCTTTCAGCA GCTGCTTCTT TAGTTCTTGC	540
	TCATACIGAC TICTICOCAG ATCTACNOCA COOCNITOOS OCTGACCOCA OCACACTTAT	600
10	GATITITIANA AGGAATOCCC GTAATOCAAN GCCCTINCNI ACCONGTCCC AATNETINCA	660
	TCAAAANGIC ANNOCCIONA TITICONCITT ICTONCAAA ACINCOCACNI TAATIGAANA	720
	NEWCOVITIC ACCOCGAGAG GTOOCCENC	748
15	(2) INFORMATION FOR SEQ ID NO:264:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 653 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1229RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:	
30	GATOGTAACA ACAAGGOTAC TOTACTGOTT ACAATACOOT GITGTACATO TAAGTOGTGT	60
	ACAAATGATT TACTCTCGCG CAGTATGACA TTGCAATCCG CCGGCACGCG CCCAGACCTT	120
	TCCGTCTGAA CACCAGTTGC CGGCCTGCTA TGGTTCAGCG ATGCTAAAAG CACCTTATTC	180
35	GTATCCATCT ATAATGTGCG AGAAAAAGAA TCATCGCGTT CTAGCATGGA TTCTGACTTA	240
	CACOCCTITCA OCCATAATCC AGCGGATGGT AGCTTCGCGG CAATGCCCGG TCGGACAGCC	300
	GCAAAAACCA ATTATCCGAA TGAACTGTTC CTCTCGTACT AAGITCAATT ACTATTGCGA	360
40	TAACATTCAT CAGTAGGGTA AAACTAACCT GTCTCACGAC GGTCTAAACC CAGCTCACGT	420
	TCCCTATTAG TGCGTGAACA ATCCAACGCT TACCGAATTC TGCTTCGGTA TGATAGAAGA	480
	OCCGACATCG AAGAATCAAA AAGCAATGIT COCTATGAAC GCTTGACTGC CACAAGCCAG	540
45	TTATCCCTGT GGTACTTTCT GCACCTCTAG CCTCCACTCC CGAGAACTAA GATTCGATAG	600
	CACACTITICA TETTIETATO ACACTEAATO AATOAGGACT TIACOTTETO TAC	653
	(2) INFORMATION FOR SEQ ID NO:265:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 528 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIGINA	L SOURC	E:
	(A) OF	CANISM:	PAG1229UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:	
	GATCAGATAC CGTCGTAGTC TTGGCCCATAA ACTATGCCGA CTAGGGATCG GGTGGTGTTT	60
10	TOTTATGACC CACTOGGCAC CITACGAGAA ATCAAAGICT TTGGGTTCTG GGGGGAGTAT	120
	GETCGCAAGE CTGAAACTTA AAGGAATTGA CGGAAGGGCA CCACCAGGAG TGGAGCCTGC	180
	GOCTTAATTT GACTCAACAC GOOOGAAACT CACCAGGTCC AGACACAATA AGGATTGACA	240
15	GATTICAÇÃOC TCTTTCTTCA TTTTGTGGGT GGTGGTGCAT GGCCGTTCTT AGTTGGTGGA	300
	GIGATITIGIC TOCTITAATIG CGATAACGAA CGAGACCITA ACCIACTAAA TAGIGCIGCI	360
	AGCATTTGCT GGTTGCGCAC TTCTTAGAGG GACTATCGGT TTCAAGCCGA TGCAAGTTTG	420
20	AGGCAATAAC AGGTCTGTGA TGCCCTTAGA CGTTCTGGGC CGCACGCGGG CTACACTGAC	480
	GGAGCCAGCG AGITATACCT TOOCCGAGAG TCTGGTATCT GTGAACTC	528
	(2) INFORMATION FOR SEQ ID NO:266:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 756 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1230RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:	
	GATCCCOGTIA GOCGTCTOOC GOCATAATGT CTGCCGTATA GGTGGACTCT GOCTGTATTG	60
40	TCCGCAGGG AATGGCATGC TTCTTGTAGA AATACAACCG ATCATAGGGC GAGCTCATAT	120
	CCACCGTACG TCGCTGGGAC ACGTACTTTT TGACTGAGCC ATCATTCGCG CTGTTCATTG	180
	CGACTCTAAT CTGATTCAGA ACCCTGACCT CTAGTGCTAT AGCGCAGGGC GTACCTGTCT	240
45	GATGATGCGC TTTTCAATGC TCGAGCGTGC GCAGTGTTAC ATCGATCGTC GCGGACGATG	300
	TTTAAGCAGC ATOCTGAGCT AATATGTATC GGTATAGGCT ATTGGCAGTA GACCTGGGTA	360
	TATACGCCTA GATATGGACA AGATGCTGCG CCTAGACATC CAGAACTTAA CCAGGCTCGG	420
50	GTTAAAGCCA CCCAGATAAC ATTTGAACAT TAGAACAATT ACCACCGCGA ATGGAGGGGA	480
	ACCCAGTCGA AACCCCCACGG CATCCAATAG TTTCCCCCCAA CNGCGAAANG GCAGAATGCA	540
	CCCCCAATG CTCCCCCAAC GCCCACGCC ACCCTGACCC CATTGACCTN GAAGCCCTGG	600

660

GOCNAAACTG CATTITIACCC CCCCCCATIN GGAAAAANTG ACCGAATAAA ANNCCCCCCN

55

	AAAAAAAAAA GOOONOOOOO AATTACTTTT TINOONNOGG OOOONAACOO ONGGOONAA	720
	AAAANNANTG GGGGGGGGTT TCCCGNNYTTT AAAAAGG	756
5	(2) INFORMATION FOR SEQ ID NO:267:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 784 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1220UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:	
20	GATCTTCCGC TCCACTTGGT TGGGCTGGCG CATGTCAAAG GTTAGTAAAA GCCCCGAATC	60
	GTGTACTGAC GCGAACTTGT TGGATCTTCC GGAAGAACAC AAGGACGTAT CCGCGCCCAA	120
	GGACGOGAAA TCATAGGTOG GCATCCACTT TACATCACGG ACGGAATCTG AGCCTGAATT	180
25	GAAATICAGG TOGCIGOGGT TCACCTIGIA AGAGIGOGAC COCAAGTOCC ACACCTIGAT	240
	OCAGOOGICO TOGOCACOOO TGATAAGGAG ATGOGTOTIGG COCATGITICA AGTOCACGOT	300
	CITCATOCAA COCCACIOCT CCCACACOCT CCCICATCAG COOCCAATCC TTTOCCCACG	360
30	COCOGTICAT ATCGTAGATG GAAACCGAGG TCGACGTCCC GCATATGGGG ATGTAATTCT	420
	TOTOGTOGTIG GAACCCCOCC CTTGACGTCC CGAAATCCGT GCTAATCTTG COCCATGTTC	<b>4</b> 80
	CCCCCCCAT CCTCCTCCAA CAACTTCCTC CCCCCCCC	540
35	GITATICCGT GCACCCIGCT GCTCCCTGTA CCCTCCGTCN AACTIGITCA GCCCAAATGG	600
	TOTTCCCCCN CCCCCNCAAC CATGCCCCCT ANCTICTTIG ATTITTTTCC AACCCTGCCA	660
	CCCCCGGTTG CCTGCACGGG GGGTIACCCCC CCCAAAAACCC CNCGCCCCCC CAATTINTCCC	720
40	ACGCCCNCCC GAAITTIGGTT INCCINNOGG NCCCCCCNCGG GNOCHNAAAA CCTCCCCTAA	780
	ACINA	784
	(2) INFORMATION FOR SEQ ID NO:268:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 751 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1231RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:	

	CATCATCTOC GTGAAGOOCG ACAGAAGCCT GOCGATGGAA ACATTOGAAT TGATGCATTA	60
	ACOCAAACAC ATOOGTCATT TOCTCAAACT CAACAGAAAG OOGACGAAGC TOCOCACACA	120
5	GICOCTOCAA ATCTTTAGCC GAGTTCTGAA AATTCAAAGT COGTAGTTCT CGTATGTTGA	180
	AGCCAGATICC ATAAACTATC TITCTCACTCG CCGCATGCAA AGTATCAAGG AATAGGCGAC	240
	AATCOGTAAT GATTOOCTCG AOCTCACOCA GATATTOOCG CACTTCTGAT ATCCGTOOGT	300
10	TOTTOGATOC ATGATOCACA TGAATAAAAG GAAGAAGCTT CGAAAGAGGT ACACGGCCCG	360
	OGTAGOCGTIG TGATGAGAGO TGTTAGTTCG OCTTCAACAT CAGCAAGTTT CTCTATAGGG	420
	GACOCAGOGT CGTCAACATC ATTTATTAGA CACTCCCAGC ATTTGTTCTT GAAAAAAAGT	480
15	NGTGCATGNA CAATNOCNOC CCCCCCTTTT GAAANGCCGG AGAAAATTTC CCTNNAANAC	540
	NAATNICING GINNAANIGC TINNAAANCC CCTINAATIA AACCCTINNN GCCNCAAAAA	600
	AATTNITTAA ANCCTITITNA ACNCCCCGGG AAACANAAAC CCCCCCCCCA AAAAAAAACA	660
20	NGITTINICC NCCCCCCCC CCCCCGANNI TITNAAAACC TITINAAAAAT CCCCCCCCCC	720
	ONAAAAANCC CNCNAATITT TTTTTIAANC C	751
	(2) INFORMATION FOR SEQ ID NO:269:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 762 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1231UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:	
	GATOGTCAGO GTOCATOGAC TTOGCATTOC AAAGOGATGT GATOCCTGAG GOGAGOCTTG	60
40	CAGCAGGCGC GCTCCTTGTT TCACATCATA GGCTGTCGAG GCCGGACTGA TTCAGCTCTC	120
	AAGBOGAGCA COCTOCCAAC GOOCAATAGG GGOOCCCTOC TGGGGTGTGC ACGGGAATAC	180
	CICAGACACT GOGITAAGAT ATATGTATIT AAGAGGGCAC CAGCTGGCTA TCAATTGCCC	240
45	TOTOTOCTOT TOTTOCAACA CCAGOCAAGT ATCATGATGT CTOCTOCAGG AAAAATGTTC	300
	AAGAACAACG COCAGAAGGA TGAGOOGAAG AATGOOGGOO AGAGAGAGAGA GOGOCAGTAC	360
	AGGGTCGGCG ATCAGCAGGG CTTGGGCCGC CAACAGCAGG CTGACTTGGG CGCCCCAGTA	420
50	CCAGCAGGG CCACGCTCGC AGCAGTTCGA CGACACTTGG NOCTTCCCCNA CATTTGGGCC	480
	CCCCACCAAT TOGENCCCCA GCAAAATNOG CCCCNCNNCT TINATITING GGGCGAATGG	540
	GOCINAAACCT ATCCCCAANT TGNGGGNAAC TCCCCCCCCA GNANGAGAAC NCATTTTTGC	600
55	ATTGGAAAAC NCACCTINNN TITGNNAACG CCCCCCCONA AAAGCCANGG GACIGTINIT	660

	ITHIGHAAAG GOCCCCTIT MIGICACAAA AAATTITT CIAAAATTIG CGAGAATICC	/20
5	TCCCTTGGGG CCATTCCOVIT TTTACCCCTTT TAACCCCCCCC CC	762
-	(2) INFORMATION FOR SEQ ID NO:270:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 746 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1232RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:	
	CATCHIATTA ATGAATTITT CCCCACGAAG CTIGICGAAT TIIGATICIA IGCTIIGCAA	60
	GCACTCAACT TGGGCTGTGG TCATGCGAAA CTAACACGCC GCGAAACAGA TACTGCCCAA	120
25	OCCUTAGOCAC TOOCTOTTIG COGTOCTACA AACAAGTGTC GAOCATTAGC GTGTGACTTA	180
	TITAGOGTIG GAATATACAA AAGTAAGGCG TACATGCCGA TATCTCTCTT GTGTTGCTCT	240
	CICTIACCIA CATCIAGATG TAITCAGGGA ACTICCCCGC GAGATTCACG GCCAAGGCCG	300
30	TOCAGOCCET ANAGIGCTOC ACCOGNIGAC CHTICCATCG TICTOGNIGH ATTGNICOGN	360
	AACAAAAACC ACCITICCCC AAANICNAAT AATIGNITCA ACAGGTIGIT CCCCCCATIG	420
	AAAGGGATAN NOGITTAAAC CCGGNCNAAA CAANNAANGG GWAGNITITI TIGGGCANAA	480
35	ACCCCCCCC NAATINAACC GCGIGGGGCC CINCNCAAAA TINITTITIT CCCCCCNIGG	540
	GGNCCCCNCC NAANAACCCC CGNNGTTNNA ATATATCCCCN CTTTTNCCAG AAGNGANTCC	600
	CCCINIAACCC GNOGNGATINT TITTIGTIGNIT TAAAAANNCC CCCCCCCCCC CCNOGGAOGG	660
40	NIVITICATION COCCANCATTI INNACONAGON GAGTITITITIT TOCCTOCOGG GOGAAAAAAAC	720
	ANIGITIVIT TINVINCONA AAAAAA	746
	(2) INFORMATION FOR SEQ ID NO:271:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 777 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1232UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:	

	CATCAGITTG CCGIAAITGA TACAAAAGGC AACTGGTGCG TGGGCGACGT TGCGAGGAGT	60
	AAAAAGAAGT CCCGGCGACT GCGCTTGITA AGGAAGTTTA GCGGGACTAT TITITGACCCA	120
5	GAGGAGTACT CCAATTOGAA TATGATAGAA TOGTCACATA TICACACAAG ATTOCTTGTG	180
	ATGAATAGGT CAACTITICAT GGAAATTGAC TITTGTAGACG GATGGCAGCA GGAAATTGTC	240
	CAAGCAAAGA CGTGGTCTAA CTTGCGGGAT TTTAAACGCC TTTCCGATGA GAGCAGTGTC	300
10	CTACTCACCT GCAAAGAGAT TATATTCCTA GACCACAAGC AGCAGGGAAC AAAGAGGGG	360
	CTATCCTOGA AACACAATTG OGATAOCAAA GATTCATCTC TAAAGCTTGC TATACACATT	420
	TOTOSCASCO ATATGAAACA ATATTTACAT GCATTCCTAT TTCCACCATG ACTCCCTGCA	480
15	GROCITATGT GROCITICITIC COGGROCGAA AACACTITICC ATTITITICAG COATCCCCCC	540
	OCTENTIGIT ITITINCCATT TACACNOONS NITTTACOGA AATTACCTOC COCNTGINCC	600
	NAGAAACCGA GITINANAGA ACCACACCCC CITTCATTIC CCTANNIGIG CCCCCCCCC	660
20	CCAGGGCAG AGTITIGGGN CCCCCNITTI NIGNACCAIN TINCCCCNCC CCNCNAGGGI	720
	TOCCCACCNY AAAANCOCTG AAACCCCTTT TOCCCCCCAC ATTTINGGIN GOOGAIN	777
	(2) INFORMATION FOR SEQ ID NO:272:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 734 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1233RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:	
	GATCACAGIG CIGIGGOCAT TOCTOCTOGT CGTOCTCTIG TGCCCCTCAA GCGCCGAAGT	60
0	AGACAAOCTG CCAOCAAOCA CTGATTOGTA CAOGAGCTTT TTGTTCACGT TCTTAAGCAG	120
	GTTCOCOGTC GAGTCCOCGT TGTTCAAAAC AGOOCCCGC TGCACGCTCG AGCTCGACTC	180
	CCCCCCCCCC CACCACCCCC TOCAATACAC CTCTCATCCC CCCTCCCCAT CCCTCCCTC	240
5	COCAGTCCCC CCOCAAGCAA AAAATTCCTC CACOGATGTA TTCCCGTGGT TOCCCAGCTG	300
	COCACCOCC GTACCCCCAG COCTGTTGAC ATTOGACCTG ATATTCTCCA TCACCACCTG	360
	CGAGCTGATC CCCCCTCGGG CGCCTGTCTT GCTCGCATCT GTAACGTCGT CAGACCCGGA	420
o	GITTIGITCT GICGICCACG AACGAGACGT TCAACCATGT GACGACGCAG GCOCGITTIGG	480
	CCTTCACCAC CNNATTIGGG CCTTTCTGCT GGAACNCCAA CCCCGGGGAAT TTCCCAACCT	540
	NIGATICCON AANIGOCCOG CONCONICCO AAATTANAAT CCCCAATTON GWIGAAAIN	600
5	GNOVARATNA AACCCONTTT TOOCCTINNIN CHNINOCONG GCOCHAANGA GCOGNICGGG	660

	CHITAAANNO COCNACOCCO AAANITATAC CCITITITIG NICCONCOCC CONCOCINI	720
	TTTTINCCC NICN	734
5	(2) INFORMATION FOR SEQ ID NO:273:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 761 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1233UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:	
20	GATCCAGCTT CCATATAAGC TCGTGTTTGC GGTCGCGACC TCTACAGAAG TGGTGATATA	60
	TGATACTGTT ACCACGAAAC CCATTGCAGT GGTGGGAAAT TTGCATTACA CCCCGCTAAC	120
	GGACCTCAGC TGGTCTGACA GCGGCCACCT ACTCGTCGTG TCATCAACAG ACGGTTTCTG	180
25	CTCCIATATC TCAATGGAGG ACAGCCTATT TGGCGAGCCA TACAGTTCCG AGGCACAGCG	240
	GACOGATTCT CTCATACCTT CGACTCCAAA AAGCAACATC TTCAGGAACA CCCTGCGGTC	300
	CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCGGC CACAACGACT CACCCATAAA	360
30	OCCOCCTOCC AAAAAATGTC GCCGCTTTCC CCTGTGGTCG TCGATGAGGG ATCTGCCCCG	420
	GCACACAACC GCCTACTCCT AGCAAAGATC TCAAGCCTCC GAAGGCGCAT CCAACCCGTC	480
	CITGITIAAT GACAACAACG GOGGCACCTA GTATCCCCNC ACGCCATCCT ANAAGITING	540
35	ATTCONVIAT ACTIVAAATAC AAACCCGANA ANCINITTTIC TIGITINACAA ACTITITTITT	600
	CACCTOCATO ACACTATOCO GONGNOGICA TICITOCOGA ATOCCOCCIC COCCITANAA	660
	CNCCCNIACN TAAACCTTCC CNCNICCATA TITIACTCATG AATCNCNGCG AANTCNCTGC	720
40	GCATCNNCCA NCTITIGOGI AGINITCCCC TITTIGITCC C	761
	(2) INFORMATION FOR SEQ ID NO: 274:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 728 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1234RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:	
55	GATCACAGIG CIGIOGOCAT TOCTOCTCGT CGIOCICTIG TOCCCCTCAA OCOCCGAAGT	60

	AGACAAOCTG CCAOCAAOCA CTGATTOGTA CAOGAOCTTT TTGTTCACGT TCTTAAOCAG	120
	CTTCCCCCCTC CACTCCCCCCT TCTTCAAAAC ACCCCCCCC	180
5	CCCCCCCCCCC GACGACCCCC TOGAATACAC CTCTGATCCC GOGTCGGCAT CCCTCGCTCT	240
	COCAGTOCOC CCOCAAGCAA AAAATTCCTC CACOCATGTA TTCCCGTGGT TGCCCAOCTG	300
	COCACCOCCC GTACCCCCCAG COCTIGTTIGAC ATTIGGACGTG ATTATTICTCCA TCACCACCTG	360
10	CCAGCTGATG CCCCCTCGGG CGCCTGTCTT GCTCGCATCC TGTAACGTCG TCAGACCGGA	420
	GITTITIGITC TGTCGGTCCC ACGAACGGAG ACGTCCAACC ATGTGTACAA CAACNCGITT	480
15	TTCCCCTTCA CACCCATTIC CNCITTTCTC GINGAACGCC AACCCCGGAT TTCNCAACNG	540
15	CNATTITOCOVI ATNOCCCOCC CCCCONCONNA AATANAACCC CAATGINGNN TGAAANGGNA	600
	NAAAANAACC CCCTTTTCCC CCTTTTCAAA CCCCGGCCCN AAAGGCCNNT GNGTGNNTAA	660
20	ANCCCCCCCC CCCAATTTAA TCCCTTTTAA TTGCCCCACC CCCCACCCTT TINITINANC	720
20	CCINNNCN	728
	(2) INFORMATION FOR SEQ ID NO:275:	
25	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 782 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) SIRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1234UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:	
	GATCCAGCTT CCATATAAGC TCGTGTTTGC GGTCGCGACC TCTACAGAAG TGGTGATATA	60
	TGATACTGTT ACCACGAAAC CCATTGCAGT GGTGGGAAAT TTGCATTACA CCCCGCTAAC	120
40	GGACCTCAGC TOGTCTGACA GCGGCCACCT ACTCGTCGTG TCATCAACAG ACGGTTTCTG	180
	CTCCTATATC TCAATGGAGG ACAGCCTATT TGGCGAGCCA TACAGTTCCG ACGCACAGCG	240
	GACGGATTCT CTCATACCTT CGACTCCAAA AAGCAACATC TTCAGGAACA CCCTGCGGTC	300
45	CAACCCGGTC AACGTAAAGC GGAAGCACTC TGTAGGCCGC CACAACGACT CACCCATAAA	360
	OCOCOCTOCC AAAAAGTGTC GCCGCTTTCC CCTGTGGTCG TCAANAAGGN ATTTGGGCCC	420
	OGACCACNAA COCCTACTOC TTANCAAAAA ATTTTTCAAA NOCCCCAAAG GOOGTCCCAA	480
50	CCCGNCCCTT GITTITITGA AAAAAAAANG GGGGNCCTCA TITTITINCCC CNCCCCCNCC	540
	CCAAAATTTI GGGGATCCCN NINCONAAAA AACAACCCCC AAAANCCTTT TICCGGITAN	600
	NAAANNITINN CHNINGACCC CCNCCCCCCC TICCCGCCNCG TCATTININC NAATNGCTCC	660
55		

	GGGAAAATTC CCINCNGGGAN NINNCNANITT TICTIGGICT CCCCCTINITT NITCCCTTINA	780
_	œ	782
5	(2) INFORMATION FOR SEQ ID NO:276:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 747 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1235RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:	
20	GATCCTTGAG AAGCCAGATA ACGACGAGGA CGAGGAGCCC AGTGACGATG AGGATGCCGA	60
	CGACTACGAC TCGGATTCTC CCCGGCCCGG CGACAGCGGC AGGGAACTCA GAGACCCTCC	120
	TOCOCCOOC ACATTCOCTA COGAACTOCA COGATCCACC GTCCTOOCCT CCCCGTTGAC	180
25	CTATICCTE COCTOCGICA TOGICCACIA TOGCACACAC AACTACGGAC ACTACATEGC	240
	CTTCCGCAAG TTCCGTGGTG TGTGGTGGCG CATCAGCGAC GAAACAGCGT ACATCGTCGA	300
	TGAACCTCAG GICTTGTCCA CACCOGGGT TTTCATGTTG TTCTACGATA TGACTATGAC	360
30	CACCCACCE COCACTICCE TEACCACTIC COCTOCCTAC ACCACCCAC TCCCTOCTCT	420
	CAGATOGOGA COGAAGAATA CGACTCATTG ACCOGOTCCA CCAAGACCTC GATTCAACGA	480
	NCCASCIGIT GCTCCCGCCA ATAAACTITG TTTGGGGCTG GCCGGCCCATA ININCTCCAT	540
35	OCATGUTCAT GOCCCCACCG GACATGUTTG ATCCANATAC TUTTIGUTUN GUINCOCCCT	600
	TICACNONIT COCCCINAAGO AAGATICITA NICTACTIGO CINGITIGITO CONCCINGITI	660
40	TOGNACCCCA AATTCCINIT NINCCNITINI OOCCCANCCC NINGGNAAACC CNCCCITITIT	720
40	TTTCAAACCA GGVITNCCCT TTTNGCN	747
	(2) INFORMATION FOR SEQ ID NO:277:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 776 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1235UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:	

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	GATCACACCC GIGITCITIT CAAAGGICAC CIGCAACTIC TIGITATICA AGATGATAGT	60
	CTCACTGTCC TTTGACACGC TAGCAGGGTA AAATACCGAC TCCTGCGGGT CAGCGTTTTC	120
5	TOCAGCCATG TTATCCCATT GCAAGGTGCC TATTGGGACC AAACTTTCCC CTCCTGTGTT	180
	CAAGGCCTCC AAAGCTCTCT CTATGAACCG ATCTGCTAGC TGCACGACCT TGTTAAGCAT	240
	TOGIATIOCT TCATATITICT ATACCATTIC TATACATGIC CCCCCAAGGA CATCGICGAA	300
10	CTGGCATAAC AAGATATCTT CCCATAGAGC GITAATATCA TTAACAGGGT ACGTGTACTT	360
	GITAGGCOCT AGTAGCGAAA CCTTTGTGGC AATCCACTCC AAATCATGGA TCTTAACCTC	420
	AGATAGTCTC ATCAACCGTT TAACGTCTOC CTGTGTCGTA TACGTGCCTC CTATGGAAAT	480
15	CAAAGITIACA ATCCOCCCAT CCAAGITTOOC CAATGNGTTC CCANTGTCTG NCTTCNOCAT	540
	AATATCACCG TAAAAAACCGT TTANGGAATC CCCNACCCCC NACCTTNGGG AANAACATTG	600
	CATTCCCCCCT TAAAATTGAA CCCANACCCC CCATTTGTTC CACCNCCCCC TGTTTGAACC	660
20	CONCOCCION CNOCCAPACCO NNAAAAAAAAA COGTTOCCANA ANGITCATTIN AAAGTTTTGT	720
	TCCCCCCCGG TTTAAAANCC NAATTTINAN AAGCGTTCTT TTTCCCCGGGG GGGTIG	776
	(2) INFORMATION FOR SEQ ID NO:278:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 722 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1236RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:	
	GATCTCCCTC CGGTCGAAGT ACGTCGACTG TTTGAGACTC TGCAGGTCGT CTTTTGATAG	60
40	CTTCGATGCC TTAGCTCCCA TGTCTACTAT AACGCTGTCC CGGGCCTCAG CTATGTGCGG	120
	OCTOCCTATC THACTOCCTA ACTICTIOGAA OCGTICAGAGG CCATAAGCCA CGATCOGCGA	180
	GCTGCTCAAA TIATGTCCTC TGAAAGCGGT GTGTGGGTCC ACTTTCCCAG ACCCAAGGCT	240
45	ATRICOGGITTA COTGACCTOC GGTCCGGATG TGACGCTGGG AGRCGGTGGG ATGCCGGCCC	300
	TCATOSCTGT COGTCGCGAA GGACTATCTA CCAGGGACTT GGCTGCCTGC GCAATTTGCA	360
	CTOCAGCTTG CAGTGGAGGT CTTGGCGAAG CTCACCGGCA GCGGCAGGCA GTTACAGCCA	420
50	TOOCACAGOC CAAGCCCCOC GAGTTGACCG GAGTTGGTTG CCAGATATTG GOCCGTCCAA	480
	ATTICTGANTA GCCCTTTATA TNAGANCCCC NCCGTTGAAC CCCAAGNITT TTTATGCGGA	540
	TOCTTOCAAT TONOCCCCT GOCTTAACCC CCCCCGAACC CCTNCCCCCG GCAAAANCAA	600
55	ATCCTNCCCC NGTTCNAAAA ANCCGAACNC NNAAAATTTT AAAAGAGACA AATCANNACA	660

	CCCGNGAAAA AGAGCCCTINT CTTTTGAGAA TICCCGGGGG GGGGCNGTAAA TINAACCTTT	720
	GA	722
5	(2) INFORMATION FOR SEQ ID NO:279:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 789 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1236UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:	
20	GATCHTOGTC COCTTOCOGT CAGGAAATTC AAGCOGGATG AGCTCTTGTT TCAGHTTACC	60
20	ATAAAAGAGC TGTTTTACAA GGTCGAATTG CTCGCCCTCT TCATCCAAGC TGAGCGGGAC	120
	GGACGCACTC TCAATTTOGT AGAGGACGTT CCCAATGCAT TCCGTCACAT CTTGCTGTCT	180
25	GCCAATCTCC AATGTGTTTT CTAGCTGGTC GGAACTAATT TTCGCAACAT AGGTGGAAGT	240
20	TICAGGGCT TOGGCTCTG GACTCCCGAC CATOGTGATA TCTTTACCTG AGTCATCATT	300
	CTCAACAGCC TECCTATCCT CAAGCGGACC TECCCTGGTG TTTTCACCCN TIGGGNGCNN	360
30	GAANICCAAT ANNOCCCCTT TCTGGGGTTC TTGGGAAAGNA TTNGGANAAT TINNTGGCCC	420
	GETTINITIACC NITTINGANA GAGACCCTIG GINTINICINAN ACCINAAATINI TCCCINIGEEG	480
	CNOCCOGONOG AAINITITIN INICCAAANI TICCNAAANN CONCITTINI GCITTICCCC	540
35	NITTINGGNGG NAGCOCCCCA GGGGGNCCCC CGAANITAATC NGGGGGNTGG AAAAANAAAA	600
	NAATTICCCA NAGGOGINIT INITITICCN TCNGAGAAGG GNOGITANAA AAACCCATTT	660
	THICCCCCCIN NITAGANIAACC CCTITTINCING CGGGGGIVICC NGCCGGGGG ATTINITIGNIGG	720
40	GNOCNITIONN NACCTOCCTT CCCCNCTATA NAAATNOCCC COOOOOOG TTINNTTTIC	780
70	CCCINDAAAN	789
	(2) INFORMATION FOR SEQ ID NO:280:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 676 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPCLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1237RP	
55	(xi) SPOUFNCE DESCRIPTION: SPO ID NO:280:	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

	GATCCGGGTT GAAGACATIG TCAGGIGGGG AGITIGGCIG GGGCGGCACA TCIGITAAAC	60
	GATAACOCAG ATGTCCTAAG GOOGACTCAT GGAGAACAGA AATCTCCAGT AGAACAAAAG	120
5	GGTAAAAGTC CCCTTGATTT TGATTTTCAG TGTGAATACA AACCATGAAA GTGTGGCCTA	180
	TOGATOCTIT AGITCCTOGG AGITTGAGGC TAGAGGTGCC AGAAAAGITTA CCACAGGGAT	240
	AACTOSCITE TOSCAGICAA COGITCATAG CGACATIGCT TITIGATICT TOGATGICOG	300
10	CTCTTCCTAT CATACCGAAG CAGAATTCGG TAAGCGTTGG ATTGTTCACC CACTAATAGG	360
	GAACCITICAC CTOOCITTAC ACCCICCCIC ACACACCITA CITTIACCCI ACTGATGAAT	420
	GITATCOCAA TAGTAATTGA ACTTAGTACG AGAGGAACAG TTCATTCOGA TAATTGGITT	480
15	TIGOGGCTGT COGACCOCCC ATTGCCGCGA ACTACCATCC GCTGGATTAT GGCTGAACGC	540
	CTCTAAGTCA GAATCCATGC TAGAACGCGA TGATTCTTTT CTCGCACATT ATAGATGATA	600
	CGAATAGTTG CTTTTANCAT COCTGAACCA TACAGCCGCA CTGTGTTCAA CGAAGTCTGG	660
20	CCCTTCCGCG ATTGCA	676
	(2) INFORMATION FOR SEQ ID NO:281:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 709 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1237UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:	
	GATCCCGTAC ACGAAGAAAA TCGGACGGGC CAACCAAACC CAAAGTTCAA CTACGAGCTT	60
	TTTAACTGCA ACAACTTTAA TATACGCTAT TGGAGCTGGA ATTACCGCGG CTGCTGGCAC	120
40	CAGACTIGCC CTCCAATTGT TCCTCGTTAA GGTATTTACA TTGTACTCAT TCCAATTACA	180
	AGACCCGIAT GOGCCCIGIA TCGITATTIA TIGICACIAC CICCCIGAAT TAGGATIGGG	240
	TAATTTOCOC OCCIOCIOCC TICCTIOGAT GIOGIAGCOG TTICTCAGGC TCCCICTCCG	300
45	GAATOGAACC CTTATTCCCC GTTACCCGTT GAAACCATGG TAGGCCACTA TCCTACCATC	360
	GAAAGTTGAT AGGGCAGAAA TTTGAATGAA CCATCGCCAG CACAAGGCCA TGCGATTCCG	420
	AAAAGITAIT AIGAAICAIC AAAGAGICCG AAGACAIIGA TIITITAICI AATAAATACA	480
50	TOTOTTOCAA AAGTOGAGAT TTTAAOCATG TATTAGOTOT AGAATTACCA CAGATATOCA	540
	TGITAGITAA AGAACTATCA AATAAACCAT AACTGATTTA TGAGCCATTC CGCAGITTCA	600
	CTGTATAAAT TOCTTATACT TAGACATOCA TOCTTATCTT TGAGACCAGC ATATGACTAC	660
5 <b>5</b>	TOGCAGATTC AACCAGATAC TATCTTTAAG ACACCCGAAA TOCCCAACA	709

(2) INFORMATION FOR SEQ ID NO:282:

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 820 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1238RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:	
	GATCACOOCA ATGAAAAACT ACOCAAACGT TACAGACTIT GAGTGGTACA TCGCCCTGCT	60
	TTCGGATCTC TGCATAGTCT CCCAGGACCT GCAAGACAAG ACCCTCGCGC AGAAACTGGG	120
20	TGAGCAAATT AGAAACATCA TGGTGAAGGT TCCTGACCTG CGGGATGGCA CTTTGGCGCA	180
	GATTOTOCAG CTOGTGAAGA OCGAGGACAT CACOOCCOG CTGCCCGGTG TTCTGAAGGA	240
	GTOCATCTOG TOCCTOGOOG AGTATTOGTC GTTOCTOGAC AATAAGGATG AGTATATTCT	300
25	OCTATIOSCA GAAAATICGA AATTATATGA OCCTGAACTA CAGCAAACTI ICATCCCTGC	360
	CATTITICAAG ATTIATACCA ATTICGIGIAA CGAGTCOGIG GTCGACACCG GTCCGTATTA	420
	AATGOGTTAC CGAGCGGATA ATCACCCCAC TAGAAGATCT AATAATCTCG AAGAACTTCG	480
30	AAGTOCAGGA GOGGTCTTCC GAGGCTCTCG AATTCTACCC TTNTTTCTGG ACNCCCCCTC	540
	CNAAATNATO TGNATOOCTA NONGOTOGCA NOTTAGNAAT TOOTNGOOCA NITICINCAAC	600
	CCTTTGAATT NACCNONNIN CONTOCCCCC CCCAAAAANC TONNNNAAA CTNTTNITTON	660
35	ATGOGAACCC CCTTTNCCCN AAANGAAGCC ANANNINVACC GNAAAACNCN CTTGAAGNGA	720
	TITCCCCCGAG TTITGANAAC ATTTCNNCCN AATTTTCCCCG GACGGCCAAA AAGGGTTTIN	780
	CAAATTANIT COOOCOCCA ACCOCCAANCG GOOCCANONA	820
40	(2) INFORMATION FOR SEQ ID NO:283:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 875 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1238UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:	
55	GATCAGAAAC GOCCGOCTOC AAGAATGGAT GOCGATGAGC TTCGAGCAGT TGAGOCATCG	60

	CITATOCAAA AAAAGAAATT CCICAGATCA CGIGACAAAG TIIICGICAIC ICIAAAIGIC	120
5	GACOGITOGG CGAAATGIGC CGICCTCIGC TATAAAATAT AAACTAGITT CTCTACCACT	180
	AGACTGATTG GGAATATCTA AGCTTTCACT TGATAGCAGC AGGAGCACTT CATAATCCAG	240
	TACCTTCTTT GOCTTATCCA CACTAGTCAT CICATCGAAA ATGTCACAGC CAGTGCAGAG	300
10	AGCCGCCGCT CAATCCTTGA TATCCAAATA TGTCAATAAG GAAACGCTAA AATACATGCT	360
70	TACAACGCAC TICIGGGGCC COGIATOGAA CITIGGIATT COGATIGCIG CGATITATGA	420
	CITICAACAAG GACCCICAGT TGATTITCCGG CCCCATGACG TTGGCGCTCG TGGTATACTC	480
15	AGGIATITIC ATGGGITACT CGATGGCCGT CACTCCCAAG AACTACCTCT TGTTTGGGTG	540
,,,	CCCACTITAT AAACGAGICC CCCCCAACTC GGACAGCGTT CCCGCTGGCT CAAGTITCAA	600
	THACTTCGGC GAGAGCCCTG CTGTCAAGGC ACCCGAGAGA CCCGCATAGG TGCGTTTGCG	660
20	TCCGCACACG TTGCATTACA GCGTCGACCA CTACATAGAA TATTATTAAG CCGACTATCC	720
20	TACACGITTIC TAGASCTAGT CGAGATGCCT TIGGCTGATA CTGCTGCGTT GGGCCAGGCC	780
	GTATCTTOCT CCTCCTOOCT TIGCTOCGIT GCGCAGCTCC CANTIGNCCG TICNCGATNN	840
25	TOCTIGIGIOC OGTATOCATT GNOTAAATGT CTOCC	875
	(2) INFORMATION FOR SEQ ID NO:284:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 716 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1239RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:	
40	GATCAACTTA GAACTGGTAC GGACAAGGGG AATCTGACTG TCTAATTAAA ACATAGCATT	60
	OCCATOCTICA CAAACTICATC TTCACOCAAT CTGATTTCTC CCCACTOCTC TCAATGTCAA	120
	AGTGAAGAAA TTCAACCAAG COCOGGTAAA COOCOGGAGT AACTATGACT CTCTTAAGGT	180
45	AGOCAAATOC CTOGTCATCT AATTAGTGAC GCGCATGAAT GGATTAAOGA GATTCCCACT	240
	GTCCCTATCT ACTATICTAGC GAAACCACAG CCAAGGGAAC GGGCTTGGCA GAATCAGGGG	300
	GGAAAGAAGA COCTIGTTIGAG CTTGACTICTA GTTTGACATT GTGAAGAGAC ATAGAGGGTG	360
50	TAGAATAAGT GOGAGCTTCG GCGCCAGTGA AATACCACTA CCTTTATAGT TICTTTACTT	420
	AFFICAATTAA GCGGAGCTGG AATTCATTIT CCACCTTCTA GCATTTAAAG TCCTATACGG	480
	GCTGATCCGG GTTGAAGACA TTGTCAGGTG GGGAGTTTGG CTGGGGCGGC ACATCTGTTA	5 <b>4</b> 0
<i>5</i> 5	AACGATAACG CAGATGTCCT AAGGGGGGACT CCATGGAGAA CAGAATCTCC CAGTAGAACA	600

	AAGGGTAAAG TOOOCTIGAT TIGATTICAG TGTGAATACA ACCATGAAGT GTGGCCTATC	660
	GATCCTTAGT TCCTCGAGTT TGAGCTAGAG TGCCAGAAAT TACACAGGAT ACTGCT	716
5	(2) INFORMATION FOR SEQ ID NO:285:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 793 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1239UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:	
20	GATCATCTIC GATCCCCTAA CTTTCGTTCT TGATTAATGA AAACGTCCTT GGCAAATGCT	60
20	TTCCCAGIAG TTAGTCTTCA ATAAATCCAA GAATTTCACC TCTGACAATT GAATACTGAT	120
	GCCCCCGACC GTCCCTATTA ATCATTACGA TGGTCCTAGA AACCAACAAA ATAGAACCAA	180
25	ACGICCIATI CCATTATICC ATOCTAATAT ATTOGAGCIT GCGCCTGCTT TGAACACTCT	240
20	AATTTTTCA AAGTAAAAGT CCTGGTTCGC CTAGAGTACA AGTACCCTAG GTTAGCCAGA	300
	AGGAAAGGIT CGGTTGGATC CCGTACACGA AGAAAATCGG ACGGGCCAAAC CAAACCCAAA	360
30	GTTCAACTAC GAGCTITTITA ACTOCAACAA CTTTAATATA COCTATTOGA GCTOGAATTA	420
	CCCCCCCCC TOCCACCAGA CTTCCCCTCC AATTGTTCCT CGTTAACGTA TTTACATTGT	480
	ACTICATIOCA ATTACAAGAC COGTATOGOC COTGTATOGT TATTTATTGT CACTACCTOC	540
35	CTGAATTAGG ATTOGGTAAT TTGCGCCCCT GCTGCCTTCC TTGGATGTGG TAGCCGTTTC	600
	TCAGOCTCCC TCTCCGGAAT CGAACCCTTA TCCCCGTTAC CCGTTGAACC ATGGTAGCCA	660
	CTATCCTACC ATCGAAAGIT GATAGGGCAG AAATTIGAAT GAACCATCGC CAGCACAAGG	720
40	CCATGCGATC CGAAAGTITIA TATGAATCAT CAGAGTCCGA GAACTTGATT TITTATCNATA	780
70	ATMONOTOTIC CAA	793
	(2) INFORMATION FOR SEQ ID NO:286:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 836 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
<i>50</i>	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1240RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:	

	Guerran intermedia regularian intermedia diacantan includigi	60
	ACTAAAGGAT TACCTGGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
5	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTTT AAAAATAAAA	180
	TAACCATOCA TTOGIAATCT ATCTAAATTA CCTGTAATAC CTAATOGATT TGATGAACCA	240
	TGTACATGTA ATACCATTAA ATOCATAATT ACTATTOCTG CAATAATAAA TGGTACTAAA	300
10	TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT	360
	CATAGTACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGTA	420
	GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA	480
15	GITAAAATAA AGATAATAAC ACCAACTGIT CCATACAATA ACTCTAGGTG ATTTATAAGA	540
	ACCATAATAT AAACCITTAC CAATATGAAT ATACATACAA ATAAAGAAGA ATGAAGCACC	600
	ATTAAGAATG CATATATCTA ATTATCCACC TATTGTACTC TCTCANAATA GITCCTACCT	660
20	GATGANAAGC TATCCATATT ANAAGAATAT GCATACCTTA AAAATACOGT TANAATTGAA	720
	TACTAACATA ACCTATAANA CONAATTCAC CATAATAATG AGAGGGTGAG GNGAACCATA	780
	CNIACNATAC TAATITAATT ATTGATTICT TICCCNITTT ATTATTAAAT TITAAT	836
25	(2) INFORMATION FOR SEQ ID NO:287:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 860 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1240UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:	
10	CATCTAGAAT TATTAAGICA ACTATTAACT AATATCTATA ATAATAATOG TTTATCATTA	60
	AAATCATTAA AGATAATTAT TAATAAATTA CCATTTAATA ATGATATATT ATTATCAAAA	120
	TARTARIAA TITARTARIA ATTARTORIT TARTARARI ARATAARIA ATTORTIAA	180
15	AAAAAAGATT TAATTAATTT ATATACTTTA GATAATAAAT TATTAGATTT AAGIATTCTT	240
	AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TCCAATTAAA GOGTAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
50	TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
	ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAAATTAAA	480
	TTAAATACTA TTTAATAAAT ATCTATAAGT AATTTCTTAT TTATTTTATA ACATTTTAAA	540
i5	ATGITTIATG TTTAAATAGA TAATAACAAT TAAATAATAA AAATTAAGAT GOCACAAATA	600

	TICCATTI CCTTIAIGAA TCAATTACTI AIGGITTECT ATTIATITTA CTATTITATC	000
5	CITCTATCIT ATGINITITA CCTAACAATT TAANAATATA TACTCCTAAA TATATATTCC	720
3	NAAATTATAA TAGTTATTAA ATTITAATTA ATCCANIATG ATCCNIATTT ATAAATATAT	780
	ANGAANATTI TAATATATAT ATATGAATNI TATATONOON TGAACCATTG NAATNNATTA	840
10	TAGTITIACAC CCCCTANATC	860
10	(2) INFORMATION FOR SEQ ID NO:288:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 837 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1241RP	
	(sei) CENTENTE DESCRIPTION, CENTEN NO. 200.	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:  GATCTAAATA TATATAATTT AATTTATAAA GATTAATATA AACTTTTTTA TTATAATATT	60
23	TAASTATTAA ATEATTIAAA CATTATTAT CATTATTAA TAAATTAATT ATTIGATTAT	60 120
	TAATACTTAT TATATAATTA TTATATAATT TACTTAATTC ATCATTATTA ATATTTATAT	180
30	AATTATAAAA ATAATATTA ATATGAATAC TATTTAGTCT ATGITCAAAT TITAAATTAG	240
50	TTATTAAAAT ATTATTAGAT ATTATTATTT TCTTTAATAA ATTATTAAAT AGATTATCAA	300
	TAATTAATAT ATTATTTATT AATTGTTTAT TAAAATAATA TATTTTATTA TTATAAAGAT	360
35	TIAATTIATI TAAATATIGT AAATTATTAT TITTIATTATA ATATCTATIT TIATAAATAT	420
	TATGITGATT TATATTATTT AATCTITTTA TAAGAATTAT TATTAAAATT AATTITAACT	480
	TEAATTICTT ATTATTAATT TITATATTAT TTAATAAATT ATATTTCATT TTATTTATT	540
40	ATTIVATURA TEAATTAAT TATTIVATEA ATATTIVATO ATTATTIVAT TAATTAATAA	600
40	AATATTATAA AGAATGTAGT TAAAAATACT TATAAAAGGA TOOGAACCTA TATTATTGTT	660
	TATCAGACAA ATOCTITTAGC CCATAACCTA TATAGTITIGA CTATCATTIG AGANITGGGT	720
45	NUNCCOCCIA TOCTINICATO CTGNIGTOCO CNUTAAANGA ATTINITTINI TINANANAIGA	780
	AAAANTTATT TATCAAAGAA TIATAATTITI TITAANAAGGG GNANAAGGAA AGACCCG	837
	(2) INFORMATION FOR SEQ ID NO:289:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 856 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	vi) ORIGINAL		E:
	(A) OF	CANISM:	PAG1241UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:	
	GATCIGIATA CTAGAGCITA TITTACTICA GCTACTATAA TIATTCITAT TCCTACTAGT	60
10	ATTAAAGTAT TTAGTTGATT ACTAACTATT TATOGTOGTT CATTAAGATT ACTAACACCA	120
	ATATTATATC TATTATCATT TITATTITTA TITACTGTAG GIOGITTAAC TOGTGTAGTA	180
	TTAGCTAATC TATCATTAGA TGTAGCATTC CATGATACTT ATTATGTAGT ACTACATTIC	240
15	CATTATGTAT TAAGITTAGG TOCTGTATTC TCTATGTTTG CTGGTTATTA TTATTGAAGT	300
	CCTCTTGTTT TAGGITTAAA TIMTAATGAA AAATTATCAC AAATTCAATT CTGATTAATT	360
	TTCTTAGGIC TTAATATTAT TTTCTTCCCT ATGCATTTCT TAGGIATIAA TGGIATACCA	420
20	AGAAGAATTC CTGATTATCC TGATCTATTC CTAGGTTGAA ATTTAGTATC TTCATTTGGT	480
	TCTATAATAA CTATTATATC ATTAATGTTA TICCTTTATA TIATTTATGA TCAATTAATA	540
	AATOGTTTAA CTAATAAAGT TAATAATAAA TCTATTAATT ATATAAAACT ACCCTGATTT	600
25	TATTGAATCA AATAATATTI TCTTAATGAA TACTACTAAA TCACATCTAT GATTTATATG	660
	AATCACCACT CTTAATCNAT CAATTAAACC CTCTAATCCA ACTITIAAATA NNCTTAATTA	720
	TAAATTANNA ATAAATTTAG TOGAANAATT AATNGTAANC AATNTTTINA NOGANTTTAT	780
30	CTCNVICCAA CCGAAACTAC TTTTATCCTT AANNAAAACC TTTAATNAAT GGACCNCANA	840
	MICHNAACHN GITTIC	856
	(2) INFORMATION FOR SEQ ID NO:290:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1242RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:	
	GATCACGIGC TAAATGICCG GGTACATTAG TGCACCCGTA CACCGCATTA CGACATTACG	60
50	ACGCTTCTTG ACTAACCAGG TTATCACGTG TATATAGTTA CATACGAACG TCTGGTACAA	120
	GGAAGAGCCG GCCGGAAGTC CACTTCACCC TTAAATTGCC ACATTTCATG AGCATTTACA	180
	ACAGAAGCAC AGCTGTAAAC GTTTCTOGAA CTCGTGAAGT TTCATATTGT TCCTTAAGGG	240
55	COCHIGATICE TICCACITICAA COTACITICITE TITOGCACACTI CONCUENCIA TAACIICONICA	300

	ATTGTTCATC GCTTCGTCAA GGATTCGTTC GATGAGTTCC GGGAAAGCAC AATCGGCGCC	360
	GCATTICTGT CCCGTACCAT CAAGCTGGCG GACCACGACG ACGCAATGAT CAATTTGAGA	420
5	TCTGGGACAC CGCGGGACAG GAGCGGTACA AATCGCTGGC TCCGATGTAT TACAGGAATG	480
	CGAACGCCCC GITGGTGGTG TTATGACGTT GACACAGGAG GATTCTCTAG CAAAGGCACA	540
	GACCICCCITI GAACGAAITA AGACCACCIT CCIGACGAGA AITICICCITAT CTICCCITCIT	600
10	GCGCATAATT GATTNGGGGA NGAGGANCGG AACCNAGGTG ATTGACNCGA GAACNCAGGC	660
	TCCCCAAACC CNGGGTGANT TCCCCNAGGT TINNNCCAAA CCGGCCGGTT NCCGGATTIN	720
	TICCNOOGAT TOGGGGAANN CIAAAAACNGG GCNAITCCNI NGGGGCCCCC CCGGNICCCC	780
15	ANTITICONTE CAAGNOCCCC CAAAGAACAC CCTGGGGGNIT ACCCCCTCCC N	831
	(2) INFORMATION FOR SEQ ID NO:291:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 878 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1242UP	
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:	
	CATCTIGICG ATIGICAAGG AGGAGACGAA AAACGCTACC ATCAGIGITG CCGTCGAGAA	60
	CAAGCAGCTIC ATCCCATTCA TITCGCTGGG GGACGTGGAG ATTTCGCGAGG ACGTGACTGT	120
35	CAACCCTTC CCTAACCCCT CTCACAACAT CCTTCTTIATC CCCCCACCCC ATCAACCCAA	180
	GGAAGCAAAG GTGAATGITC AGAATTACTT GAACACTTTA GCAAGCAAGG TAICTGAGAA	240
	AAAGATTITCG ATTCCTCGCA AGTTCCAGCC TCTGATCGAT GCAGAGGATG TCAGGGAGAA	300
40	ATACAAGGIC TCCGTTATCT TCCCAACCGC CCTTGGTGAT GATACTGTGT CGTTCTACGG	360
	ACTIGICOGET AATETTIGATIG ACGOGATOGE ATATOCTOGE CAGTICGTETA AGCAGTACAT	420
	OCTAGAATCT TTOGAGGIAT CCAAGOCTCA COGAAAGAAT GTCOCTCATG CAAAGAATTT	<b>4</b> 80
45	AATGITCIAC TICGCCAGIT ACGAACTCCT CCAAGGATAT TAAGGAATTC GTTCCAAGGG	540
	ANTIGAANIT TIGINCIACC CACTCCCGGA GGGATTIGCC CGNITIAAAN AAGNITTINA	600
	ATNOACANTT TITICCAAAGG GNGAATTTTG GOGNACAAAA AAAANTGINT TOOCOGNONA	660
50	TNCCTTATTT NITTAACNACC CCCCCTCCCC NGTTTCCNCC GNTGAANACC NAANTATNAC	720
	CCTTTCCCCC AGNGATTIAC CNGGGCCAVIN CAGGGGANIC CNCTTTTTIN CTCCGGANIC	780
	AANAAAGGGA AANACCNGNN GCTTTTGCCA GGNTGANAAA AAATCCNCCC CCCCCAGAGG	840
55	TAAGANCONN GNAAGGNGNG COCNTTIGGA GAATNCCC	878

(2) INFORMATION FOR SEQ ID NO:292:

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 844 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1243RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:	
	GATCOCTAAT CCCGAGGITT GITTIGAAGT CIGIGATCAG TIGGITCTCC ACATCITTIGA	60
	GAATTCTAAT AGCCTCCGAT GGCAGTTCCT CCAATTCCAT TCGCACCTGG GCAGACTGTA	120
00	TOTTTAGAGA GIVATTITICO ACACACAAAG AGICAATOTT GIOTTGAACA TOGTCAATOA	180
20	TATACTICAG TACATCGTIC ATGITITGGTA GATTCACTGA GCTTTTCAGT GCGCCTTTTC	240
	CTAGCOCCGA AAGGITCCCC GCTTCATTCG ATGAGAAGCC TAGAACTGAC ATCATGGCGT	300
05	GOCAGCATGT CTTCCGCAAC TGTGACAACC AATAATTCAA GACTGCGGGG CCTAGATAAC	360
25	ACCOCCCTTG CCCGTCTGAG TCATACCCTG AAGCCTCCAA GAAGGATTTC CATACGTTAA	420
	CATAATTATC ACCCTCTATC GGTGAGAATT GAAGITGGAT TAAGTAATGA TGCTGCTTTG	480
	GGATTITIAAT CTGATATICG ACATCATICT TIGTATGACG GATACAAACG TIGAAACGTG	540
30	GGATGATATC AAGAAGTTCT CTTGCCGTGA AAGTCACACC GTTGACACGT TGGAGCTTTG	600
	CGAATTTGTT GCGGGATCTA GATGCATCCG ATTGTTGCCC AGTTCCCTGG TATTCTGGCA	660
05	GACTIGTIC GATATACTIT GGAGATCCCT TGAAGGGATG CACTIGCCATT AGAAATACAC	720
35	CTTGAATCCN CTAGTGAATG ATAGGTNTAC CCGAACCCCC ANTTTTGATA CCCNOCAGAG	780
	THIGHNOATO GOCCCCTION NOTICOTOCC CACATIGCOT COCNATITIA TOCTGAAATG	840
	CTTA	844
40	(2) INFORMATION FOR SEQ ID NO:293:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 865 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1243UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:	
<b>5</b> 5	GATCTCGTCC CACCACGGCC GCACGAACGT GTACTGGCCT TTTGAGATCA ACTCTGTCAG	60

	GACGTCGATC TTTTCGTCGT AAAAAGGCCG GAAGCCGCAC AACACGGTGT ATAGGACGCA	120
	GCCCATCCCC CACATGTCGA CCTTCATGCA GTAGCGTTCG TCCTTCACCA CCTCGCCCCC	180
5	GGTGTACCCG ACAGTCCCGC ACGGCGTCGT GGTGTTGGTA GCATAAATTT GCTTCGAGAG	240
	TCCGAAGTCT GOGAGCTTTA TCACACCGAT CCCGCCGCCC CCGATGCCAG GTCGGAACAG	300
,	eccencatat taititaiai tiessicaic ccaetaicic ascieciese ectieciese	360
10	TATAAAATCA ATTOOOGACA ACAGCAAGIT TICTOOCTIG ATATCCCOGT GGACAATGCC	420
	AAGCCACTOC ATGTGTTTTA CCCCCACTOC CACCTCCCTG ATTACATGTC TACAAACGTC	480
	CTCCGAAAAA TAAGTGAGTC GCAGGATTTC TCCAAAAAATC TCCCCCCCGG GCAAGCAGCT	540
15	CCTOGACTAT GAAGTAGTAT GACTOGGTCT CCCTOGAAGT CGATAAACGT CACAATGTTT	600
	TOCCOCCACE ACACCOCCTT GIOGRATCHE ATCTCCTTCA CAACTCCTCT COCCATCTCG	660
	CCTGTTTCCC CCCCTCCNCC CNCTININNC CCCCCCCC NCGTCCCCCC ATCGTTAANA	720
20	GENNOCTITIT GCTGATCNCC TTGACGGCNC CGTTTNVTAC NGNCNAAGTN CCCTTTCGGN	780
	CONCCTICAG COGNICONNOG ANNOCIONOGN AAACCCCONCC CNAITTINCCC NAACTINTCC	840
	CIVICAANCICAA GIVINOOGAANC COCCCC	865
25	(2) INFORMATION FOR SEQ ID NO:294:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 851 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1244RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:	
40	GATCCTGCCT TATCACGAGC GCCATCCGAA CTTCCCCCGG GATGTCGTTG AGAGGTAGCG	60
	AGCTCACCTC CACAACTTCC TCATCTGAAT CGTCTTCGTA TGTACTATCT AGCTCTTCAG	120
	CGICGCCCCA TGCAGATTCC GCCCTGTCTT TCACCTGTTT CAGCACCGCC TGTGCCGTTAA	180
45	OCTUACAÇÃO OCAGOCATOT GIUGUACUCU OCTATATUTO OCUCAGOTAA TACUCOGIOG	240
	CCAGCGAAGC CATCGTAACG CTCAGTATGA ACGGTAAGTT GATACCTGCC ATCCTAGTTT	300
	CTGTTTGGTA TTCTGCATGC TGAGTGCGCA AGCCAAGTTG GTTGAAAATT CCTTCAAGCT	360
50	CACAATOOCT GCTCCTGCGC GCACTTCAAC ACAGCAAAAC TCACAGAGAG GTATAAACGC	420
	CATATATAGG AGGAGACTAC TCTATTCACT GCCTATCTTT TCAGCCCACA GTTCCTCTGC	480
	CTOCAGAATT GTGTTGTGAT TCCGCCAGCA TTTTGTTCAT CGTCTCGACA TATTCGTCCG	540
55	TTATGATTOG GAATCOGTOG AACATTCCOC COCCAGOCTG TTAGATTAGG CCACACOCCC	600

	CHOTIASAC CATASIGCOC GASIGCOATT ACABOTTATC CATCOSTAGA	000
5	ACCAGIGGCT ACNOTOCOGN GTTAAACCCC TACOCTNCCC TTCCACTNTC CGATAGICCA	720
3	TACOCOGAAT TTGGGGGCC AAAAAAGTGC CCNGCAGGAA CNCAAACGAA GNNTCAACGC	780
	CNIGINITGG GCNOGIGCON TITICCNCAAA NCAGIGCGTA NITINIAANCC NGCCNCTTAT	840
10	TNTCCCCCAT T	851
10	(2) INFORMATION FOR SEQ ID NO:295:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 859 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1244UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:	
25	GATCAATCIG ACAGITOGAT IGATACCAGG TOCTATCICC TTATCAGCCT TTACAGIGAC	60
	GAAGGAGGA TIGGATIGGG GAATGGAGAA TAAAGATATI TITGATCCAT CACCAGAAGG	120
	ATTIGATICO: TCTTTCAGTG AGCATGCCCA ACTITTACTC TCGGAACGTA TAATGGGAAA	180
30	CTTTCTCGTT CCAAAGTCTG GCATCTGGAA TTATGCATTT ATGGGTGCTG GATTTAACAG	240
	AGAGCIACGI TACGAGCIAT CICICGACAI ACCACTOGGA TITTATGATG AACAGCACOG	300
	TOCAACOCAT TITCTACAAT TCAACGAAGT GOCAGCTGAC GATACTITIGG AAGCAGAACA	360
35	GGAAGATTIA TICICCTAAG TACATATTAA GGATAGAGCC AAACTIGCAA CTAGCTICAG	420
	TIGOGIATGA ATCCCATATA IGIATATATC AATACACGGG CCACTCATGG CTGGTGACCC	480
	ATTIAAGCAA ATACCATATT TTITAATGIT GCGGIGATIT TATAATCICG ATATCATGAT	540
40	TTTATTTATA GGAGATGACT TTTCCCCTCTA CAACGCCACA TTATAGAAGA COGTCAATGC	600
	AGCACCCAGG CTGAAGCCAG AACGGAAATG TTGGAACCAG AACAGGCAGG TTTGAATAGC	660
15	TOGACATATG AACCTCCCCA GAACATGTIT TITTIGAACA TONAATGANT TICTGCCAAA	720
45	AACANGAAAA TOGACNOONN GCATCATTCA AAAAAAAACCN TOCTTGAACC TGACAAAAAA	780
	TATOCACCON GATTITITGA TCACOGANNG TITTCTTTAC NCCAATTAAA TAGGNCCCCC	840
50	NGAGATITIT ACACCCNCC	859
30	(2) INFORMATION FOR SEQ ID NO:296:	
<i>55</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 833 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOROLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1245RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:	
10	GATCAAAAAC AGAGTACCCT CCGCACGAAC TICCCATATG AGGCCCAGAG AGAACAACAT	60
	COCCEATCAC CTATATCAAC AACOGAGACC TIGGICIOCC GAGAACGICA CAGCITATCI	120
	TATTATOGAT OGAATOGATG TIGGAAAGAA GATACAAAAT AACOCATAAT TOCTGAATAT	180
15	ATTOCACOCT TCTAACOCAA ACGACGAGOC TCACOCTCAG ATTCCATCAA GACCAAGATG	240
	TOGTTOTOTO TAACTOOOCC CTTGACGTTT CTGACAATOG TTCTGGAAGT GTCGTCCAAG	300
20	AACTCAACOC OGACCTOOGT GACACCACCA CGAGAACCOG TTCTACCTAG AACCTTGATA	360
	ACCITAGCIA GAGIGACTOG OGICTIOGAG TCCATTITICA TCIATIOCIT CITOGATATA	420
	AAATATCIAG TAAAAAGTOC TGAATAOGTG AGAGGAAGAT ATCATGAACA GOCOGTTTTT	480
	TITGATGCCC CGAAAAATIT TICAGGTCTG CGATGCCCAT COCAGGTGAA ATGTCCTTGG	540
25	GTTCTTGAAA AATCACATCA TACGATAACT ATGCGTGCAC CCAAAGGCCT TGGCAGCAGC	600
	GAAGTGCGCG AAGGTTAGCC AGCCCAGAAC GAAACCTGAG AACAGGTTAA GCTCAGGTGA	660
20	ATTGTTTGCT TCTATTGCCT TACAGTTCAT CTTCCGGTAA TTGCAGTATC CGTTGATTCC	720
30	CONCAGCIGA CCAGCOGTIN ATTOCCGTTT GAACTITICAG AGNICNIGAA ACCCINGINT	780
	TITCAACCON TGACACNIAT ATCNCCCOCT TATAIGACIT COGICNATING COG	833
35	(2) INFORMATION FOR SEQ ID NO:297:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 864 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1245UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:	
	GATCCGGGTA ATACAACGCC TCGGACCCCT CGGCGGCTAA CGAGAAAATC GCGCTAAGCT	60
50	TCCAGCCTAA TCATAATAAA AGGGGCATTG GTGGAAGCTT TCTGGTACTT AGGCGAGTAA	120
	ACAAAAGOOG CAAGGACGTT TCAGAAGAAG CCAGAAGCAG CAATGAGCGA GATCAACTOG	180
	ATCATTCACA GAGTGAATGT ACTOGTCTCA AAACTOCCCA AAGAGAACGA TOCAGOCCTG	240
55	CAGAAACAGT CCCCCCTCAT CAAGTTCCCC GCCATGGTAT CTAACCGCCA ATCCCCCCTG	300

	TIGITTOGAG AACTOOCOCA OCAGATOGAT COCACAGOOG TOCTACOGCA GCCATOGATT	360
	GICGAGITIG TIGIOCOCIT 900CAACGAG CIATOCCOOC GIGOCGAGGI 900CGAGACC	420
5	TTCTGGGGCA AGATATTGGT TCCGTTGGAT GGACAGACCC CGTTATTGAC AGTTACTAAC	480
	AAGAATCCAG GGTGCGAAGT TITICGCGTAA TGTTGCGGTC CATGGCCGGT TGGTGGAGGC	540
	CCTOCTOGAC COCCCCTTGT COCCTACCOC TCCCTGTCCG TCCCAGAATA TCCCCTTGTT	600
10	OCTOCAGCTG TOCTATIONAL CONCOGGATT MICCOGGAAGT TENTGOCCC CCTTTACCCC	660
	CCCCCTINICN AGNATOGITG GNGACCINITI GINCGINTING CAACTICCIT NINICCCCINCT	720
	TITTITICNAC NITGAANCNA TITTITCCCCC TINAANICAA CCNACCNGIT NINNCAACCC	780
15	CCCCCCCCTT TOOGAAAANN AGNAAAAAAN ACCTTTTCCA CCCNOGATNC CCTTTOGNCA	840
	NCTOGRACING NUMBUTTONC CCTC	864
	(2) INFORMATION FOR SEQ ID NO:298:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 830 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1246RP	
30	(A) ORGANISM: PAG1246RP  (>ci) SEQUENCE DESCRIPTION: SEQ ID NO:298:	
30		60
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:	60 120
30 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298: GATCAACAAT GATIGIGGGG ACCCCCCCC GCCCCCCCCCCCCCCCCCCCCC	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGTGGCG ACGGGGGGGG GGGCGTTCAA ATTCTACGAC GTGCTGCTGT  CGGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGGACTGC CTGACGAAGG	120
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGTGGCG ACGGGCGCG GGCCGTTCAA ATTCTACGAC GTGCTGCTGT  CGGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGGACTGC CTGACGAAGG  GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG	120 180
	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGIGGOG ACCOCCOCCG GGGCGTTCAA ATTCTACCAC GTGCTGCTGT  COGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGCACTGC CTGACGAAGG  GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG  GCGAAGGCAC GGTGCATGGG GTGGCCGATG ATGAGATGTA CCCGTACATG CTAGTGAACA	120 180 240
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGTGGGG ACGGGGGGG GGGCGTTCAA ATTCTACGAC GTGCTGCTGT  CGGAATTTCC GGGCGTGTCA GATTATCCTCC GGCTGGAGGA GATGGACTGC CTGACGAAGG  GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG  GCGAAGGCAC GGTGGATGGG GTGGCGGATG ATGAGATGTA CCCGTACATG CTAGTGAACA  TAGGATCCGG GGTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCATG GGTGTGGGCG	120 180 240 300
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGIGGGG ACGGGGGGG GGGCGTCAA ATTCTACCAC GTGCTGCTGT  CGGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGCACTGC CTGACGAAGG  GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG  GCGAAGGCAC GGTGCATGCG GTGGCGGATG ATGAGATGTA CCCGTACATG CTAGTGAACA  TAGGATCCGG GGTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCATG CGTGTGGGCG  GCTCGTCATT GGGCCCCGCC ACGTTGTGCG GACTACTGTC GCTAATTTACT GGGCCGAAGA	120 180 240 300 360
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATIGIGGCG ACGGGCGCG GGCCGITCAA AITCIACGAC GTGCTGCTGT  CGGAATTICC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGCACTGC CTGACGAAGG  GGTTGGACTT CITCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG  GCGAAGGCAC GGTGGATGCG GTGGCGGATG ATGAGATGTA CCCGTACATG CTAGTGAACA  TAGGATCCGG GGTCTCGATT CTGAAGGTGC AGTCGCCCCAA CGAGTGCATG CGTGTGGGCG  GCTCGTCATT GGGCCGCCGC ACGTTGTGCG GACTTACTGTC GCTAATTTACT GGGGCCGAAGA  CGTACGACGA GATGCTGGCC TGGGCAAACC AGGCCAATTAA CGCCAACGTG GACATGTTGG	120 180 240 300 360 420
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGTGGCG ACGGCGGCG GGGCGTTCAA ATTCTACCAC GTGCTGCTGT CGGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGCACTGC CTGACGAAGG GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG GCGAAGGCAC GGTGCATGCG GTGGCGGATG ATGAGATGTA CCCGTACATG CTAGTGAACA TAGGATCCGG GGTCTCGATT CTGAAGGTGG AGTCCCCCAA CGAGTGCATG CGTGTGGGCG GCTCGTCATT GGGCCGCGC ACGTTGTGCG GACTACTGTC GCTAATTACT GGGCCGAAGA CGTACGACGA GATGCTGGCC TGGGCAAACC AGGCCAATAA CGCGAACGTG GACATGTTGC TAGGCGACAT ATACGGCACC GACTATCCGA AGATCGGCCT GAAATCCACT AATATTGCAT	120 180 240 300 360 420 480
35 40 45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGIGGGG ACGGGGGGG GGGCGTTCAA ATTCTACGAC GTGCTGCTGT CGGAATTTCC GGGCGTGTCA GATATCCTCC GGCTGGACGA GATGGACTGC CTGACGAAGG GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG GCGAAGGCAC GGTGCATGGG GTGGCGGATG ATGAGATGTA CCCGTACATG CTAGTGAACA TAGGATCCGG GGTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCATG CGTGTGGGCG GCTCGTCATT GGGCCCGCC ACGTTGTGCG GACTACTGTC GCTAATTACT GGGCCGAAGA CGTACGACGA GATGCTGGCC TGGGCAAACC AGGCCAATAA CGCGAACGTG GACATGTTGG TAGGCGACAT ATACGGCACC GACTATGCGA AGATCGGCCT GAAATCCAGT AATATTGCAT CGTCGTTCGG GAAGGTCTTC CAACGGGAGA GCGTCACCGC GCCCCTCGGC GGGCCTGACT	120 180 240 300 360 420 480 540
35 40	(xd.) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATIGIGGGG ACGGGGGGGG GGGGGTTCAA ATTICTACGAC GTGCTGCTGT CGGAATTICC GGGGGTGCA GATATCCTCC GGCTGGACGA GATGGACTGC CTGACGAAGG GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACGA GCGAAGGCAC GGTGGATGGG GTGGCGGATG ATGAGATGTA CCGGTACATG CTAGTGAACA TAGGATCCGG GGTCTGGATT CTGAAGGTGG AGTGGCCCCAA CGAGTGCATG CGTGTGGGCG GCTCGTCATT GGGCGGACG GACTTGTGGG GACTACTGTC GCTAATTACT GGGCCGAAGA CGTACGACGA GATGCTGGCC TGGGCAAACC AGGCCAATAA CGCGAACGTG GACATGTTGG TAGGCGACAT ATACGGCACC GACTATGCGA AGATCGGCCT GAAATCCAGT AATATTGCAT CGTCGTTCGG GAAGGTCTTC CAACGGGAGA GCGTCACCGC GCCCCTCGGC GGGCCTGACT TCGGCCGTCTG CGACCTGGAC GTGTGAGATC CGACATTCGA AATGAGAAAT CCNNCACGCC	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:298:  GATCAACAAT GATTGIGGGG ACGGGGGGG GGGGGTTCAA ATTCIACGAC GTGCTGCTGT CGGAATTTCC GGGCGTGTCA GATTATCCTCC GGCTGGAGGA GATGGACTGC CTGACGAAGG GGTTGGACTT CTTCATCCAC AAGGTGCCCT ACGAGGTGTT CACATACAAC GACCTGGACG GCGAAGGCAC GGTGCATGGG GTGCCGCATG ATCAGATGTA CCCGTACATG CTAGTGAACA TAGGATCCGG GGTCTCGATT CTGAAGGTGG AGTCGCCCAA CGAGTGCATG CGTGTGGGCG GCTCGTCATT GGGCGCCGCC ACGTTGTGGG GACTACTGTC GCTAATTTACT GGGCCGAAGA CGTACGACGA GATGCTGCCC TGGGCAAACC AGGGCAATAA CGCGAACGTG GACATGTTGG TAGGCGACAT ATACGGCACC GACTATCCGA AGATCGGCCT GAAATCCAGT AATATTGCAT CGTCGTTCGG GAACGTCTTC CAACGGGAGA GCGTCACCGC GCCCCTCGGC GGGCCTGACT TCGCCGTCTG CGACCTCCAC GTGTGAGATC CGACAATTCGA AATGAGAAAT CCNNCACGCC GAATNITCCC ATCCCTCNIG TACCCCATCTC CAACAAATCG GCCAAATGCT TNCTGCAGCC	120 180 240 300 360 420 480 540 600

(2) INFORMATION FOR SEQ ID NO:299:

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 861 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1246UP	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO:299:	
15	CATTOTIAGAG CETGAGACOG CACTOCOGGA GOCCOCAGOG COGGACOGTG TOCAGOCAG	60
	GOOGTITICCT GAGCTGTACC GOCCOOCAGC GATATCTAGC TGGCCCCAAC GGCTGCAGAA	120
	GAAGAATOOG CAGOGCAGGC COCCCCCCCC GCCACCCAGG CGCAGAAGAT	180
20	CCACAAGGAA AACATGGCGT ACATGGAGG GCTGTCGGAG GAGCAGCGGA CGGCAGAGG	240
	CCGCGGCTG TINCACACCC TGGACCCCAA GGTOGTGCAG GCGTTGTACC GTOGGTTGGA	300
	TIGCACTICA CCACCICACE CAACGCCCC CTITACTICCC CAACTCCACE CACCICCACE	360
25	CAGGIGGGG GCCGCACCACCACCACCACCACCC GATGATGCCG GCCTGGATG ACGCGACCGT	420
	OCHOCOCCO CINCOCCC CACACCTIC CATOCCACAC COCCCCCA CCIACCACCT	480
	SCCASCOCC CTGCACGATG CGCACGACAT CGCCCCCAG GAATACCAGT TCATCAGCAG	540
30	ATOGACCATA TGAAGGACAG GACTTOCTAC GAGATATOCA CTTCCTCCCC AATGAGACTG	600
	TOSOSCICAG ACTOGAÇATO AACGACOCCA ACTITIATGAG CASCITOCACG AGAATACTIC	660
	CGGATNITCC GAAAGAAANA AATAACTNGA ATGGATGAAG GCCACTGAAC CCTGACACTC	720
35	TICINCTAAC TOXCOGATIT TOCOGAATGC COTCCAACTT AGGGCCCATG TOCOCCCCC	780
	COSCAATTIN MICCOONNAA CHOCCIONNC COTTOSAAAA COCCCCTTIN COGGONITOC	840
	TOCCATTITOC ACNITOCCCA C	861
40	(2) INFORMATION FOR SEQ ID NO:300:	341
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 810 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1247RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:	
55	CATCTOCCCC COCACCTOCC CCCTCGTATT CCTCCCCTCC GTTACTCTCC CCCCCCCCCC	60

	GIGICTTATT COOCATCOCG TACGCGTCAC TAAGCCCCCTC CAGGACOOGC ACAAAAAGCG	120
_	CAGGGCCCTC ATAGAGCACC ACAGCGTCTG GGTCGGGAAG CACGTGCATC CGCGGCGTGT	180
5	OCTIOCICAE COCCICGIOS GCCITOCCCE OCTCIGCCAE COSCOCAGO: GITOCAGCCC	240
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	300
	CCACCOCCTT GATGACCCCC TTTTCCCCCCCG CCCCCCCCCCC	360
10	OCCCCCCCTG CACACGCATC AGCATCCCAT CCACCGCTTT CCTGTOGTCT TCCACCACGC	420
	TETUCCCICA ACCAGACTET GOCCTATETE CTCCCCCTCG GACGAAAGCC CTCGTCCCTG	480
	CICGACTORC TOTOCCOSTA CTTCCGTOGA ASTACGCGCG CAGTGCCGCC GCGCCCTTCG	540
15	CCTCCGCGGC CGCCGGCGGC GCGAAGGGCA CGTTAGGGGG CCGAGCCGCC GTCAGACCCT	600
	CCTCATCGAA TCCGAACCGC TCGCGCCGTC GCGCCAATCG CCCACGGAAC CANCCCCCCG	660
	GOCCOCTING NOOCCOCCCC GOCCCCCTCC TITINAAAAC GACNACCNCT TGNAAANCCG	720
20	TTACCCCONCN CHATTCAAAC NCCNGGAAAA ATTTTCGNCN ANAANAANN CCCCCCCCCT	780
	NINCINNEAA ANAANGNCCN GOCCCINNOO	810
	(2) INFORMATION FOR SEQ ID NO:301:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 630 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1248RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:	
	CATCAGATAC CETOGTAGTC TTAACCATAA ACTATOCOGA CTAGGGATCG GETGGTGTTT	60
40	TCTTATGACC CACTOGGCAC CTTACGAGAA ATCAAAGTCT TTGGGTTCTG GGGGGAGTAT	120
	GETCOCAAGE CTGAAACTTA AAGGAATTGA COGAAGGGCA CCACCAGGAG TGGAGCCTGC	180
	GOCTTAATTT GACTCAACAC GOOGAAACTC ACCAGGTOCA GACACAATAA GGATTGACAG	240
45	ATTCAGAGCT CTTTCTTCAT TTTGTGGGTG GTGGTGCATG GCCGTTCTTA GTTGGTGGAG	300
	TGATTTGTCT GCTTAATTGC GATAACGAAC GAGACCTTAA CCTACTAAAT AGTGCTGCTA	360
	GCATTTOCTG GTTGCGCACT TCTTAGAGGG ACTATCGGTT TCAAGCCGAT GGAAGTTTGA	420
50	GGCAATAACA GGTCTGTGAT GCCCTTAGAC GTTCTGGGCC GCACGCGCCC TACACTGACG	480
	GAGCCAGOGA GTATAACCTT GOCCGAGAGT CTGGGTAATC TTGTGAACTC GTCCCGTGCT	540
	GGGGATAGAG CATTGCAATT ATTGCTCTTC CAGGAAGAAT CCCTAATAGC GCAGTCATCA	600
5 <i>5</i>	CTTGCGTTGA TACTTCCCCT GCCCTTGTAC	630

	(2) INFORMATION FOR SEQ ID NO:302:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 700 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1248UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:	
	CATCOCTAGA TOCCCAGGAT GAGACTGTTC AGGTTAGGCA GGTGTTGTAT GCGCCGCCAG	60
	AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGCCATC ACCCATGTCT TOCGCTGTAT	120
20	AGAGACTAAG GTATCTGAGG ATCCCTTAGC GACTCTCTCC ACCCCTCGAC GAGGCCATTG	180
	ASCICTTACG AACTGCACAA ACCTACTOGA ACTCTGTTTC CAGACTTCTT TCTGTTTGTC	240
	TICAACTOCT TICOCATGAA GIACCCCCCA GOCIATITIT CITACCCGCC TOGIGITTGT	300
25	CTATATACCC GGITGTATTI TIGATAAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA	360
	TATCCAGTCC TIAGCOCCAT OCCAAAATCT OCCTTTTTAC COCTGTTTCT CCCAGTCTTA	420
	GCACTGCCAG AAAAAAGATG TATGCCGTAT AGGCGCTGGC CCCCGCAAA AAAAAAAAAA	480
30	ATAGAAAAAT AGAAAAATAA AAAGAOGTOG OCCOCCCCCC QOGCAGACGA AGAAAAAATA	540
	GOCGCCCACC CCTCCCAAGC AGACGAACAG GOCAGACATA ATAAATCCCA CACCAGGGAA	600
	CAAACTCTIG TOCACOCTCC COCCTCATAC OCTOCCATCT GITCCATCCG GNITOCAACC	660
35	AGTATOGATO TICAAGCATO TOOGANOCTO COCTOCCTTO	700
	(2) INFORMATION FOR SEQ ID NO:303:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 837 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1249RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:	
	CATCATOCAA CATTICTICT TITICCOCCTT TCTGCCTGTG CCGCACGGTG TGTCCCCGCC	60
	CCGCACCICT GAGGAAGAGC TIGCGGACTG CAGCGAGCAT GCCCACAGTA CCTGGGGCGA	120
<i>55</i>	CTGCTGCGGC ATTCCGATAC CCAGCGCGGT GGCCGCCTCC GAGGCCACTC GCAAGCATTC	180

	TAAACCACTT CCATTCGATT GAATCAAATT ATATATACCA TIAAGTAGAG CTACCATGCG	240
	AACCITIAGCT GGGACGCAGT AAAGAITIGGC GGITTICCAGA TCAGCTTICTIC GGGGTCGATC	300
5	GATCOCCTTT TCTTCGCTAT CASCTTCTCG TACCTTAGCA GCACGTCCTC GTTCAGGTAC	360
	AACATGTOCT GOCCCTTGTA ATATCGCAGT ATGTTAAGAG CCTTGGCTGT GTGCAGTATG	420
	TOTGTAGTOG TGAGOGATGT CATOCTACTG ATTTCATOGA TOGTGATCTC GGTGCCGTTT	480
10	TOGACTAGCA GCTTGATCAG GGTATCOGAC CAATAGOCTC TGTAGAGAGC AGCCCAAGAT	540
	CAGAGAGCOG CTTCTCCGGC ACCCAACTTG TTCTCCTTCT TAGAGAGCTC CATACGAAAC	600
	TCAATCAGCA GOCTGCCGTA CCCCATCCGC TGGTACTCAG GGAGCGTCCA GAATACACGC	660
15	CACATTGTAC CCGTCCGCCA MTCCTTTCCM TTGGANAATM CCCACCAAGT NGGTGCCCCA	720
	CTCACTCCCC TGTGTTCTTG CANTAAAAA AAGGTCAANT TCCTATNACT CNTGTGNTCC	780
	AAAAAACITT GANAAAGNIN GITGOGNACC ACTICCINNI NCCCCGICAA TICAAAT	837
20	(2) INFORMATION FOR SEQ ID NO:304:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 853 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: ENA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1249UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:	
35	GACCIGCOGA TOGACNOCOG TIGOCAGGIG ACTGCCCTAC GGICTITAGI CCCCGCAAAG	60
	COCATOGOCT TIGICOGCAC ACOCAAGAAC TIGOCAATGA TGITGACCAC GICCATGGIG	120
	TOCTTATTICT COTTIGUACAT TGTGAAGTGC ACGCAGTTCT TGGAGGGGCC GTACCCCCAG	180
40	TTAATGACAC CGFTCTCGTC TCTTGTCTCC TCCACATAGT CCTCTTTGCT GACTCTGGTT	240
	TTACOGTTOG CCAGOGCAAT CTOGAATGTG TTOGACOCCG AAGTGACCGA TTCAAGCTCA	300
	TIGITGAACG CCTTTCGTAG CACCTGGTGG ATCTTCGTCC GTGCACCTTT GTCGTCAAAG	360
45	CTCCTGGTGG TTTCCATTTT CGTGACGTTC CTGTACACGG CCTCAATCTG CTGCATGTCC	420
	TCCTCGCCCA GIAGCTCTAC CAGCTGGTTC CGCAGCTCTG CCTCCACCGC GIGGTTGTGG	480
50	COCCUTTOSC SCICTICASC CISCIGISCC TICACCISGI COSCAGASCI TIGSCITIAG	540
5 <b>0</b>	CAGGCATTTT GAACCCATTG TCCCGCAAGT ACACCACTGT TCCATCCTTC TGGATCTCAT	600
	TGACCATGAA GTCGGAATAG COCTOCTTGA TCTGCCCGCT AAACCCTGGT ACTCTGCTGA	660
55	CACCTACTOT GTCATCCAAC GTCCATTCCT TCACTCCATC CCTCTCCCVT TTCCCCCCTT	720

	TONONATITO ONVININNOC TACCINAACO CITGITNAAC CITOCACCON ANAANTCATA	840
	AATATICCCC NCC	853
5	(2) INFORMATION FOR SEQ ID NO:305:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1250RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:	
20	ATCITAATIT AAAATTITAA TIAACTATIT ATAATTIAGA AATATATAAT CTAGAGATAT	60
	ATAATCTTAA AATCATAGGT AAAAATACAT AAGATAGTAA GAATAAAATT AGTAAAATAA	120
	ATAGAAAACC ATAAGTTAAT TGATTCATAA AGAAAAATOG AATTATTTGT GOCATCTTAA	180
25	TTTTTATTAT TTAATTGATT ATTATCTATT TAACATAAAA CATTTTAAAA TGTTATAAAA	240
	TAAATAAGAA ATTACTTATA GAATATTTAT TAAATAGTAT TTAATTTAAT	300
	AATATACCAT TITTATTAAT AAATAGATTA TIAAGTITIAT TAATATTAAG TGATATATAA	360
30	TTTAATTTAT ATAAATTATT TAATTTACTT CATTGATATA TATAATTATT AAATGTACCT	420
	TTCATAATAT TTATTTTIAT TAGTCTAGTA ATATTTCTAT TTAATAGTCT ACCCTTTAAT	480
	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT	540
35	AATAATTTAT TATCTAAAGT ATATAAATTA ATTAAATCCT TITTTATTAT TATTTAATTA	600
	TTATTAATTA GIAAATTATA TITATTATTT TATTAACATA ATTITTTGAT AATAATATAT	660
	CCATAITAAA TOGTAATTIA TTAATAATAT CCTTTAATGA TITNATGATA ACCNTATTAT	720
40	TATGANATTA GITAATAGIG ACCTTAATAT CCCNATCCNA ATATAINTAT TTATTINIAA	780
	NAACANANAA CITCITATINI CATATTIANI TINANIATIN ACCUITIOCU MUNI	834
	(2) INFORMATION FOR SEQ ID NO:306:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 847 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1250UP	
55		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

	CATCAAAATT TCAACAATTT CCATTICATT TAGTACTACC ATCACCATGA CCAATTGTTA	60
	CATCATTTAG TITATTAGGT TIACTATTAA CITTAGCTIT TACTATACAT OGTATTATTG	120
5	GTAATATTTA TCCTTTATTA TTATCTTTAT TAGTAGTTTT ATTACTAATA ACTITATCAT	180
	TTAGAGATAT TGTAGCTGAA CTTACTTATT TAGGTGATCA TACTTTAGCT GTAAGAAAAG	240
	GIATTAACIT AGGITICCTA TIATTIGTIG TATCIGAAGI ATTAATIITT GCTICTITTAT	300
10	TITGAGCTTA CTICCATICA OCTATAAGIC CIGATATICT ATTAGGTAAT GITTGACCAC	360
	CAGTAGGTAT TGAAGCAGIT CAACCAACAG AATTACCATT ATTAAATACT ATTATTTTAT	420
1.5	TAGCATCAGG TCTAACTATT ACATATAGTC ATCATGGTTT AATTGAAGGT AATAGAAAAC	480
15	ATCCTITATC ACCITIACTT ATTACTTICT CATTACTICT TACATITGTA TTATGTCAAT	540
	ATATTGAATA TAGTAATACA TCATTTACAA TTACAGATGG TATTTATOGG TCCAGTATTT	600
20	TTOCTOGTAC TOGITACATT CTTACNTATG GTTAGTTTAC TAATTAGGTA GGINCTATTA	660
	NGAANAACAA GAAATTNOOT TTAACNOOON COCCTOOGIT NGANATNNAA CONCACCTAT	720
	TATTACNNIT TTINAAAATA NIGAANACCC CANNATTGIT NIAANGAAAG GNVIAACGIN	780
25	NACNCACCON TAGNITTING GTCCCCCCCC NTOCTACCCC ATTITICNCCC CCCCCACAAN	840
	AACCCCC	847
	(2) INFORMATION FOR SEQ ID NO:307:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 825 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1251RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:	
	GATCAGGAGG GITTIGCOGT OCTOCCOCGAC GOCGGGTTAG AGGTAATGCT CCTGCGAGAG	60
15	GATGACAAGA CIGICGCTGT GIACCGOGAA GIGOCAGAAT AGIGIATACT ACATAGICAT	120
	AGTTATAATA AACAAGCCGC GGCGGCTCT AACGAAATGG GGAGTTGCCC ATGCCACCGG	180
	COCCCCCCCCC CCCCCCCCCCCCCCCCCCCCCCCCCC	240
50	COORDINATE COORDINATION COORDINATE COORDINAT	300
	COOCCUSTICIACO COCCCATOCA ATATCATECO COCCTICOCOC TTCCCCCCCC	360
	GAAAGGGGTC AAACGGGTTT GGCCGCTTCT GGCCGCCTGG ATACAGGTCG CTGTCGCCGT	420
55	NGCCIOCAGG GCIGCCAGGC AGCGGCIGCG CGGCGCGGC CGGGGGGGAG AGAACCICGI	480
	ACTICOTOCTIC GAAGOCAGGC ATGTCTGCTG GCAGCCTGCG TGCAGGAACC TGCGCGCGCA	540

	LIGACACHAS CACACCICCA CICARRACCI, CINIANICACC GERCICIOCL TILIOCOCNOC	600
	GCTTCTCNTC COCCCACCAG GCNAATTICC CINCNAAACT INCCGAACTC CNCCCCCTTA	660
5	AAACTOGCON CNCCCTTTIN CCINNCNOCT NICCICCTGC NNCCCCNITI CCCCCTCAAN	720
	ACCONCCTAC CONTINICINT NENTTONING CCTACANCCT TTONICCTING TOCCCOCNCC	780
	ATMICCIONI TMIATONNAA AATTIONIIN CITTITIACCO COCCC	825
10	(2) INFORMATION FOR SEQ ID NO:308:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 856 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1251UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:	
25	CACTGITCOC TGTTCACCAA GATAATCAAT ACCGGAATCC TCTCACCTTT GCTTCGCCCT	60
	CCATTOGCT ATTACGAAAT TOGCGTGCTG CTCCTAACGA TGTTGTACCG TTTATACAAC	120
	COCUTOTICA TOCCUTITA CCACAACCC CITTITICAC CCACACACAT CACAACCITT	180
30	GCTACTICIC CGATCCAGTA TIGTICAGTG CTGTAGTCAT CTTGCCATCG TTGGTAAACA	240
	CATATACCCC ATCOCACTTG GAGAAGATCG ATACCACGIT CCTTTCCCTC TCATTTCACC	300
	CATTAATTIC GCGCCTTTTA TIGTAAAGGT GCAGCACCAC AGAAATACTT GATAAAATCT	360
<i>35</i>	TAGGCAATGG CCATATTGGG AAGTTTATAT TACTAGCACG ATGGTTGCTC ATCCCGGCCT	420
	TGIGCIGITC GITCTACOCG CCCCTGITAC TACCITTAGT CCTGIGTTAC TCACACCTTG	480
	TTACCGGCCC GGGCTTCTAT GCAACTATTA TATTTGCTTC TAATATATAA GTACTCACAT	540
40	TITICATACCE COCTACCTAC COCTOCTTIG TCTTCCGGGA CTCTCTTCAG AACACCTTCT	600
	TOGRATTATO TIGIRCIATO ARCCATOGRG ACACTOTIRO GOCACACOCO GROCAAAAGG	660
	AGAACCGAAG GACAATTTIG ANCCTCCCTT TCCCCCGAAT TANGGNITNI GAANATATNA	720
45	ACCOGGACCG GGITCCCTNN TCCCCCGGGT ANITNCCCNT TAAATTCGIN TAAANITANN	780
	AANGCTINTAT GOOGNGAANG AACCCCANCT GACCCNAAAN GITNCNIGOG GITTAACCTIN	840
	CINVINCOCC GINCOG	856
50	(2) INFORMATION FOR SEQ ID NO:309:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1252RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:	
10	GATCTCCTAT TAGTGGGTAG CTAGCTAGTC GCCCCGCTG GCCCGCCCG AACTGGTACC	60
	GGGTGCCAGG CCCAGTGACT AACACTCCGG GTTCTTCTGT CTCTTGCCAT GCCGAACATA	120
	ACCATOGOGA CTTATATAAG TICOGOCOGC GTOCAGTCGT ATGAGCCCGT ACGAGCAAGA	180
15	CGTCCAGCAG TTTGCAGCOC GGTAGTCGGG GCGTTGCAGT TGTGTATATA TTGCCACCCT	240
	TOCGAACTIG GACAGCCGTA TOCTOGAGGC GGTCAGTAGT AAGCAGGAGC CGGTGACTCA	300
	AAGTAGAAGT COGATTIGTAA AGGACAACAG ACCAGTIGOOG GTACOGACAG CAGCOGGCCA	360
20	ACGTAGTAAT AAAATATGAC GAGAGATATA CAGAACCACC TACTCTTOGA GACGCCCACG	420
	GAGGTAGGGA ACAAGGTCGG GGGCATCTAC TCGGTGCTGA AGTCGAAGGC ACCGGTGACC	480
	TOCGCTCAGT ACAAGGACCA CTACCACTGT ATTGGGCCCC TGAATCCAGA CTCGGTGCAG	540
25	ATAGAAGTGG AGGCCCTGGA CTGGGAGGAT GACAGCGTGT TGGACCCGGG AGATTGCTGC	600
	COGGIAAAAC GICCCCIGCA GCACAIGCGG AACCCCGCGT TGAACTCCGT ATATGCCGGT	660
30	CETTIVETCAA CETIVECCCCE CITATCTTET TCAACCTETT CCCGTACCCC CCTCCTCCAC	720
30	AATTGAAGCC ACCTGTTGAA CACTGCGGAT CCCCCCCCCC	780
	CCATCOGTTA GGINCOCCING NCTGTCCCCCG AAATTAANOC CGANCONCINC TCAN	834
35	(2) INFORMATION FOR SEQ ID NO:310:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 858 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1252UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:	
	CATCHTTATC CCAACNITHT OCHTCTGTTT CCACTTACOG CCCTCCCCCAA CCACACCCCAA	60
50	AGCCCAGCT CCCAGTGTTT TOCCGAATAT GTAGTCCCCT TTGTTCACAT ACCAGCCTCG	120
	TTGACCTGTC ACCTTGTGGA AGAACTTGGT CAACATGTTG GCCTGAGACG GAGGACGATC	180
	CTOGGGCTTC GATGCGTCTT CGTCGTGCTC CCCTACACCC TTACCGAGTT TTCCGGTGGA	240
55	ACTAGIGAAC ACTOCCATAG CCTCGCAGIT AAAGTGATGI GGCAATATTA TATTGTAGIT	300

	TIGITCITT CTTGATTGIT TTAGGCTGCC GATAGCCCAC GAGGTGAAGT TTTGTACACT	360
	TCACACATCC CASCACTOCC ATCACGACAG ATGTTGAAGA TCAAATTTCG CAGCTACATG	420
5	CTOCATTGTG GTOCTTOGGT TAGCAGTAGC GOCTAAGTTG CAACTACATT GTCCCCATTC	480
	ACTCAGAAGT ACCTCGGTTA AGCTCACTAT GCGCTTATTIG CCGAGCGAAG CCGAGCATTIG	540
	TTACAGCAAT GATGAGAAGA GOCTATTGGT ATGTTAACAT AACGCCAGTA GTGTTATATT	600
10	TACCACTAAC CATAGAAAAA GTACAGAATA TOOGTAGOOT ACGAACTGAA TGAATATNIT	660
	SCTTCCCCNC CCCGNCCNTA TACCAATGAA TAATAAATTIG GATTTGCTAA TATCTNCCCC	720
	ATATOCNOCO GOOCOCOGA NNOCOCINCAA CITATIOGIN CACNONOCON TOCCNOCONON	780
15	TITINITIN TONNOGAACC CCCCCCCCCT CATCNICCIN TONNINAANA TGANIACCCT	840
	CCCTTQVICC CCCNCCCT	858
	(2) INFORMATION FOR SEQ ID NO:311:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 841 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1253UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:	
	GATCCTAACC AAGCTGATTG ACTOCAACTT TOCACTTOOC ACATTOGACA AGCTGTTOCA	60
35	GASCTCCACG GCCGTGGGGG GTGGTGGCTC CATATTGGGA TCAGATGGTG GGTGTACAGA	120
	CACOGAGOCA TTOGGACATG ACCGAAAAAGG CAAGAAGTTG GAGCCCCGCT TCCCGGGGGCC	180
	TCCGCCGAGC GTGGCACTGG GCCCGCCCA TCGCCGATAT AATTCTGAAT TGGGCCTCAA	2 <b>4</b> 0
40	CTACTICOCC GAGACCAACG COCAGCCCAG CGIGATCCTC CCCCAGGIGC AGCAGCCGTG	300
	GAACACAGOT CCTOGACAAC AACOCAGACA ACAGCATAGA CAACATGGGC AGGCOGAGGA	360
	AACOGGITCA CCACCAAIGG CICTICOCTA TCCCCCTCCA ATGITAAIGA ACAGCAAITA	420
45	TACATTCCCT GCCGGCCCCC AGCAGCCGCT CGGCCCGCAT CCACAATGGC GTGCCTCGAC	480
	OCADCAATCT GATGTCCCAG CTACCCTCCC CGGAATATCG GCGTAGCACC ATCGTCCCAA	540
	CTTCCCACAG CCCCCACCGC TGACTAGTCT TTTGTCTAAA CATCAGCCTC ATCACTCGCA	600
50	OCCIAATGAG CIGCCIACCI CCCAIGCATA TGIACAACAG ATTIGCCIAC TCCAATAGCC	660
	CAGITICIGAA GICTIGCTIGC THACGITIGC COCTICTCCCC THOGOCAATN TATCCTTGIN	720
	NNNAAAACCN AACCCNNGTT CCCCTGTGCC NGAATTTCTA CTTTTACCGT CCGTTATTCC	780
55	NTAAATCATA ACCCOGITCA ANAACCCTTT CCTTGACNAT ATCNCATTGN GCNANCCCNT	840

	С	841
	(2) INFORMATION FOR SEQ ID NO:312:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 842 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1253UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:	
	GATOGACGAG TROCATGITG AGACGITICAA GAAGCIGITT GOGAACTGCA TROCAAGGA	60
20	TOTOGRIGIG COCCAGGITG TOGCOCAGINA COCACTGATA GTOCCGTGTG AGGAGCCGGG	120
	TOSOGTOCCC COCCCOCCC CCCGTCACCC COCCCACCC CAAACCCCAAC CCTTTTCCCA	180
	CCAACACAC AAACACATTA CCATCATTCT COCTCCAAAC CCAATTCCCA TTCACTTTCT	240
25	AAACAATGIG 100GAGAACT GCTGTGTGCT GTACCGTTTC TATCACCGCC CGACTTTCAT	300
20	CACGAACCIG GACGACCIGI AIGAGACAGA CCCCCCIGIGAG TACACCCACG ACCACCIACC	360
	CHICHTOCCG THGHGCHACG CHGHCAHGCC AGHGGGHGCG CHGHTCHCHA GCHCCAHGCH	420
	CCCTGGTCGG GGAAGCGAAG ATGCGGGGCTC TGCAGGCAGA ATAACAGCGG CTACATTCGC	480
30	GGATACGGAC ACACGGCACG CTTATCTGCA CGACGAGGGC TACCGGTACT ATGTGGCTGC	<b>54</b> 0
	GAAAAACCTA GTGATCTCAC GAACGCCCCGT GACACCGAGG CGAATCAAAC CTTGTTCCCCG	600
	TITIGIGITET COCAAGITOC GOGOGGIONO COCGGCATOC GITTITICIGE CONSCIATNA	660
35	ATTOCNOCON COTINNAGANT COACCOCACOC COCCOGANA ANTAAAAAAA TTTCCCCCCC	720
	CAACCEGAAN TCCCNCCCCG NITTACCCCCC CTTANAAANG AGGITTITTIA AACAAANCGG	780
	GENECOCIONO NOCOCOCEENN CINNINACATICO COCOCOCTAAA TOCGGAANATT INNOCEGAAACO	840
40	œ	842
	(2) INFORMATION FOR SEQ ID NO:313:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 836 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1254RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:	

	GATEGRECAL ATTRICCETS ASSECTATION ASSESSED ATTRICCETES TO ANGACES	60
	TGACGACATT GTCATCGACG CCGAGAACAA TGCCATCAAC CTCCTTGTGC CAAAAGAAGA	120
5	AATTGAGTCG CGCCGCGCTC GCTGGACCCA GCCGGCTCCA CGCTACAAGA GGGGCACGCT	180
	CGCCACCTAT TCTAAGTTAG TCTCCAACGC CTCCAAGGGT TGTGTCTTGG ACAGCGACGA	240
	CTAGCACCTC GACGCAAGTC ACTATTTATT AACAAGATTA TGTATATAAG CACCCGCCA	300
10	TGTCCATTGA ATGGACCOCA TATGTAACAA AAATGGAGGA TOCTTCCCTA TGGTCTACAA	360
	ATCTCAGGAT GITGAGTACC TTTCAGGTGT CTGACTGAAA TAAATGTTGA ACTTTGATAG	420
	TACTITIATG TITGAAAAAT TITAAAATTI TATTGTATGG CTGTCACCAC GAGTACTCAT	480
15	CTTCACCOGA CATTACGOGT ACCTGAAGAG CTTATCTATC GATAACATGG CGACTCAGGA	540
	GOCOGTATIT ATCOGGOCOCA ATAGOCAGAC GAAGGITTOCG CACTICIATIT TOCCGACCAA	600
	GACTIGICCAT TOGACTOGAA AGTIGCATOCT CTATOGAATC CGTTGGACGA ACNCATOCNG	660
20	GNGTTINNOC CATTGAAGOC CNCAACCCGA GNIACTCGGN AATTTATGGG GCNAAAAACT	720
	TTTOGTCACN CTCNNCGAAG CACAATNCTT COOCAAGNAA NAAAAANGGA ATTGNCCNAT	780
25	TTOGAGOCON AAACCINIAC NINGONIGON GWOOGTANC TOONNITOON ANGTON	836
25	(2) INFORMATION FOR SEQ ID NO:314:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 850 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1254UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:	
40	CATCTCTGGT ACCCCAGGAG CCCTGGCGGG GACGTGGCAT TGGTGACTTC TCCCCCAGGT	60
	AACCOOGTIGT OCTOTICAGOO COTTOCOCCAC ATTIGAAGTTA AGOTTIGTTIAG COGTACTOCOG	120
	CTTCATTITC TGTGCCCGGT CGACCGGTAG CGTCATAGTC CCGCCGTGTG GCCGACCGCG	180
45	GGCCGCCATC ACAGGTATCT ACAGTTCAAC GGCCGGTGG CGATCCCAAG CGCAGTCTGG	240
	AATCTCGAAC GCTGCTACAA AGAACGGATG CGTGGCAGAT CGAAGCTATC CAGAAGCTGG	300
	TOGOGGAATT GAGTGAAAGT ACACGAAGGC ACGGTGTCAG ATCTCGTACC TCTCGCATAC	360
50	AGTACGAGAA GGAGTICOOCG ACGGTIGTTICA GAAATCAGCG CAGTIGTICCAG TIGCOGGGGAAG	420
	COTOCAAACO GAACTICOGAA ACAATICOGAC OGACCTACTO CCAGGTICCAA OCCCTTTICCA	480
	COGIGICACA GCTAAGATOG TGACTOGCCA ATAATTIGIC ATOCTOGTAT TOGIGIGIOG	540
55	ACCATTATCT ATTCOGTTCA GOOGFTCATA TTTACGTCOG CTCCAAACGT GGTCACATCA	600

	CGATTOCACT GTATATATGA TOGAGTAATT COCATACACT GAAAATCNTA ATAATCAATA	660
	ACCCATROCKN CNACTOGNICA ACTITONICONIC TITONICOTICON GGTICAAAATCC CCTTCACTIAN	720
5	TTTTTTTCAT TOCCCATTINN ACCGAACTTT ACNAATNATG CAATGANAAC CNCCCCTCCC	780
	AAACCTANAT CCTTTINI'IN NGGGICCCONN ACNGTINCON TICCNENCNA NCCCNCTTIN	840
	ATTCCAANAC	850
10	(2) INFORMATION FOR SEQ ID NO:315:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 827 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1255RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:	
25	GATCGTGTCG TCACCGTGCA TTGCAGTGCG CCTGAAGACG GTGCGGACTG ATCCCCCCC	60
	GAAGAAGCTG TCGCAGCTAC AGGCGATTGC GGCTGTGGGT CAGGGCCGGC TTATTGCGCG	120
	GIGGGACTOC CTCTTCAGAC CGTTCAACGA GAAGATTGCG CAGATTTTGT TGACACGGAA	180
30	CGACATAGIT GACTOGICOC AGIATAAGAA COCOCAGAAT ACGITICCACG AACTOCTOCC	240
	GATGOGOGIG ACGCCGATIG TGAACGAGAA CGACACGCIC TCAATCAGCG GAGIGAAGTT	300
	TGGGGACAAC GACACGCTGA GTGGGGATCAC AGGGGGGCTG ATCGGGGGAG ACTACCTGTT	360
35	CCTGATGACG GACGTGGACT GCCTATACAC CGACAACCGG CGGAGGAACC CGGATGCAAA	420
	OCCUATOTTG GTGGTGCCGG ATCTGTCACA GGGACTGCCC GGCGTGAACA CCTCTAGTGG	480
	GTCCCGTTCA GGTGTGCCCA CCCGCCGCCAT GCCCACCAAG ATCCTTGCTG CAGACCTGCC	540
40	AACCAACOCC GOCTOCATAC GATTATTATC AAGAGTGAGC GOCCGTCGAC ATGGTGCGA	600
	TOGTOGAGIT CATOGAATOG COCAGCAGTG CACTOCAGTT TCTOCTGACG CGAGACTTGC	660
	AGACOGACGA GCTGAATTTG TTGCAGAGCA CGGCGTCCCA CTACACACGC NCTTGNTGCA	720
45	ACTITICACO TOCTIGAACNA CNGATTONTG ATOCONOGTO TIGTIGACNOGG NOGTATOTAA	780
	CAGGGGCINA GGCCCCCCA AACAACTGNT CCCACGTTNT CCGTCAG	827
	(2) INFORMATION FOR SEQ ID NO:316:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 836 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIGI	NAL SOURCE	Ε:
	(A)	ORGANISM:	1256RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:	
	GATCTAATGG CATTCTCCCT ACCAAATGGG CCCAATTGTA TATTGCCGAT CTTCCTACAG	60
10	CENACTICETT TACOGATCCA CCGAAGATCG CCACAGTTCA CCTCTTCGTIA TTGCCCACAT	120
	TGTGTCGAAA ACACCAGCTG CAAACTTGAG GCCATATGTC ACTGTCATCA CAGGTCCACT	180
	TATCCGTGTT GTTGGCGAAA GGTCTAGCAG TGATATTAAG GCTGCTATCC TATATGCCCT	240
15	ANATOTICIC TITTOGANGG TICCACANTI CCTGCGGCCA TICATACCTC ANCTACAGAG	300
	AACATTIGIT AAATCICTIT COGACTCAAC CAATGAGACC TITAAGATTOC GGGCCGCGAA	360
	GOCACTAGGI ACTITICATAC AATATCAACC AAGAATTGAC CCTCTOGTOG TOGAGCTAGT	420
20	AACAGGCGCT CAGCAGGCCA CTGAAAGGGG AGTAAGGACG GCTATCTTGA AGGCATTGTT	480
	GGAAGTTGTC TCCAAAGCTG GCAGCAAGAT AAGCGAAGCT TCCAAAGCTA ACATCATTAG	540
	ACTIGIOGAG CAAGACATOG CATOCACAGA CAGCAAGTIT GCAGTOGCTT ACCCCAAGCT	600
25	TCTAGGIGCA CITTCIGAAA TCATGICTOC GGAGGAGGG CAGACCATAC TICACGAAAA	660
	GIGCTICATC CAATHTICAA CANGCACNGT AAATTIGOOGT CNCACCCCAC TCTATCCTNC	720
	TACCCCIGIA CNITCICCOG CCATNCACON AINITIGACIN TINGIOGIOC ACCGATONON	780
30	ATCCTTCONN CACACGITIN CCONINGNAT ICCCCCCONAA NGAAAGINAN CCCCCC	836
	(2) INFORMATION FOR SEQ ID NO:317:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 841 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1256UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:	
	GATCAACTOG TCGGGCGGC TGCACCACGC CAACAAGAGC AATCCTTCGG GGTTCTGTTA	60
	COTGAACGAC ATTOTTOTOG CGATTCTGAA TCTOCTGCGC TACCACCCAC GCGTTCTGTA	120
50	CATTGACATT GATCTGCACC ACGGAGACGG TGTCCAAGAA GCATTCTACA CTACTGACCG	180
	CGIGITCACG GICTCGITCC ACAAGTACAA TOGICAGTTI TITTCCGGGAA CGGGGGATTT	240

300

360

CCATGAGATC CCATGCTCGC CCCCCAAGCA CTTTTCCCTG AATGTCCCCC TCAATGACCG

CATCGATGAT GATTCGTACA TCAACTTATT TAAGAGCATC ATAGACCCGC TAGTTACATC

55

	ATACAAGCCA ACAGTAATTA TICAGCAATG TOGAGCAGAC TCTTTGGGGC ATGACAGACT	420
	GGGGTGTTTC AATCTAAATA TCAGAGCCCA CGGCGAGTOC GTCAATTTGT GAAGTCGTTC	480
5	GOGATACCIA TOCTATOTOT COGTOGTOGA GOTTACACCC CCAGGAATOT GTCGCGGCTA	540
	TOGACCTACC AGACACCCAT CCTTAATGAT GTGCTCTTAC CTTCACATAT CCCACAAGAT	600
	ATTCCGTTCC GCGAATGGTT CGGTCCAGAC TATCTCTGCA CCCGGTCCTT GGATGANTIN	660
10	TCCAAAATAA ACNCCCAAAT TACTOGANAA NATACGINCG GNITTAAAAN NIAAATINIG	720
	CNECCCCAT TITICACATGA ANOCGAATATC CTCCAGATTT CCGTTTAACA AAAAAAAAAA	780
	GATCOGAANA ACCAAAANAT NCCTTGNTAA CANTNAAGAA NTTTOCCGNN ACTINITANT	840
15	С	841
	(2) INFORMATION FOR SEQ ID NO:318:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 841 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1257RP	
3 <b>0</b>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:	
	CATCACTOGT GTCACCAAGG OCTACAAGTA CAAGATGAGA TATGTGTACG COCATTTTCC	60
	CATCAACGIC AACGITGICG AGAAGGACG CGAGAAGTIC AITGAGATCA GAAACTACTT	120
<i>35</i>	GGGTGACAAG AGAGTTAGAG CTGTGCCTGT CAGAGAGGGC GTCAGCGTCG AGTTCTCCAC	180
	CAACCAGAAG GACGAGATTG TTTTGTCCGG TACCTCCATC GAAAACGITT CTCAGAACGC	240
	TOCTGACATC CAGCAAATCT OCCGTOCCAG AAACAAGGAT ATCAGAAAGT TCTTOGACOG	300
40	TATCTACGIT TCTCACAAGG GTGTCATTGC CGAGGAAGCC TAAGTGCCTT ACTGACCGTA	360
	TCTTGATAAA TAATATGAGT ATTATGTAAT CAAAGAACTC ACTGCTTTTT ATTGGTGGTG	420
	TTITOGICAA ACOCTETTAT TAGCOCCOGG GTTAGAGIGT GOGAATACTG GOGITATATG	480
45	CTTTAGAAGT TATGITAAGT AAATTTAATG TCCTATCAGG GCCACAGCCT TAGCAACTAG	540
	GIGCAGGIAC TOCTITAGCT TGCCACTGIT CTGCAACACA AGATATATIT TATCTGTCTC	600
	CTTGGCACCA TOCTAGACAG CTTCACCGCT TOCTTGCAGG AACGATGGAA CGCCAGCTTT	660
50	CCGCGGIGGA AGTIATAGGA ATTAIGGATT CCAATGACAG TIGGIGIGIT AACNANCCIG	720
	ATTIGICCAN TITICCCGICT CNGAAGCINC ANIGNTICON TGACCNANCA AACCCGGGAN	780
	ACCCCTAGGG CTGNNAGGCT TGAATGCNIT AAAANANITT CNITGANAAA NCATTGNTAA	840

	(2) ENFORMATION FOR SEQ ID NO:313:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 856 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1257UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319: GATOGOGOGO CTCACACACT CAGSTACCTC AAAGGAATAC GAGTTTGTCG CAGGCTTCCC	60
	CTGTCCACAT CCACACAAAA TCGATATGTA CATCAAGCAG CCGCAAAACA AGTACCTCTT	120
	TICCOGAACA GAGTACACIT TOCAAATCAT CTGCAGCCCT GCAGACCCCC TCACTCACGA	180
20	TCCATACGAC GCGCAAGCCG CTGCGCCAAA TGTGATAGTC GTCCAGTCCC CATCCGGCAA	240
	CATCTACCGT CTCAAAAAGG CGCAATCCGA TGTCGAATTT GGCGTATGCG AAGCTAGGCT	300
	AAAAGTOCAC GAGCCAGGOG TCTGGCTGGC CCTAATTACC TCTGAGGCAG GTGCTGGTTG	360
25	GIGCACTITC OCGAAGIGGA TCTGIGITTA ACACCTAGAT GCTACACAGT CATCCACCCC	420
	ACCAAATTAA TACATAGTAC GOGTACATAC AAGCCCTATA GTTTCTTAAT ACACTTOCCC	480
	TATATTGAAT ATGICTACGA AGTATATGGG CGAGGCACTT TCAAAATCGG TGAAAAAAA	540
30	TOCACCACTT CGAAATCCAT GITTTATGAG CTTAAACAAC AGTOGITGIT GAAGAACAAT	600
	ACCCTOCCAA GCAAATGTCA GGTACTCCAA CCAGCTCTCA ACAGATTCTT AAAGATTCCC	660
	AGIGITGIAA CCGAATCCAC GITCOCTGAA TOCTOGGACC GACATCAGAC CCTTOCATTG	720
35	GTACAAAATC AGTCTATACG CNGAGCGCCT GTNTGCCCNA AAAANAAANA CCACGGAAGG	780
	ACIVEATTETC ACTIGNACIE ACIVEATETE TIVENETEACE COGNITITITE CUTTENACEC	840
	CCAAGGACAA NAACGC	85€
40	(2) INFORMATION FOR SEQ ID NO:320:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 724 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1258RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:	
55	GATCCAACCT TCTACTAGGG TATTTTTCCC TACCTCAGGC TGCAATTCCA TGCCATCGCT	60

	AACCAAGATA ATATTCTCCT CCAGTAGATC CATATTCTCT CCCGACTTCG CACTAATCCG	120
	CATCACTOOC ACCITICCAC CCAGATCTIC ACCATGIATT TCATGCTGIA GCAAATCATT	180
5	CATTATTITE TIGATCACAG TITICCITTIC TITITOCCGAC COGAGITIGI CCACCTIOGI	240
	TATOSCGACA ATCACCICAT TCCCTGATTT TTTGACATGC TTAATCGCTT CAATGGTCTG	300
	GGGTTTAATT GAGTCTTCGG CAGATACTAC CAAGACAACG ATATCGGTAA TATTCGCGCC	360
10	CCGITCCCTC ATCITCAAAA ATOCTTCGTG CCCGGGGGTA TCCAAAAAACG TGATCTTCCG	420
	CTTCGAAACA GGTGTGACAA CCTGGAACGC ACCAATGTGT TGTGTAATGC CACCAAACTC	480
	CIGCGAAACG ATOCTCGACT TCCGCAGATA GICCAATATG GTGGTTTTGC CGTGATCAAC	540
15	GIGACCCATA ATOGICACAA CAGGIGGCCG GICCTICAGG GCCTICGGGT CTGCAGGCTG	600
	CTICAATICA TOGIAAACGT TCTCCGGAGT GACAATICCC TGCCGGAGGG CAGITGGTAG	660
20	CTATCTCCTC CCAATATAGC TCGATGTAGT CTCCTGGAAA TATGTAGTCC GCCTGGCTTT	720
20	TCAA	724
	(2) INFORMATION FOR SEQ ID NO:321:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 853 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1258UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:	
	GATCCTGTTT ACAACTAAGT TCGCATCCCT ACCAGGGGAA AATATGAAAT ACCAAGTGTT	60
	GTATTCCCGAA COCTAGAATT CTTGTACAAA AACCGCGGCA TTCAGGAAGA AGGTATATTT	120
40	AGGITAAGCG GATCCAGITC TCTCATAAAA TCTTTGCAGG AGCAATTTGA CAAAGAATAT	180
	GACGIGGATT TGTGCAATTA CAACGATAAA GITTCTGTCA CACCAGGAAA CGAAAATCAG	240
	GOCGGICICT ACGICGATGT GAATACCGIT TCAGGITTAT TAAAACTATA CCTAAGAAAG	300
45	CTTCCTCATA TGATCTTTCG GGATCCTCCA TATATCGATT TTAAGAGAAT CGTCGAAAGA	360
	AACCICAGATG ATACCAAACT AATACCACTC GAGTTCACCG CATTIGGTTAA TTCCCCCACGA	420
50	ATTOCCAAAG AATATGTCOC CITAATGTAT OCATTGTTCG AGTTATTOGT GAAGATCACC	480
,,,	GAGAACAGCA AATATAACAA GATGAATCTG COGAATTTGT GTATCGTATT TTCGCCAACG	540
	TIGAACATAC COGIGAATAT ACTACATOOG TTIATCACIG ACTITOOCIG TATATTOCAA	600
55	GATAAGOCOC CGATOGAGAA COGACACOGT CAACATACAC ATCCCOCCAAT TTAGTTCATA	660

	TTAGECONAT TGINTAATAA TTGAATATGA ATGONITAIT NICICINANI CAAINIGICA	780
	CCATTOGATT TACACCNOCG TCTGTAANGA CNTCTAGCTT GGTCATCCCA NTTCTCANIT	840
5	NCTCCCGCTT NCA	853
	(2) INFORMATION FOR SEQ ID NO:322:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 836 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1259RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:	
	CATCACACGA ATATTICCGOG AGTATTTICTIC CATCGTTCGC CGCAACGCOG CCTGCGCATC	60
	COCCUTEACC CATTOGCCCT CCTTGATGAT CACACTCTTG TACCTCCCCG CTACCCCCTC	120
25	CGATCCOCTC TOGAAATCCA CCTOCTCCAT CTOCOCCAATC TCCTTCAACA ACTOCTGAAT	180
	CACGATCCOG TCATTGTOCC CCATGTOCT COOCGTGATC TCGATGTOGT ATGGGCTGCT	240
	GACGACGITG ACCICGACCI ICTIGITAGA TOCCOTAACA AATTCCCCCA CATCAATCIT	300
30	TAATTIGIAT ACACCIGCIC CAAAGATACT TOCAAGGAGC COCATGCACC GIGICITCIT	360
	CCCACTICCA TICOCCCCCT AAAGTAAAAT ATCCCCCACG TCCTTCCCAG AACCTCCTAA	420
	ASCCTOGASC TECTTEGTAA GOGATECCGT ATGTGAAAGG CTGGTCAACG ACTTCGGTCT	480
35	ATOCTTOTICA ACCCAAAGTG ACATATTCCT GTGTATCCTG AGATGGGCTT TTGTGTGTTG	540
	TAGGGAAGGT GAGCAATTCA GTCGCAATTA AATTCATTTA GATTCGCGTT TTAGCACAAA	600
40	ACGATATOCC CTCAGTAAGG CCAGAATACA TACAGGTACT TOGCCTACTA CTTTTGACAG	660
40	AAGTAAAGCT CTCACGAGAT COCTOGAGGA GATGOCATGT ATATAACCCN CAATTACTCT	720
	GATOCNAAAA ATGITOCACC CNTOCCITIT TANITCNGTC GACAACTANN AGAGCCINTA	780
45	TONAGTOCAA ATITINOCAA ANCTOOGAAA ACCTININOC GIOGINIAIN AACACA	836
	(2) INFORMATION FOR SEQ ID NO:323:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 851 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
5 <b>5</b>	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1259UP	

	(xa.) SEQUENCE DESCRIPTION: SEQ ID NO:323:	
5	GATCACCCCC CAAATCAGCA ATAACTOGAA AACTGTGCCC AGTACCTTTC AACGCGCATG	60
	AACCTAACGG CGCGCAGCGG TCATGGGTAC TCGACTGCCT TTGTATCCCT CACACTGCCC	120
	CTCTTCGTGT GCCGCACGTG CTTGTTGATG GTAGCGGCGC GGCCCGGTGG ATCTAAGCGC	180
10	ACGICTETTI GTACGIGGGI CTCACGIGCA CATCGICATE CATCCGCTIG CGAATCAGIA	240
	GATCAGCACG GAGACCATGC TAGGCAGGGC CGTTGGGGCAA GGTGGAAAGG TTGCAGCATT	300
	GAGGTGGAGC AGCAAGATGA CATCACAGGA TAGTAGTCGG AAGAAAGAGC TATGTGCAGC	360
15	GTACAGOGTA GTOGATGAGO GGGTTTCGOCG CAGCATGGAA GAATGOGGAC GTAGAAGGTC	420
	GCAGGITCTA TIGCITGCCG TITCIAAACT GAAACCTGCG TCGGAIGIGG CGATACTGIA	480
	CGAAGAAATG CCCCTCCCCC ACTITICCACA GAACTACCTIG CACCACCTICG TCCCCAACCA	<b>54</b> 0
20	AGCAGAGCTG CCGGGGGATA TCCAGTGGCA CTTTATCGGG GCGCTGCAGA GTAACAAGTG	600
	CAAGGACCTG GCGAAGGTAG TGAACTGCAT GCGGTGGAGA CCATCGACTC GCTAAGAAGG	660
	COCOGAAOCT GAGGAGGCG TGCGAAGTTC CAGCCGAGCC CCCGCATCTG TGTTACATTG	720
25	AGTIGAACNOT CTGGCAAGNO AAAGNNGTTN CNCGATGAGC NACNGTGCAC TGTGATTCTT	780
	CINCCAAAAC AAACCTTCCC TGCCCGACGA TAAATGGTCC TGGACCCTCC CCGCGAAGGG	840
	AACCGATCCC C	851
30	(2) INFORMATION FOR SEQ ID NO:324:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1260RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:	
45	CATCCTCAGA COCCCCCAA CAACCTTCCC CCCAGACACT AACCATCTTT CCCCACCTTG	60
	TOCTOTATCA CAGTIGAGCT CTAGGITOCA CTTTCOGAAA GAGCOCTACC GTAGCTOCAT	120
	GAAAAAAAG TAAGGCTCAT CAGTTTATGC AGAGGCAAGA ATAAGTTTGG TAGAGCCTTA	180
50	CTICACAAGC GIOGCICTAG CGAGCCATAT TATICTATGG CCGGCAAGAG AAGACCGAAG	240
	AAGOCCAGAG CTCCATATCG AAAGTACGTG GCGGGTCAAG GGTTTGTGCA TACCTACGGG	300
	GITTICCAGTA CTGAGAGTTC AGCACACGAT GAAAGCGGTT TGTTCCCCGC AGACAGTGGG	360
55	GIOCAGGIAT CIGACGATGA TATTOCGAGA CGACTIGITG ATATGACACT TICCOCAAGC	420

	OCASOGITTO COOSTOCACO GOCACCCATA COGIATOCOG GACACTICAAT GOTOCTTICOC	480
	TOOGAGCTOC AGTITITIGGT TCTGTCCAAA TOCAAAACTA TTGAAACACA CTTCATOCAA	540
5	GIGIOCAGGO GGIOGIATAT CATGIGICIG CCATTGATCT ACCGAGCACC AAGGCTCTCC	600
	AGCAAGACTT CTACAAGTTT GTGGAGACAC TGGTGGCAGC CCGTAAACAG AATTACCGGC	660
	AATATTOCTO GATCTOGACO GIOCATGAAT ACCINVANCOO AAACCTTTTC CAAGGTOCTO	720
10	COGTTOCTCC CACCCTTGAC ATTCCGGCCC CAAACACTCG TATCCCCCVTG AATCTTACGG	780
	CNNCCCNNTT GCAACCGATT TGTCTNTTCC CAACGTTANC GAACNCNTTG AG	832
	(2) INFORMATION FOR SEQ ID NO:325:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 846 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1060UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:	
	GATOGACCOG COCCCACOC COGTIOCOGTIG GGTGAAGTICG CCOCCCTOGA TCATGAAGTT	60
30	GGGGATGACG CGGTGGAACG TGGAGTTGAT GTAGCCCGCG GAGGCGTCCT GGCTCTTTGC	120
	GAGOGTICACG AAGTTOGOGA COGTICOCOG AGOGACOTOG COGAACAGOC CGAGCACGAC	180
	ACCCCAGT COCTOGTOCC COTOCTOCAG ATCGAAGAAG ACACCGTGTG TGACCGTGGG	240
35	GTCTGCGAGC GCCAACGCGC AGAGCAGCGC CTGTGCGAGA ACGAAGAGGA CCTGCATTGG	300
	GOGTGGCTGC GGGAGGCGCG GGACGCCGCG GGAAAACGCC CGCTTTTATA CGCGAAAAAG	360
	CIGCTICGGC TACGTAGCTA GAGATACAGA GOCGTGGACT TGAGGCTCTG CAGCATCAGG	420
40	COGTICCATICA TICTICOCOCCET CAGCACGTICC GAGTIAGCCCC COGTICGCCC GTOCAGCCCC	480
	GCGGTCAGCG CTGGCGCAGT GGCGCTAGAC GCGGTCGTGC CACTGGCCGG CTGCACGGAG	540
	TICIOCICCA CGGGCACGAA GGCCGCCCC IGGCCAGGCT GGAAGCGCGC CAGACGCTGA	600
45	TOOCGCCCAG CGCGGCCGAC AGGTGGAAGC CGGTCGACAG CAGGCCGTTC TGCACCACGC	660
	TGTACGCCGT GGCGCCTGTA CCTTCCCCNA ANANGINTAT CTTGACGCAT CACCGTTCCG	720
	CCCCCGCTGC TTCCGAACCA AATCCGTCCC NCTTAACCAC CNITTCANGC CNTCACTTGC	780
50	ACNOTIGNOCA CACNOTTONO GETTIACOTOC CAATGOOGTIC TOOCCNOGGO GOTTAGONOG	840
	ectegr	846
	(2) INFORMATION FOR SEQ ID NO:326:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 835 base pairs	

	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1261RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:	
	GATCATAAAC GAAGAATTCC TAATTAACAA TTTGTCCTCC ATGTACTTCC TCAGTGAGAA	60
15	ATAGCGATAT AATCATTAGA AAGCTTCCCC GAGCACTTTA GCAGCACCGC ATGCCAGCAT	120
	AACCCCCTGG ACTCAGGGCA GTATGCCGGC TGGCACCTCG GCACCTCATC GCAGGGCGAGA	180
	CAGTOCACCA CIGOGAGCAC OGTAGTATIT ATACTITICC AGGTIGAAAA ATTITOGACC	240
20	GCCCCACGCC GCAGAGGGCT GGACGCGCAT TAGGGCTCAC AGCGGTCGAC TGCCCACTGCT	300
	OCCCCAACAG COCCOCCAT GTAACGIGAA ATGATATATT ATACCTTCIG ACTACAATGT	360
	GAAATATACA AAGGTGGCTC ATAGGCGCAT TGCATTTATT CAGACGCAGT AGCTCTGGTG	420
25	TAGATACCCT CCTTCCAGTC CTTCCAGATT CCCTTCATCA TCCCCTCCGCT CTCCAAGTCT	480
20	CTCAAAGCAA CICTGGCCAT GGAACCGCCG ATCTTCAATC TGTGGACCAA CACGGACACA	540
	GAGACGIATC TGTAGGTTGG GACCTCCTTT AGGATTCTGT CAAGCTTGTC CTGGTCCAAG	600
30	ATGACGOCGT GCTGGGCCTT GTCCTTGTGG GACTTCTTGG ACCACTTCTC TTGGACTTCT	660
00	TACCACCOOC CATGOCCCCC GCOCCTTCTG COCCTTAAAN ATNITGTTTT TOGTGCATAT	720
	ACNOTIGIOCO CIVITATACTIGT CCOCACCACT COCINTCTICTIG CONAGOGTIGG TIGAGCTTCCG	780
35	TACTOONOCC CCTACCONCC CCCCCNNGNT TGTCCNTTTC NNCNNNCCTA ANTCT	835
33	(2) INFORMATION FOR SEQ ID NO:327:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 852 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1261UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:	
50	GATCTOCAAC AACACCATTC CATCGOGAAG TCTTTCCAAT TTCTGTTCTG GAATATTATG	60
	AGGAAGTTTG AGAACGATAT TOOGGAOCGAT GATGAOGAAG ATCCCTTCCA GATCAACGAT	120
	TIGGACGAGG AGAAGACCIT GCGCATGCTT TCTAACCAAG CCTGTTTCTT CGGCTACCTG	180
55	ATGGCCGAAG GTCAGGTAAA GTTAGATGTT TTAAAACATG TATCCATTAT GGGGTTGAAC	240

	Telephone declificer Adalaticit Ciatticagi Ticigninge eleagedaa	300
	AAAGCAGAAA CTAAAAAGAA GGTGGGGAAT ATCAAGGAAT GGTCTTACAG AGATGACTTG	360
5	THOCAGOOG CCCTGTCOCA TOOGATCCAG OCCGAAAATA AAAAGATAAT CTOCAAATCG	420
	CTCAGGATGT TTATGAGGAA TTTTAGATAC ACGAACTATA TTGGTGGTCA GCCTGGCTCG	480
	AAGGAGTATC AACGTGACAT GAGAAGGTTG GACTGGGCCG TTAAGCGTTT TTTGGAACTT	540
10	ATAGATGAAG AACTOGATAG TOCAGATTGT GAAGACCTTC TIGICACTAG TCTGAATOCA	600
	TATTACGIGT AACATIGAAC ATACGIACTC TATATTAAAG TGGTGAAAGT GATGAGAGTA	660
	TGACGICCNI OCTITIATIG CATACCACIT NICAATTACA GITATICOGI GAATGACNAC	720
15	AAACANGTIC CATTACTTAC TIGITGACNI 0900N0GACC ACCAC00000 CCACACCTTT	780
	GTTTACCTTA TAAAAATCTC CACNICCONC GTATANAGCC TNAANAATTC NITCOCTCAT	840
	GCGGTTTTGA CN	852
20	(2) INFORMATION FOR SEQ ID NO:328:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1262RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:	
35	GATCTITICCA CACOCTOGTA ATGTTTCCCCA CTAACTOGTA TITTTCCTTG TCTAGATAGT	60
	CTOCCOTIANA GACTOCOGAC GIGATOGGCC GGGCACOGAC GCCCATICTGC TOCCAAGGCCG	120
	TOACAAGTIT CAGGITCTGT TOCAGAAAGC ACTOGOGAAC TACTGTCATG GTCACAGGAT	180
40	CAGITACOCG AATTOCTTCT ATATATGAAG OCTOGATACC CTGAGCCTCC AATTTGTTAT	240
	TCACCTIGOGG ACCOGTIGOCA TIGCAGCACAA TOGGATAGAG COCCACATOG TACAGGAACG	300
	CCAGGCATGA AGCCAGTICC GGCAAGTIGT CGCTGATGAT GGCACCTCCA ACTITGATAA	360
45	CCCCGAATTG CTCCTCCGAG ACCGAAGTAA AGTACTTCAG GTACTGTTCT ACTTCACCCT	420
	TAGAGCCAAT ACTGTTGAGA AGCTGGATCA CGGTGGACCG TGTCTGCAGA GACCCAACGC	480
	CCTCGTTGTT CCCGGTTCTT CCATAGTTCA CCTTCTTTAT ACCGGCAGTG CTGAACAATT	540
50	COCCCTTGTA TGCCGCACGG ACAGCCCATG GCGTCCGGTT TTAGATCCTG CTACCAGCGA	600
	AGCTICTACTA AACAGTAGAG AGTOCTOOCA AGCATICTTOG TACTOCGTTT ATOCCAGTOG	660
	COCCAGNICI ACCICIOGAA ACCAGNOCOT GIGOCITATA COCTAANNIC TCTTCOGNIC	720
55	CATAACCACA AACCGICTCN TIGNOVITICC TGANITICAA GACCCCNANA TITTCACAAT	780

	TINIGCATIT NICONONONA AGOGIOCNAT TIATINITOC AINCNITIAA A	831
_	(2) INFORMATION FOR SEQ ID NO:329:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 865 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pag1262UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:	
	GATCACAAGC TIGITGAAGC CAACTOCTGA AAATGTCTCC TACGAGAAGA AACGATTCCT	60
20	TOCACTAGGA GAGGIGIGGC AAAITTITAAA AGGAGOCAGT AAGACGCAGA CTAGCCCCAG	120
	CAGAAGCGCC AGTAGTTGTT AGGAAGCATT CCAGAGCGTA TACGACACTT TGAAGACGGA	180
	CAGCGITCAG AGAAGACAGA GACAATCAAC ACCAAACAAA CATGGAGAAT OCTCACGTAC	240
25	ATGATAATTT ACAACACATC CAGGOGGIGT TATOGAACTA OGACACATOG TTTCTCTOGG	300
	ACGATGAAGA GCACTACTGT COGCTCTGCA TGCAGOCTTT GGACATCACC GATAAGAACT	360
	TTAAGCCGTG TCCGTGCGGG TATCAAATCT GTCAGTTCTG CTACAACAAC ATCAGACAGA	420
30	ACCOGGACCT AAATGGCCGG TGTCCTGCGT GTCGCGGAAA TATGATGATG AGTCGGTGGA	<b>4</b> 80
	GIACATTGIT TIGAGCCCCG AGGAGCTGAA ACTTGAGCGA GCGAAGCAGG CGCCGAAGGA	540
	CCCCACCCC AACCACCCC ACAACACCAAA CCAAACAAAA CCAATATCCCA CCCCAACATC	600
35	TOCCOCCAT COCCUTATO CAGAAGATTIG GIATACGITA TIGOCOTGAA COACCOGIAC	660
	CCTACGACCA CCTTGCTCCC CTCTTCCCCT CCCACACTTA CTTTCCCCCT TNCCCCCANAT	720
	TTACHNATCH TCCGTGAACC GCAAAAAGGCC CCATGACCCC NACGGINTGG ATMINITICC	780
40	TTCCCNGAAA AAGAGCGGCC CNNTINCCGCC GTGGATGTNT TTTNTGANGG CCNGGTGAGG	840
	GGGTACGACC NATINIGCCIN TITTIG	865
45	(2) INFORMATION FOR SEQ ID NO:330:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1263RP	

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	(xa) SEQUENCE DESCRIPTION: SEQ ID NO:330:	
	GATCOCOCCA TICOCTICIG AATOCTICCT CACAGAAGGA TICGICTACC AATOCCATTA	60
5	GITCAGCCAG GICCICOCTA CTAACAGAAT CGICTIGIGG AACTCICTITI AGGAAGGIGA	120
	ACAGTICATC TATCCTTICA AAATIGATAC TCTGAAAGGG TTCATTTGCG GCGTTAAACA	180
	TACTAGATOC AGTCATTAGG GCGGCACTTT CTTGGTTAAT ATCGTCAGCT ATCCTTTTTA	240
10	GIGCTICTIC CICATITICA TIGGOCTICA ATAAACCICI AGCTATCAAA AACTCAATTA	300
	GIATCTTCCT CACCITAGIA GITOGICCGI CIGIOCOCCT AGICATACTC ATTAAGICAT	360
	GACGGAGCTT TTGCACACCT TTGCCAGAAA ACACACAAAA TATTTGACGT TGGTTAACGG	420
15	TAAATTCACT AGGAGGAGGT CTOCAAAATT GTGTGATATC TGGCCTGAGA AAAGAAGTAC	480
	COCAGTCAAT GACAAATGAG AGAOCTTTGG ACAAGCCATT ACCAACTCAT ATATTGGATA	540
	AATAGTCAAA TTAGTACAAT ATGATAGGTG AACTCTTTCC AATGTGTCAT TCCTACCACG	600
20	CANAGCANTO ATATTIANTA ACCICATOTO TONICIGAGA ACATTONOCA ACCOTATOTI	660
	THYAGHTGI TAATTCCCCA ATCATATAAG TATGAATTGI CCATTITIGIA CACAACNATC	720
	CNCTTCTCAT CNNCGANATC CTCATTCAAC CTTATCCCCN CCCNCAATGA ACNTCCCCAA	780
25	NGANATININ GITTITICCON CITGAAANCT CNAAATNCAT ACCCCGCTTA CC	832
	(2) INFORMATION FOR SEQ ID NO:331:	
3 <i>0</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 851 base pairs  (B) TYPE: mucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1263UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:	
	GATCITAAAA OCTOOCCTCC OCAGATAGAC CTTCTOOOCA GAGOCTOGAA ACCTCAACTA	60
	GCAAGTCGCC ACCCGAATCA GATAAGCACT AGAGTCGTTC CAGTAACAGA GGAAGCGATC	120
45	AAGGAAGATA GTAGAAGAGG ACACTGCTGC CAGGCTTGAT COGACAGAGG GTTTAGCTTT	180
	CTGTTGAATT TTAGAGTTTC GOOGCTTTGT TTACTTCGTT TCATTCTTTC GTGTAAAGAA	240
	OCTOTITIOCA COCTOCCATO ATTICCCAGI COCCAGGIAG COTATICCAG COCCACCGAG	300
50	TOGGTGAAAC AGAGCAGGAC CGAGAACGCC GATAGACAGG CGITTGTTTG TAAGCGGTGA	360
	GAGCTGAAGC AGGTCAAGAG GCCGGCTTGG GCAGGTTGTG CGGCGGCGGC AGAGCACAGC	420
	ACCOCATOCO AACAACOCCO ACCOTOCCCA CACCACCCCA GOCCOCCAA CACCACCCGA	480
55	TCATCACCAC CCACACCAAC AACAACAACC COOCCACCTC CAACCGCCGC CACCTACCGC	540

	CATCOGGGG TOCKCOAGE TOGETTALGA COCCATTOT GOGGGGGGG COCCAGALAG	600
_	ACAGCAGTAC TCCCAGAAGT TTCGCGAGCG TGTTTCGCGG TGACGCCAGC GCGCCAGAAC	660
5	TATTITICCA CTIACCAACC GOCCGNAATG CCCCCCACTT INITIGNCCAA ANACCATTIT	720
	TOCHOCAGON COCHOCOTINO TAAAAACCATT TOTTACHOGG NOGAATGAAA TOOGTTGWIT	780
	TTCCCCCCCC NGAGACACA TTTTTCCNCA CTCTGACCCG ANTINITIANT CTCCCNAACA	840
10	TTATTTTTC C	851
	(2) INFORMATION FOR SEQ ID NO:332:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 801 base pairs  (B) TYPE: rucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1364RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:	
	GATCTCGTTT TIGTAATGCT CTAGCTCATA TTTGTTGAAG GAGAAGGGTG AAAACAGCTC	60
	CGAGGCTGCA ACTACTGCAA AGAATAAAGA GCAAAATATG GCACATAAGA TGTCTTCCCA	120
30	ATTCATTTGG TACAGCTCTA ATACTGTGAA CCCTTAATCT CGGGTAGGCG CAACAGTTAT	180
	GCCCCCAACC ACCITAACCI GATAATCATG TAGCIACCC GCTGAAAAAA AGACTATGIG	240
	GAACCGCCCA GCTGAACCAA GCGCATGAGA CATGCCAACC ATATCCAAGC ATACTTGACC	300
35	ATGATGACOC AAAACTATCT AGCATAGTTA GTCTTGCAGC TGAGACAGOC TTCAATCGTA	360
	AACCICCCAC CTICACIATI GICACGIGAG AGOCAACATA ATTGATCITIG TGACTACCAC	420
	CCATACATTT TOCTACCACC CATACATACT AATTAATGGG GAAAATAGCG GCTGGTACAG	480
40	ATTCTTGCAT CTCCCTGCCC CAGAGGCCCG CGGGCCTCTC GTTCCCCAGC GCGGCCAGGC	540
	GOCCOCAGOC CGACTIGTCCT ACTACOCTCT CCCTGTTGGC CCGTGGTTTAC CGCCCCTCAA	600
	ATTACCAANC CTCCAATTIT TGANATICCC CGACAGTINI GINOCINTIT TITACCCCAA	660
45	TICCOGAATT TCCCTATTAA ANOGTAAGAC CONNVITTAC TITIGTOGAN TAACCINNOG	720
	CGINCTINING OGNVINCCIT TINITACNOG CCCCIVITCINA GOCCTITTIOG TICCCINAAA	780
	CCCGINAAAA AAAAAAAGAT T	801
50	(2) INFORMATION FOR SEQ ID NO:333:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
<i>55</i>	(an) and manages and where	

(ii) MOLECULE TYPE: DNA (genamic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAGL264UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:	
10	GATOTOATGI ATOACAACOA GACTATGATG OGACTTOGGG TGACTATGTO TOOTTTOCCO	60
	ACCOCTICAG AGAACGACTG AAAGACAAGG ACCITATITT GATGGACTCT GGTGACAAAC	120
	CTACCOCTAA TOGTCTCACT CATCTCACTA GTCCCCATGOG TTTCAAGTCA ACCOCTATCT	180
15	TTAACCTICA GAAACTICAC TIGITAACTC TOOGIAATCA TGAACTGIAT AOOGAAGAIG	240
	TOGTTCOCTT GGAATACTAT GGAACAOCAA TOGAGCCTGA GCTAAGTGAT AAATATGTCA	300
	CAAGCAATGT GGAATTTATC ACAGAAGATG GOGACGTTGT ATCCGTTCGG CAATAAATAT	360
20	AGGIACTITG AAACGCCAAA CCAGAATCTA CGIGTATTGG GGITGGCATT CATGITGGAT	420
	TTTCCCGTGG GCTGCTAAAA ATGTTAGGTT AACCCCTCTG GCCGAAGAGG TTAAAAAAGGA	480
	CTGGTTCACC CAAACTGTGG AAAAGTACCC GCTGACAAGC TTGATATTAT AGTTGTCTTC	540
25	CGTCATTTAC CAGTCACCCG TGGCGAAACG AGAGCTTCTG CAGTTACACC AACGACTAAG	600
	GGAATCTTAC CCCGACACTA TTATCCCGTA CTTCCCAGTG NNTACTCAGT CNGAAANTCC	660
	CINGITTING ANAAAACGAN TOCITTACCA ACCOCCAAAT TOCICAAACA TOCAATOCNA	720
30	TCAANANNG TTTCNCAAGA AACCAAATTT TOCATTCNAT ATGACTTACC CAATTCCTTT	780
30	TCCCCTCCNG NITNANACTC CAAATTCCNT CCAAGGAAGA ANAMINACNC CC	832
	(2) INFORMATION FOR SEQ ID NO:334:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 800 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1265RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:	
	GATCTICCTC AGAAATAACT TCCATTGTCT CCACTATTTT CTCAAGATTA CCATTTATCC	60
	ATGICACTAG GCATTGCGTT TCAGGTAATG CATTCCCAAC AAGTGGCTTA CGATCTGGAA	120
50	CAGATTGIGI TCTTTGICAT TCTGGIGGAG CCGTACCTCC AAAAGTTGAA TCTTCGTTTT	180
	CCCCCCGACCA CGAATTCCAT CCACCACACT TCTTCTCACA CATAAACTCA ACTCCCCCCC	240
	CICIATORA CATATORICO TGACTOROTI CIOCATACGI GOGGITACOT GOCTORAGIT	300
55	COLOCICAGI COCIACOLCI CINCITOCAT GCATANCOCT TOLOCICAGA TANGUINCIC	360

	Terresser Admissione Tearriging Gaterigane Analoging Tightatier	420
5	CCAGCTOCOC AGICTCTTCC AGGITTTACT TCCCATGCTT ATTAATACTG GITCTTTAGA	480
	TOGITICCCTG ACTITICCCTA TAGOCCATTIG GTTCCGGCGA CTTGTGAAGG TATGCATTGA	540
	GAGTOCTOCT OCTTAAAOCT CINCTOCCCC CCTTATTITA NCACCOCTTC CCCCCAATCC	600
10	TACACIVANTG AGTTAATIONS NGCOGGTTOS NGTTSSATIOS TGTGGGGGGC SCACCSCAGAA	660
70	COCNAACITN GOOGCACNA TITOCONTON CCAAACNNTT TOOCCNAAAA AANAATINIT	720
	CCCCCAACCN NCCANNACCC ATACCCCCAN ATCNNCTAIN TTGTCCCCCCNNA	780
15	ANCCCCINCCC CCCCNGCAA	800
15	(2) INFORMATION FOR SEQ ID NO:335:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 820 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1265UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:	
30	GATCCCGGTCG CCCCTCGTGA AGCCAGCGAC GTCGTTGTAC CGGCAAGGGC GCCTGCCCCCC	60
	GITCTACCTG GOCAACGGCC TCAACGTCAT CAACGTGTTC CCGCACTCGG CGATCAAGTT	120
	COOCTOSTIC CACCIGGOCA ACCOCCIGCT GCCCCCCTIC CACCOCTICC CCCACACCACCC	180
35	CGAGCICTCG COCCTGTCGA CGTACGTTGC GGGGGGGCTT GGCGGCATCA TGGCGCAGTT	240
	CTCGGTCTAC CCAATCGACA CCTTGAAGIT TCGCATACAG TGTGCGCCCC TGGATACGCG	300
	CTGCCGGGGT CTGCCGCTGC TAATCAAGAC GCCGAAGGAC ATGTACCGCG AGGGGGGTCT	360
40	COCACTOTIC TACOCCCCC TICOCCTICG CATTITICCCC GIGITCCCCCG TACCCCCCCC	420
	TOCACCITOG CACCITICIOG COCCICAAAC COTGETACAT TACCOGTOGO GCAAATGOGO	480
	TOOGCATCTC COGAGAACGA AGTGGTCATG AGCATCTCCG TGTGCTGCCG AATGGCGCCT	540
45	TCAGCCGTAC GTCCGCCCA CGTGTCTACC CTATCAACCT TCTACNGANG CGNTCCCAGC	600
	CCCAGGNAGI INICINCICC CCCTCCTACA ANGNITICAAN INITITCCGAA AACACCINCIN	660
	AGGCCCCCC GCTTTTACAA GGTTGGTTCC NACATTGCCA GGTNNCCCNC ATCCCACNCT	720
50	MITITITING NAAAMITAAA NNCCANCCCC CCNAATAAAG GCCCCTINIC CCCCCNACCC	780
	CNOCAATAAN GGITCGCNCT NNAAAAACCAA NACNCCCCCC	820
	(2) INFORMATION FOR SEQ ID NO:336:	
55	(i) SEQUENCE CHARACTERISTICS:	

5	(A) LENGTH: 819 base pairs (B) TYPE: rucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: 1266RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:	
15	GATCTTATCT GGAACACCCA TTCAGAACGA TTTATCTGAA TATTTCGCCT TACTAAATTT	60
15	TAGTAACCCT COCCTTCTCG GTACCCCCCC ACAATTTACC AAAAATTTCG AAATACCCAT	120
	TCTACCCCCT CCCCATCCTG ATCCTACTGA CAACCACATC CCTCCTCCTG ACCTCAACTT	180
20	ACATGAGITA TCCCAGATTG TGTCGAAATT CATTATCCGG AGAACCAATG ATATCCTATC	240
20	CANGIACTIA CCITGIAAGI ACGAACATAT TCTATTOGIC AATCTCTCTC CGATGCAAAA	300
	GOCAATTTAC GAACACTTCG TGAGGTCACG AGAGGTTGCC AAGITTAATGA AAGGTACAGG	360
25	GTCGCAGCCA CTGAAGGCGA TAGGTTTGCT GAAAAAGTTA TGTTACCACC CTGACCTGCT	420
	AGATCTCCCCG GATGAGATCG CCCGTTCTAC AAATTTAATT CCAGATGACT ACCAGAAGTG	480
	CTAGTGACAC ACACTCCGCC GCCGAAGAAN TTCCCCTTTT GNATTCCAAC GANACATTCC	540
30	ATCHAATTIC GCNATTCCTA GAACGITTIC NGITITAGAA TCCAGCCNIG ATTCNAATGA	600
	AAAAAATGIC CCNGATTICT ACNNCCCCCC ACCITGGATT TINICCAAAA AATNINNCCN	660
	CCCNCCCCON GETTINITICC CANCIGAANG NINCOCNENAA ATTAANNANC TITINAACCTT	<b>7</b> 20
35	TIGAAAAITIC CAAAACCCCC GOGAGAAITTI NICNITINIT TCCCCCCNGGN CNGOGNNGOG	780
	NICCCCCTTT NGGCCCCCG NGAANITIGA CCCCAAACN	819
	(2) INFORMATION FOR SEQ ID NO:337:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 807 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1266UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:	
	CATCTGTCAG CATTCACAGA AACCATCOCT ACGAAAAGIT TCCTACAAGT AATCCCAGCC	60
55	ACCOGNACIA CTCCCCGTTG GGTCCTGTAG CCGTCTTGGC ACCGCACAGT TTCCAGGACT	120
	TGTCTTCTGT TGGTCAGAGT ACTAGGCAGG ATGCGTTTGC TTATTCCAAT CACAGTGTTG	180

	TOSCTAATGA TOSCCAGOOC TOTTTACOGO GAAACCOTTOC COCAGACTOC ACGTTCACTG	240
	COGAGITTAA CCAOCIOCIA TCIGAATCCA GCAACIOCCT TGAOCITGAT TCTATATICT	300
5	CAGGCAACTC AGITCTCTGG AATGGCGAGA CCTTAACCTC TGAAGCAAGA GCTACCCTGG	360
	ACCOCATOT GCCATOTOC TOGGAAGATG CCCCCCACGA CAGCCAGCA AATTCTGCAC	420
	AGAATOOCCT GAAGTATTGA GTCTAGCOGA CACTGAGTAT OCGGACCTOG ATAGTTTGAT	480
10	CACTAATTIG TACTICTACC ATGCGAGGGT TCGTCCCGCG GGTCTGAACG TTTTGTTATA	540
	ATGATOGATT TTAGAAAATA TAAGAACCOC CTTGAATATG AATACNGNON NTTAACCCCC	600
	GGGGGTTGCT GATIACCCCCC CINTCCCCCN CINGGNIGAA TINITIACCCC NCGGNGGGGN	660
15	GANAAANAAT TOOTGOODING TIGGGITOON AANOOCCATT COOTTINNAA TNAAAANIGO	720
	TTOCONGNON TINITAAAAAA AAAAAACOGTIG TTOCCCCONAT AACCAAATOC OCNOGCANGN	780
	AATTICCTOG GTICAACANC COCTCAC	807
20	(2) INFORMATION FOR SEQ ID NO:338:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 792 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1267RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:	
35	GATOCATTOC ACCOGATTOC AGCAGCTAGT OCATTTOGOC ATACOCCCGA TTOCCCTTTC	60
	TTATAATGAA TOOOGGCTTG TAGAGCATCA TOOGGCACTT CACGTOGTAT TGAATAGCTC	120
	CTCATAACCG CACCGGAAGA TITICAGGAAT ATATICTOGTT GTGTAGTGTA GAGGTTATICA	180
40	CTGTGGATTC TGATATGGCT GTTGCAGCTT GAACATTCCA CTAACCTCGG TTGGAATCCG	240
	AGCACGAACA ATTITITICNC INAANCOCNA NATTITINNOC CCTANAATAN TOGNCTINNOC	300
	AAAATCVICN NNITINAATT TITICCAAAA CTTTGICCGT GACCGGAVIN GAAATGNOGG	360
45	NAAGTOGAAT GTCCAAGNOG GGNNCOCNAA ATTAGAATTC CAGGGAAAAT TOCTACANTA	420
	NANAGGIGNE ACCONOGINA ACCOCGGGGN GGGNNVACTG GNCCCTTINA ACCTGNGAAT	480
	GCGGTTNTCC AACCTTTTNC CGGGNGGCTT GGCCCCCCNN TTAATNCNAT TACCCNCCCC	540
50	TNCTTTTCCC NAAANNGATN CCCCCCCCCCG GAAAGGITCN TTWWWANCN TAGGAGGCCC	600
	CITINGGICCG CAAITINGNIN CCITTICIINIC TCCCCCCCCA AATCCNGGAC CCTGNAANNC	660
	CCTININCCC CCCNTTTTAC INVITITCOMI GNAANINCTT CCCTTGGCCC ATCCCCGGAC	720
	cerminate economical institución destination (contracte sincercasse)	. 20

	CCCCCCCTTN CN	792
	(2) INFORMATION FOR SEQ ID NO:339:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 824 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1267UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:	
	GATCCOCATC GITTTGTTGA GTCATACIAC CTOGACOCCA TGTTCOCCGA OCTOOCCGG	60
20	CCGCCCAGTC TCGCGTCACT GGTCGGCTTG TGCAACGCGG ACTGTGCCCC CTCGTACTGG	120
	TTOGAGCTAC CCAAGGACCG TATCCTGTTC CTATGTGCGA TTGCGAACCT CGTAATCACG	180
	CACCTOCTICA ATGTAGACCC ACCACCAAGG CACATGCACG CCTTCTGGGA GAAGGTGAAT	240
25	GCGCTCTTCT TGGAGAACGG CTCAGGGGGG ATGCTGCAGA AGGAGGCTTT GGTGCCGCAA	300
	COGRAGACT COGRGAROGA TOCCOCCAG COGRAROGITC CTCCCGTCCCC CATTICCCCT	360
	TOGCAGACAC AATACACATO GCACCAGGGC AGCAATTACA TGAACCCGCA CGCATTCGGC	420
30	ACCCCCCCC ATCCCCCCC CACACCCCCC TOCTICTGTTC CCCCTAACAG CCACACCCTC	480
	TCTGTGCGAC TOOCTTCACA CAACOCCTGC GCCCCAGAAG CGTCGCGCAG ATTCCATACC	540
	ACACTTOCTG ACOCAGOSTC GAGGACGCCA TCAGACAGGG AGCTTOCTOC TTTGACCAGA	600
35	AGGOCTICAG CAGGATITOCC AGGACGACAC GACCGCINCIG TAATGCAACT GITGICCTIC	660
	CNATTTGCGC CCTATCCCCC AATGGAACGC CACTCCCCING AAAAAAAAA AATTTTCCCN	720
	TOGATATTTG ATGAATTGAA TTAGAAAAAT TACMTTTCTN NNATTCTTOC GGTOCCACAA	780
40	CAATTGCGAN TNCTAGACCC GCGNCCTGGC NTTNGGTTTT AAAT	824
	(2) INFORMATION FOR SEQ ID NO:340:	
45	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 787 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1268RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:	
23	GATOCTICAGA ACACTITITIC TGTOGAGGCT TATCAATGCT CTTTCTATCC GCAGCTTCTT	60

	CCARROAGAI GAAIACIGGC AGICGCIGGA GCCIGCGCAT GTTAAGGCGT TTGCATATGG	120
	1999CTGACT TOOGAGTOOC AGCATOGOCT GCOCAGCTAT GCATTCCCGA TOCTCTTTGA	180
5	AATGICGTAC TATGICGCGT GGATACTGGG TGTGGCCACC CGGATGGCGC TGCAGGGGTT	240
	COCACATOCC ACCOCCCTGT GTGCCCCCTT GGTGCCCCACC GCCGCCCCCCC	300
	GATGAAGGCC GTCTGGGAGC TGCCGGAGGC AGCGCAGGAA CTGGTGGAGT ACTACGGGGT	360
10	TATTGTACGG GCCGCAAGT GGTGATGGCG GCGGTAGCAG CGTTCGGCGA GTTCTACAGC	420
	CTOCTOCTOC TTOCCCAAGC TCTATCTOCC ACTCCCCCAT AACCCCCACA CCACAACCCC	480
	GACGCGCGCC GTCAGCCGTT GCGCTGATGC TGACCATGAC AACTTCTTCA ACTGTTTCTT	540
15	OSOGACOCCA ACCITICATICA CTCCTTOGAG ATGACOCTICA COCCTOSCOC TCTACCATTIG	600
	ATTGAACGGG CCTCACTTGG TTCTCTNGCT TCNCCCAACT TGCGGTGGCT CTTTTGCCTG	660
20	CCTCACGCCA MIACTITITA TCTGGCNCCC TGCTMITCTT GGTGNGANCC TGTTCCCCCN	720
20	ANNOTOCNON COTTITAACO CONCOCAAGT TOCCCOGAGC COCTGCOGIN TITICAATOCA	780
	ANNAMOC	787
25	(2) INFORMATION FOR SEQ ID NO:341:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 840 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1268UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:	
40	GATOCAGGTA TACCCGCCTC CGTCGCGCAG CGAGCTGCGC AGCCGCTTCA TCGCTGCAAC	60
40	TGAGAATGCC CTCGACCTGA TGTGCGGTAT GCTGACGATG CACCGCACA AACGGTGGGA	120
	CACGACTOGT TOCCTOCTCA GTCAGTATTT TGTAGAGCTT CCGGAGGCGA CACCTCCTAC	180
45	GGAACTICCA AAACTAAATA AGTAATGACT ATGATAACCT AGATGGTATA CTCGGACGTT	240
	TIGIGITIGI OCTTIGAGOC GAIGACATIG OCTTTIATOG TATCOCAGAC GITOCCIGAA	300
	AAAGATTCAA CGTCTCGGTA ACAGATTTGC GCAGACTACT TGTTGAAAGA ACAAAGACCA	360
50	GAGCOCTIGGG ATTOCTICACOC CAATGACGAA COCACTICOGC CTTATTIGGCG CTIGGCTGCAG	420
	GTTCCTTAGC ACCAACAATA GGCCGCCACT GCACAAGATC TTTCCCTCCC AAGAAGCTGG	480
	TGAACAGGAT OCTGTTCGAC CTTGATAGCC GACTGACCTT CCCGGAAATT ACTGCCTGTA	540
55	TACCACCACT TGTACACCCC AATTACACAG TAGTACGGCG ATTTGTAGTA CCCCGCGCGT	600
	TGAGGGGGC ACGACGITTA TGATTCATGA AAAGGTGCTG AGAAGACTGG CCCGCCAGAA	660

	CGAGAGCTCC CATCGCCIVIC TACTTCCIVCC GGANAACAAC TGCTTTACTT GCTGCCCANT	720
5	GGANACHAAA ATGCACGNGC NCTNCCCTTG ANCCCGTGCA CCGNTTCGCC NAAGGNNCGA	780
5	AATGAATTIG CAATITAGNI CNGATITITAC NCTCIGGNIC CCCCCCCCA CIGANNGANC	840
	(2) INFORMATION FOR SEQ ID NO:342:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 787 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1269RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:	
	GATCCCACTC TTGGCAAGCT ATACGGTGAC ACTATCATAG CTCGCGGTGG CCTCTACGAG	60
25	ATGGAAGACA ACCTGGGCGA GTTCTTGGAC AGAGAACCCA ATAACGAGGC GTACCTCAGA	120
	GATCAGGGCC TAGCCTAAAT GCTCCTTCTT TTCGCCGCCCT TCCTGCCCTC CTATGTATAT	180
	TOCAGCIAGA GAATOGCAAG CAAGCCATAC TIAGAAATAG GATATTGTTC CGGGAACACT	240
30	CATTIACIGI COCITACICO TOCOCAAACT CACCIGTICG GIATOCAATA ATTACOCITIC	300
	GACTACOGCC AGTGTGATGC TTTCTTTATA COGGCATACT AAAACAGGGT CCTCAGTCGA	360
	ATCCTGTGTC ACTGAATATG ACCCCTCCA TGAGTTCCCA TCGCGTAGAG CGTCCTATGT	420
35	GCAGACCATA TCAACACCCT CTGTACACGC GTGGAGTTCA ATATAGGGGT AGGACGCACA	480
	TACAATAGTA CGTGTCGCCA ACCGTTATAC GAAGAGCTGC GTTCTGATTG CAGCATTTCC	540
	CAAGCCCCGG AAATACAAAA CCGCATTTTT AGCCCAGTGC GATAGATGTC CTGAACCANG	600
40	GAATTACANC GAAGGNOGAT TOCTACTACN ANCATCANCC AGGGCTOGNG TATTTCTCAT	660
	CCATCCCCCT CNAACNAAAA ATCCCCANTT TTTAAATTTC CATCCAAAACC ATNCANATCC	720
	CONTINGAT ATTONOCCAC TOGOCCCCCC NCCCCCANNT ANCNOTOGG ATCONONATT	780
45	CCCCCCCT	787
	(2) INFORMATION FOR SEQ ID NO:343:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 820 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1269UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:	
5	GATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGGAGCT GCACCGCACT GGGTGCGTAC	60
	ATACCOCCAT CIACCAATOC COCCATAACC ATTCCCAAAA CCTCACTOCC CTCCCCCTCT	120
	AGCTTCAGCT CAAGCTCCCC CAGCAGCGTT GCTATAGGCT GTTGTCCCGA CAAGGTCCCAC	180
10	ACTICAGITG CAGTAGGAGC AGGTAGCATA CGACTAGTTA TATCGAACTG GTGCCGGTAA	240
	TGAGGATGAG GGTCAATTTC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCACCAAGT	300
	CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CCGGTTTTGC ACCCCCTCGG	360
15	CCTAAGITIT CCACCGIGAC CTICGATICC TCCIGGGAAA TGCGAGAITT CITTACCICT	420
	TIACCIGICC CCICCAATAT CCCCCCACC TCCITCCCAT ACTGAGTGIT GACCGTCATG	480
	ACCACCACAT COGITATOCC CCCCCCCIGN COCCCCONAN TITICCCCCCCC CGITATTICT	540
20	GICCCIGCGC CIGCAANAAC TICCANITAC GANGCAAICT GGICCCCCIG TICTICCCCC	600
	AAAACATCTG GCCCATTIGGA NCCCATATGC CCTAGAACCN ATCCAATCTG CANCCCCANGA	660
	NITTITIGGAA ANNAATTACC GGNAAGGANC AACCCGGAAG NAAAGCCCGC CCCCCCTGTG	720
25	GASCONACTT CCCCCCCCC NAAAACONGA ANTINNITIT INNITIOGCC CIVANCONCON	780
	TITICNECCC NECCESCANG OCCITAAAAN TICNICCCCC	820
	(2) INFORMATION FOR SEQ ID NO:344:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 806 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1270RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:	
	GATCATATOG TGAACTTOGC ACATACAGIT GAATCATCCC AATACCAAAG AGAACGIAAG	60
45	ATTTACCTAG CGCGGCATCA CCTGGAATAT CTAGCATTIG CAGCGCAGGT GAAAAGAATT	120
	TCTCATGAAT TGATTGGAAA TGTGGTTCCG TGTGTTCCAT TGCTAAGCCC GCTAGTACAC	180
	GATAATCATC ATTAGACTCA CAGGITAGAT GGGCCTTCAC TGTTGCCTTA TACCAGTCTA	240
50	ATAGAACCIG CCTGIAACGA GCATATIGAT CCTGAAGAAT AACCACCGAT GCGICAACCA	300
	TOGAATTGAG CAACAATGIC GOGTCATTCA CGGTTTGAGT CATGTGACTT CCGGTGAAAT	360
	TCTCAAAGGA ATTTAATTTC GGTATCAACC CCTTCAACAA GCAAGCTGTG AAGATATCAT	420
- K	CAACATOCGA TITIGTIAAOCT AAACCTTCCC OCATCCATAG GAAATCAAAA GTOOCTOGGA	480

	ASSAURT TOGETHING GETTIGHETA ACTOCCHAST TAGASTACTA CATGROOGG	540
	CCAGTITICAA TAGCAGAGTT AGACATTCAA CGGATTCTNA GAATATAATC CTNGCGAATT	600
5	TATCCATCON COTANAAAAT INTITOONOO TIGATOOANA ACNANAAAAT TOOGITIGAOO	660
	NCIGAAGACC TATTOCINOC TITNAAAGAC CIGONCATIC TICNATTIOC CNAANGNVIC	720
	CCGITCTACC NAGAAANITC TIGCATGOON NCATGGTTIN AACCNAAACN TCCTTTGANG	780
10	NIANINACIT COCCONNOCC AATTA	806
	(2) INFORMATION FOR SEQ ID NO:345:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: mucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1270UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:	
	GATCCGATTC TCAAATTTTC TGAATGGTAT GGTAAGAAGT TTGCCCCTGG AAAGGCTAAC	60
	AGROGIGITA TATCIPTOCG TGATATTITA GCITGOGICG AGITCATTAA TAGIACCIAT	120
30	AAGGCATTGC CTTGCCCTTA TGCTTCATTA ATCCATGGGG CGGCAATGGT ATTCATTGAC	180
	GCCCTTGGAA CCAACAACAC AGCGTACCTT GCCGAGAGTG AGGAACGATT AGAACACCAG	240
	AAGCAAGAAT GTCTCAAATA TCTGTCTGAA CTAGCAGGAA AGGATTTAAA CAAATACATG	300
<i>35</i>	TCTGGTCCAT TCGATGTTAA GATTGACGAT GAAACTCTCC AATCCGGGCT TTTTAGCCTA	360
	CCCAGAGITT CITCCICATC TGTCCAACCG GTTTTCAATC TTGGCGCACT ACTACAGCCT	420
	ACAATCTCAT GAAAGTTGTC AGAGCAATGC AAGTACAAAA GCCATCTTAC TGGAAQGATC	480
40	ACCIGGIGIT GGTAAAACCA CATTAATTIC COCATTGOCT GACTGTACCG TTACGAATTA	540
	CCCNTTTTAA TTATCCGAAC CAACTGATTT GAATGAATTA TTTGGATCCG AAGONCOCCG	600
	AAAAAAAAN GOVAATTINI TITGNGITGA TGCCCCCNIT TITINAAACTA TGCCAAAGTG	660
45	GATGGITTIN TITAAATAAA ANNANATIGC NCCCCANCON TITTITAAGGN CNNACCCIGI	720
	TIGINNOCNI GENGAACCCA MICCCAAATT TAANAAAATT TNICGCCCCC ATCCCCTTTT	780
	TIGNINCCCA AACCCANACA GOOGNOGIGA AAAGOGNIGC CAANCTICCC TC	832
50	(2) INFORMATION FOR SEQ ID NO:346:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 791 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAGL271RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:	
10	GATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
	ATTATATAA TICTCCATIG GAGCAATTIG AGATTAGAGA TITATTAGGT TTAACATCAC	120
	CAATAATAGA TITTAGITIT ATTAATATTA CIAATITTOG TITATATCIT ATAATICTIT	180
15	TATTAGTAAT TITACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTICTA	240
	ATTGATATT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
20	TIGGIOGIAA AGITATGAGG TIATTATITT CCATTAGITT ATACATTITT TATTCTTATT	360
20	TITACTATAA ATITAATTAG TATAATCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
	TIGIAGIATO AATAAGIATA ATTATTIGAT TAGGICTAAC TAITATTGGI TITTATACIC	480
25	ATGITTAAAT CITTGITTAT TTTACCACTA GGTACACCAT TAATTTAGTA CCATTATTAG	540
	TATOCATIGA ATTATATOCT ATTTOCINNA ACTTATTOCA TAGGITTITIA AAATACACTA	600
	ATATATACCG GICCATTTAT AATOGITATT TAGNNOGITT AATATINAAT TNAAAACCAN	660
30	AATATTIACA TITTATOGIN NOONOOCAAN AAGGCATIGG TITGGIINIT TAAAAAGGCN	720
	ACCTATATON CCTANITGAT NITITITATN CCCCCTITITA AANANCNATT TINNCCTTAT	780
	TAAANTAAAT C	791
35	(2) INFORMATION FOR SEQ ID NO:347:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1271UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:	
5 <i>0</i>	GATCAATCTT TOGATCATTG TOCAATATTC COCACTGCTG TATCATATAG ATATTGATTA	60
	TAATTICIAA ATCAACGIGA TIGITCTAAC TITAATTAAC AATTATGAAT TITTGOCTAG	120
	TTATTATTIT TTAATTAACT AATACCTAAA TCATTATAAG CTTGACTTAA AACAAATAAT	180
5 <i>5</i>	TATTACATTA TICTITATIT ATTATTTAAT ATTTAGITAA ATTITAAGIT CATTATICIT	240
55	AATTTTTACT CACGAGTACA CCACTTATTA ATACTATTAA TTAATAATAT TAACGTTTGA	300

	TTOGCATGIG TAATGICCTT AGITAGOOCT TAATCIGAAC CAACATCATG TTCTCATTAT	360
	TATTAACTAT TITTAATTAT TITTAAATAAT TATTTAATAC GAAAGITATA GGATTCGAAC	420
10	CTATGAAATC ATAAAGATTT ATAATAGCTC AAATATTACA CTTTAAACCA CTCAGTCAAA	480
	CTTTCTTAAT ATATATACCT TATATATOGT TTGATAATTT ACTTATAATA TATAGTATAT	540
	AATTTAATGA TAACTCITAT CATTTAGGIG OGTAGOGITC ACCCCCCTAT TOCTAGTCAG	600
	CATATGAGGT ACCTCCCCCC AATGATAAAA GTTATAATAT ATAATATTAT ATTAAGTATT	660
	TAAAGAANAT AATATAATIA TITAATAATA TITTTATTTA GONAATAAA AAAAANITIC	720
15	ANNITIGAAA NANGGIGONG AGAATTANAA AAAOONAATA ATATGITCAA TITIGACOOAT	780
	TAANAATGIA GINONCIGAC ATONOCTATT TOOTATANAA ANITTANAAN AANA	834
	(2) INFORMATION FOR SEQ ID NO:348:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 813 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1272RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:	
	GATCAAATCT AGGTTCTCCG ACGGCAACGG TGACGAGTTC GTGAACGCGC TCAAGCTCTG	60
	TOOCTITITIC CATAAACACA CAGACAACAG CAATAAAATG TICAGGAAGT TIGAGTICIT	120
35	CAAGOCTOCA AAGGAGATOC TAGAAGAACG CAAAGCCAAG CTOGAGOGTA AGCAGAAGTT	180
	CATCGAAGIG GAAACAGAGA AGGAAGCTCT AGAGICTAAG COGICOGAAA ATCCAGAAGG	240
	CATCGAAGTG GAAACAGAGA AGGAAGCTCT AGAGTCTAAG CGGTCGGAAA ATCCAGAAGG AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC	240 300
40		
40	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC	300
	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT	300 360
40 45	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG	300 360 420
	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT	300 360 420 480
<b>4</b> 5	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGCCA TATGCTGCTT GTCTCCCAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGCGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC	300 360 420 480 540
	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGCGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGACG CCGAACAATG CCCCAAGGGC	300 360 420 480 540
<b>4</b> 5	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGCGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGACG CCGAACAATG CCCCAAGCGC AGTGCTGCGT TAGTTTGAAA TCCCAAAACA CTTCGAATCA TCGGTTCCCC GGAGGCCCAA	300 360 420 480 540 600
<b>4</b> 5	AAACTGGCTA CTAAAGCCAT GTATATATAA ACGGAGGTGA TTGCCTAGTC TCTTCTCAGC ATGCGATCAT ACCTTATTCG TGTAATCTTA TCAAACTATA TATAGGGCGA CCGACAGCTT CAACCGTTCC TAAAAAAAGGT TTGGAAGGTG AACAGCCGCT GGATGTTCTC CACATTCGTG AATGTAGGCA TTTGTGGGCCA TATGCTGCTT GTCTCCGAGC TTTTCTTGTT GGGCTCCCAT CTGTCGCCAG GAGCGGAATC CCGTACGCAT TGTACCTGTT ACCCTGCTGC GAACAGCACC AGAAGAGGCT GATAATTGTA GTCNCAGCAC ACCATAGACG CCGAACAATG CCCCAAGCGC AGTGCTGCGT TAGTTTGAAA TCCCAAAACA CTTCGAATCA TCGGTTCCCC GGAGGCCCAA TTATCCGAAN TTGGCTTTTA AANTCCNAAT ACAANGANTG CGCCCCNTGT CCCCTGTACA	300 360 420 480 540 600 660 720

5	(A) LENGTH: 844 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INVA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1272UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:	
15	CATOCACCCC OCOCOCATOG OCOCCTOCOG CCTOCCTOCOC CCCTOCOCCC TCCOCCTOCACA	60
	SCICGICIAC AICCICACCG ICSCCAICIT CACCAACCAC TICITCATGI CCCCCTICIG	120
	GCTGCCCACC TTCGCCGCGC GCTCCAACCG CCACCTGCTG CTCGGCTGCT CGCTGGCCGC	180
20	COLOCIOCIC OCCOLOCIOS LOCIOCICAL COOCOLONC COCCIOCICO COCLOCIOS	240
	COCCTACOCC CCCCTCCCAC ACCTCCCACAC CCCCACTTTC TTCCTCCTCC TCCCCCCCC	300
	OCCOSOCIES OCCAACESCS TOSTECTOSC OCTOSTOSTC STECTATOCA CCTECACECT	360
25	CGACTCCTTC CAGAGCGCAC TCGTCTCCAC CATTTCCAAC GACCTCTTCC CGCAACCGCC	420
	TOCCCCCCCT CTACOCCCCC CCCCCCCTCC CCCTCCTCAT CCTCCCCCTC CTCCTCCTCC	480
	GCCTGCTGGC CACCCGACAT CCTGGCCCATC TACCTCATCG TGGACCTGCT GTCGGCCGCC	540
30	GIOGIOCCCG TEATGETGET GOCTTETIGGE CGCGCCCCCG CGCGCCCTGT TETIGCCTTGG	600
	ACCIGATOGG COCCOCTICC GONDOCCTGT CTGCCGTTCTC MICTITCCCGG CCATCTATAA	660
	COCININCIN CHANGOGANC GONIGOTAIT TATTONAANG NCCCTACTIN AATAANGOOG	720
35	NNCTINNOGN GOCTINGTONT TOCOCCCONIN GGGAACTGIT TITTCCCGGCNA NAANITICNGC	780
	CTOGENNOCC GITGENOCCN CCCGGANANT CANGNTAACC NCAGGGGAAN TOCAAANCIT	840
	CTINC	844
40	(2) INFORMATION FOR SEQ ID NO:350:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 792 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
43	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1273RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:	
	GATCCCAATA CAAGCAATAT TGTCGCTACC AGAATGCCCC ATTTGCGACC CATATAATCA	60
55	CAAGCGAATC CCATCCCCAC CTGCCCTATG ATAGTCCCTA TGAGTGATGC ATTTGAAACC	120

	CTIGIAGATA CATCIGCACT ATATICITATC TCACCGIACT GATITICIGAA TACACGGITT	180
	AACATCGACA TGACATTATT TTGGTAACCA TCTGAAATAA GCGCAAATCC TGCCGCCAGG	240
5	ATACTGAATA GATGTACCCA TITICCCCTTC TTCCCCACAG CAAAACGTGC TITICCGAGCC	300
	TCCCCCTCAT ACTITACTAA CCCTGTCGTG GACATCGTAT TICTCCAAGC CCCCCCTATC	360
	CGAATAATAT CTAGCGOGTC AAGOGITAGG TTGCTGCATT CTATATTATA TATTTCCTCT	420
10	CICIACCACG TOCAAATTTA CCIGIATGAT TATOCTOCAA TCTCCOCGIT CTACTTCCIT	480
	TCTTGGAGAC COCTACCGAC TGTCTTATGA TTATCGGTGC ACCATATGGC GTCAAGCAGC	540
	ACTAGCTTTT ACCTGIGATA CCTTCCTTTA CTAACTGNAT TCCGAACTAN TTTGNNCCCA	600
15	TACTATATOC TICCOCTAGA GIGAAATAAC CITCCATTTA GGITINNICOC ATTCCCNGAA	660
	ACAGITITITA AANAAANACA ACCITTATOC TINAACCOCA AACGCCCCAA AAANAAAATT	720
22	TCCCCATTIN CIAGGITTIT TGNGCCNGGA GGGAAGAAAC CCCCCCTAAC CCCCCTAAANA	780
20	ATTCCTCTNC CC	792
	(2) INFORMATION FOR SEQ ID NO:351:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 833 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1273UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:	
	GATCGGCGTA TAAAACTGAA AGTTCATGTA TGCTGTCTTG AATGCAGAGA CGCGGCGCAC	60
	TTTACACATC GGCAAGCCTT GTGTTGCGAA TGAAACATTA AGCTTATGTC AAATACCATG	120
40	AACTGTATGC CAAATTTAGT AAAACTGGTA CGTGCTGGCA GCATAGATAG AGCTGTTACC	180
	CATATOTOCO TICAGOCTAA AGCOCAGCAT TOGGTATTAA CTIGOCTIGCA CTATTOCCAA	240
	TCAGAGCTTT CAGATTOGTC TTCATCATGG TCAGTCATCA AAGTOGTOGA TGTAGGATGT	300
45	TCTATTTTCC CACCOCAATA AAGTOCAGTA TICATOCAGT ATTCAATAAG CTTACCTCTC	360
	ACCTOGATAT CTAGGACATO AGCTGGAGOG GAACCTAACO AGACACGAAG TTTAGTGGCC	420
	ACCICTICGA CGAGIGAAAA TATTICTIGG TCCCCCAATG ATCCTCATCC CCCATTATAT	480
50	GGCGTAACGT TAGGTACATA CCTGTGACAC CCAACAAAGT ACAGTTGCTA ACGTCCCAAT	540
	ATCTTARAGE ANCOGRITIAA ACCNOATATT AAGGIGAAGT TTATGAACCT TTGANAGTAA	600
	CTGNVICNIT ATAGCGGAAT ACCANANNAA TAACGNCCTT GITANGGNAT CTATCGAAGG	660
55	MITACTICCN MITCGANCAT TITATACTIC MINCIATTAC COCCGANAAA TITGAACAAC	720

	CVIGAGAAAA GTININNOCN CNOOGAAANG AAAANINING TINIGANIOC CCCCGITIAC	780
5	CTTGAAGNIT CTCCATTCNC GAGATTCAAA TTTTTINTAAN AAGGANITIN TAA	833
	(2) INFORMATION FOR SEQ ID NO:352:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 803 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1274RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:	
	GATCAGAACC AAAAAGCAGT TOGAGTATAT CAGTAAGCAC TGGGAAGTTT GGGAAATAGC	60
	AGIOCIGAGA GITACOOGAC AGATIGOCAA AGACACATIT GOGATOGAAT TIAATICOCC	120
25	GCAGCCAGAG CACGCACAAT TACACATTCA CCCTAAAGGT GCAGCCCGGC TGCTGGGAAA	180
	ACTOCACOCG GAGOGTCOCG TGATGCACCA CGAAGATAAC CAAGAAAAACC GOOGCCGOGGA	240
	AGGACCOCTG ATTCCCTICAC COCCOCTGTC ACCACGAATC GGGCCCGAG AGAACCCGGG	300
30	OGCOGINGGA ACGGAATOCC OGAACOCTIT TINITACCCC AACTIGGNIC CONGOCTIAN	360
	TITICAAACCG NITINCAAACC CONNOCCIGG GITTINITINGC CONVINCOCA NITANITIGGGC	420
	TNCGGGGGGG GGGGCCCNCN CCAAAAAAAA ANGGGGTNTN CCNGGGNGC CCCCNGTTTT	480
35	ANCAAAANAT TINCCCCCCC GGITCNCCCC CONAAAAGGI TITTCCCCCCC CCCCGGGITT	540
	ACCAAAAANC CNGCCCCCCC TTTGGANGGT TTCCCCNVTCC CCATGGGGGG TTTTCNCGGG	600
	GCTCCCCCCN GGGGAACCCC AAAAAAAGGGC CCCCCCTTTT NTGGGCCCCC NAAANNCCCC	660
40	CHINNTTTIC CAGANGGETT NOCNCCCCCC TITTTTTTTCC CCATTANNCG GGAANTCCCN	720
	NINTTCCCCC CITINNCCCC CCCCCAAAA ANNAATTITIT INNATTAAAA GAGGCCCCCN	780
	NGAAAAANAA NACCCINICCC CAC	803
45	(2) INFORMATION FOR SEQ ID NO:353:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 814 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
66	(A) ORGANISM: PAG1274UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:	
	GATICAATTIGE GGATACACGA GGCACAGGGC GATIAGGCCAA GCTTICCAAGA ATGGGAAGAG	60
5	TACCTAGTCA GOGTCGTCCT GGTAAGACTG AACCGCTGCA AGCAGCTCTA TACACAAAAT	120
	GTAGAGATTC TATTOGATAT ATATOCOCAG ATAGACOCCC CATAAACACT AATGATACOC	180
	TAATTCATAC ACCTACACCG TGTACATCAA ACACACAC AAGTTTGATG CACACGCTTT	240
10	ATTIGITECT TOCACACACT TGATTTAGAC OGTCAACACC CTCAAGGTGT TAGAGTGGCC	300
	AACACCAGAC GOGAAACOCT GAATAGTGAC AATAGTGTCA CCCTCGCTCA GGATACCAAG	360
	CICCITIOGAC TICICCACAC CGAAGITICAA TCTGGCCTCG ACGTCATCGG TCCACTCATC	420
15	AGCTGCCTCC TGTTCGTAGA CGAATGGGAA GACACCTCTG TGCAAGTGGC AGTATCTGGC	480
	COCTCCTTGG TTTCTGGTCA CCATAACGAT TOGAACGTTT GOCTTGTACT TGCACACCAT	540
	CTGTGGTGTT CACCCGAGGT TGATACAGGA ANATGCCTTG GCTTCTGCTC GAANINCCGC	600
20	GAAAGCAGCA CACAAGNOCC OGAGGTTGAA TTGGCTTGNT CATTTCCTGA GTCACCGTAT	660
	TTGAACGITT GGAAGOCCTG CNCCACNATIC AAAATCTCGC CAGNONTAAA CGTNAATGGT	720
	TGANACCCTG GOGNICCCCN AAAAATAANA TCNCCCGCCN GAAAAGTTCC ACTTCGAACN	780
2 <b>5</b>	CCCCNGINGT CTOGTTTTGN TOGTANCCCA ACCG	814
	(2) INFORMATION FOR SEQ ID NO:354:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 754 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1275RP	
<b>4</b> 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:	
	TGACTOGOCT TOGTGAGGAA CTGACGCTTT TACTACATGT AGATTGAAAC COGTTTTCCT	60
	GCATCGCCTC GTCTCGTTGC TTGGTATCTT TGCCAATCCT CCTGAGTGGA CGCTGCCTGT	120
<b>4</b> 5	AGAGGATCTT COCGATOGOC CAAACACOCC CCACCAGCCC AAAGACGTTG GAGAGAGOOC	180
	TGAAGAAGGT TCATTGACCT CCTTTATGGC TTCAAATGCT GACGGAAGTG ACAAATGGTT	240
	CCCAAGACGC ATGTCCCACA ATTICTICTCAC GGTGGACTGC AAGACCTGGA TGCCCCTGTGC	300
50	CCTGGICTTT GATATTCTAT GGATAGIGGC AATGICCTTT GAGAGIGICA TGTTCTGGIT	360
	TGTGAGGITT AGGITATCAA GITGGGCAAT AGCGAGCTGC TCTGCAAGIT GGTGGTTTTC	420
	TOCACCAGET GIGOCTICIGI GIGITTICAGG TETGICATCA GITTICITTIAA GECTETECTT	480
55	ATCOSCOCAT COTOCACCIG GACTONIAIN TITTINCCAC NOCCATINNN CCATAATTIG	540

	MINAAGNAGG INCCCCNCCG GAAITINGNI CCCGITICCA NAGNICGGNC CGGGGATAAT	600
	TTAAACNITT AAAAATTANC CCCGGCCCTA NITCCTTTTN CCNAATNNN GWCCCCCCN	660
5	QVAANVITIT NCAANVCTIN TONNOCNIAN CCITTITINNC CCCACOGITT TINNICCCCC	720
	CCCNICCCCN ATINNOGANT TOCCCCCNITN CCCC	754
	(2) INFORMATION FOR SEQ ID NO:355:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 842 base pairs  (B) TYPE: mucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	٠
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1275UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:	
	GATCGCCCAC ATTATGICTC AGGGTACTIT GTACGTTAAG AAGACCTGCC GCTCGATGCT	60
25	COCTCAGAGC ATTOGICGAGC ACTACAACTT GGACGICTCT ATTGTCGATG CCCACAAGAA	120
	CCACCACTIC CACAACAACT TOCCATICAA GOSCOCTOCA GOGITTIOCT GIGOSOCTOC	180
	AAATCTAACT GAGACCATGG CCATCACCTA TIACTGTAAG TIGCCACCGA CIACACACCG	240
30	AASCATGGAG COCTAGTGTG ATGAGAAAAC CTTTCGAAAA AACAGTTATC CCTGTCTGAA	300
	TOGOCATAAT ATCTOGTTGC ACATGTGTCG ACACACCATA CTCTGATTTA GAOCTACATG	360
	CCACCTICCG ACCAACACCT ACTAACCGAA CAACACTGGT CAACCTAATC CACCACGACA	420
35	AGECCAAGEC TECTICTECTT GECTICCACEC TACAGGAGCA GECACAGGTG TTGCECTGGG	480
	AGICTITGAC CAACACCAAC TICATIGACG ACGIIGGCIC IGCCICCIAT ACCIAGAGAG	540
40	GETGTGGTCC CNTTNCACCA ANNCNACATG GAAAACGNCN TTCCCCNGNGG CGAAACNITN	600
40	CCCNACNOTT TIMMAAAAAA GAAATAACCN CITCCCTCCC TTACCCCCGG AAANITTIMT	660
	TINCCOGGAN NCCNIGNONN TNGGGGGGTT GAACHNANIT CCCCACANIT NGGGGNGNIN	720
45	MIGRENCONE GCCCCCCCCC CCCNNNNANE GTTACCCCTT GGGTANCCCC NUMINAAAAA	780
	CNNCCNCCC CCCTTNGGTC GGACCNAAAG GGGGGGCCC CAAANGAAAA AAAAAAAAA	840
	AA	842
50	(2) INFORMATION FOR SEQ ID NO:356:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 77 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
55	(ii) MOTECULE TYPE: DNA (genomic)	

	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1276RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:	
	CATCCTATT CTTCTCACC ACTACCACTT TTTTCATCTT CCCTTCGACC ACCACCTCCC	60
10	CCACGTTACC GACCATC	77
	(2) INFORMATION FOR SEQ ID NO:357:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 77 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1276UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:	
25	GATOCTOGGT AACGTGGCGG AGGTGGTCGT CGAAGGGAAG ATGAAAAAAG TGCTACTGGT	60
	CAACAACAAA TACGATC	77
	(2) INFORMATION FOR SEQ ID NO:358:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 822 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1277RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:	
	GATCCGTCAC GGACAGACTG AATGGTCAAA ATCAGGTCAA TACACAGGCT TGACAGACCT	60
45	TCCGCTGACC GAATATGGTG TCGGCCAGAT GCGGCCCACT GGTGCTGCGA TATTTAGCGC	120
	AAAATACATT GATCCTGCGC ACATAACATA CGTATTTACT TCTCCACGCC AACGCCCCGC	180
	GAAGACTGTG GACCTGGTTT TOGAAAGCCT CAGTGAAGAT GAACGTGCAC GCATCCAGGT	240
50	GETGETGEAC GAGGACCTAC GEGAGTGEGA GTACGETGAC TACGAAGGETC TGCTGACAAG	300
	CCAGATTATC GAATTOCGTC GTAGCCGTGG CTTGGACTGC AAGCGCCCAT GGAATATATG	360
	GOGOGACGOC TGOGAGAACG GOGAGAGCAC CCAGCAGGTG GGOCTGAGGC TATCACGAGT	420
55	CATTECCCCC ATCCACCCAT TACACCCCCA CCACCAACCT CACCGACCGC CCACCCATAT	480

	ICIGIGITI GGGAIGGC AIGCICICG TIAITITICI GGGICIGA IGAAAIGG	740
	COTTCGAAGCG COGACCCCAG ACTGCCCCAT GCCCTCCAGT AACCCCGAATG ACCATCCGTG	600
5	COCTTOGTOC GGCTGGAGCA ATCCGTTACCT GCAGGACACC CCACTTCTTG CTAGACGCAG	660
	GIGOCATCOG IGIGITIGICC TACCCCCNON ATTIGAGACC ANICIACION CCIOSCONIT	720
	CNITIOCCCCC COGAGATICCC CCCACOGTINA GTCCCACCGA AAATTTITEAT ATCTACAAGN	780
10	CNGICCCCCC ATGAATATAC CNTATCTTCT TAATCGTCCN CN	822
	(2) INFORMATION FOR SEQ ID NO:359:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 818 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1277UP	
25	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:359:	
	GCCGTCCTTC TGCGGCCAGC GCGAGTCCAG GTGCCGCAGC ACGCCCCACG AGCGCGACCT	60
	GCGCAGGCGA TAGTACGCGT ATGCGACCAG GCCCGCCCCC AGCACGTTGC TTGCGCCGAA	120
30	CAACCACAGG AACCGCCEAGC GGCTAACCAG CTGCACCAGC TGTCCGTAAT CGTGCCGCAG	180
	COCCTCCCC CACCCCACCC CCATGOCTCT GCCCACACTC CCCAGCATCA CGCCGCCCCC	240
	GCAGATICAGC ACCGTICCCGA CGCACGTAAG CATACAAAAC GGCTICTGCGA GCAGCCAACA	300
35	CCAAAACCAG CTGTTGAACA GCAGTCCGCA CGCCTGCAGC GGGGCCAGCA TCACCAGTGG	360
	TAGOGTOGCA ATCTOCATOG TOCTTOCGAA CACGITOGCT AGAATGAATA GOGTCAGACC	420
	CATCIGCCAT AGGCCCCTAC GGTACACCAC CTGCACAGTT CCCCGTGCCA CTTGCAGCCC	480
40	AGOCTIGOGO IGAAAGIACO AGOCCCAAAA GACIGCATAC GOTIGAAACT ACCGCCACCA	540
	CCACCCATAA TAACCAGTTG ATCGACCATT COCTTGGATA CCCTGCACCC TTCGCTGCAG	600
	AGUACUCUAC UGUGGGGGCC TUTUGGCUCU AGGUCUCUAC GCUAUGCCAA ACAUACUGC	660
45	TOOGGIGOGT CATGITOGAT OCTGIATGIC ACGTGACCGA TGACAGGGTA CCTGICGGTT	720
	CICTICOGGI TOCAGGENAT GATACOGAAA NCCGAAAATTA NCCGGATGAA TITICCCGACC	780
	CTGCGANUAC GACNCCAACN GGAGACGCNG TITTINTGT	818
50	(2) INFORMATION FOR SEQ ID NO:360:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 828 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1278RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:	
10	GATCTTCAAC CTGCTTCCGC CTATGAACAT TCTGTTGTGA TTGAGAGCG ATACCGCCTC	60
	CACCTITICIT CGAGCCTGCC CGGITTTGGT AATCCATACG TICTTCCCCA TICTTTTGGT	120
	ATTOGTATAA GOGATOCAAA TGAAAACAGC CTICTTGAATA CAAATOGACT TGOCTIACGTA	180
15	TAAAATTATA TTTTTATCAG AAACTTGGCG AGCATCAAGC TCGGCTTCAT TGATTCATAT	240
	ACTABACAGA ATACACTACA TOCTACOGTC CGAAAACGAA TAATCTATTT CCAATATATA	300
	TATATATATA TATATATATA TIATAGITGI ACTITATAAA TOTGAACTAG GTOATACAAC	360
20	TCTCAAATCA AACGATATTT ATTCTACATA TAGCACGGGC GACGCACCAA TTGAAGACTC	420
	TAGGGCGCCT GAACTTGGCG CTGCCCTGTA TCTTTAGCCT GTTCCTTTAC AGGGTCATAA	480
	ACATAGTACA TACCOCOCTIC TAGTTOGTICA TACTOGATGT TOCTCTGTTT CAGCTGCGGC	540
25	CAATTITICGT GAGGGATATC CCACCCACAT TICTGAGCTA TGAAAGCTGC AACGTCGTCG	600
	CACACCCCCA GIAACTTAGG TCAATTCGCG TGCTTAACGG GTCTCCTATG ATAGTACTTG	660
	TOCTACCIGA OCTOCACCNI CITITACATON COGAAACTOC OCNOCTICAN CINITICNATO	720
30	ANCNCAATOG CATNCANVIT CTOGCNANIT TTTTTGANIC CATGACCCCC CCNAAANINT	780
	TICCOGINNG ACCCACACCC CCTIGAAAIN NCIGAINIGN AGANGONC	828
	(2) INFORMATION FOR SEQ ID NO:361:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 855 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1278UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:	
	GATCHIGGAT GIACIGOGGG CICATACTIC GOCTICIGIT TCHIGICCIT THIGCOCTIC	60
50	TGGCCCTTGC CATACGTCGA TGCTCCTTGG CCCATCTTAG AGATATCTGC TGTGCCGCTA	120
	TOGAGIAACG CTICIOCTIG CGAACTCIAA GIAGIGITAT CAACTIGIGI GIATCATTIT	180
	TOCCACCTOG ANTOCATICAA TITICACCTAG COCCAACCCAA OCTOCGACCT ATCAAAAAAAC	240
55	AGGAGCAGGA AGCTGCCTGA AGAAGCGCTC CAGGGGTCTA CCGACGGGAA AAACTACGAG	300
	GACTOGTOCT ATGACATCCT TCCCCGGGATC CATCCCGAGT TCAGTOCTTT CGAGCTGTAC	360

	AATTIGOGTOO GAGOGGTOGG AGOGCAAGOG TOGTIGACAAC ATCAACGACO GTATOCAGGA	420
	GCTGCTCAAC GTGATTCCAG AGGAGTTCTT CCAGGACTAC TACCAGAAGA AGAAGGACCA	480
5	GCAGTCCCAG ACCCCCACCC CCCCCCCTCT CCCCCAAAAAAC AACCCCAACTG CCACCCCCCCA	540
	COGCAAGCCC AACAAAGOCA GATTCTCACG CAGGCCGTCG AATATGTGAC CTATCTGCAA	600
	ACCAGTOGAT CTGCGCACCG CGAAGAGGTG GAGCTGATCC TGAAGGTCAG GAGCTGTGTC	660
10	OCCAGACOGG CAGCATCGTG AACGACGTGA ACTAGAAACA CCATTOCCGA CTCOCGCTGG	720
	GAAATOGOGT TOGGGNCTOC AGOGTOCTOC OGAATTINTOC OGCGNCAGGG CAGCACACCC	780
	NGCCAGCACA CCCCCCAGA CCACACACTC ATTTGGGTCC CATTCGGACG CNIAGATTTT	840
15	CNCCTGGNCT GITTT	855
	(2) INFORMATION FOR SEQ ID NO:362:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1279RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:	
	GATOCITCIG GATGCTOGIA GCICCCATGA GGAAGTCGIA CITTTOGIAA TGICACTOCT	60
	CCITAACCAT CTACTITICAA ACCGTGATAT ACAGAGACCG TITICCTAAAA GTOGTGGATA	120
35	TAGGITACIG TICTOCATAT TAAAAGATAT CCAATCOGGG CITTACAGGAA AAGICACGAA	180
	TCTATTGTGC ACCTATGCAT TTGGAAATCA TATTGTCCCA ACACACAGCG AAAGCACGTC	240
	CCTTCTTATT AGACCGCAAG GCGATGGGCT ACAAAGGATA GTTTTCGAAC TICATTATTT	300
40	GOCAATTIOCA TIGITIAGAGA TAGCOGTGAT AAAAGCCCCCA AAGGAGGATC AACAAGAGTT	360
	GAGTAAAAAC ATTATTACGT ATATCAACGA GITGOCGTTA CTTCATAGTA CTCACTCTCG	420
45	AATATOGCTT TITIGATOCAA GOGIATOCCA ACTITCATGAG AGATTGTTAA CTTTGTTAIT	480
45	AACTITIGACA GATCCCAAAT ATCAGGGTIT CTATATACAG GCTATTCTGG ACATTGAACT	540
	TOTATIGAGI AACAACATAT CITTCACTIA AAGAATGAIG ATOCACCACC TITTIGGAACT	600
50	ACTIGCAAAA TATTITOGIA ATGAAAGOGA CATCCGATTA GICCTAGCAG ATTACAGITA	660
	GTAACAAAGG TOCAATTATA TTGAGACCAC TATATTNIAA AATTGTOCCC NIGTTATTGA	720
	AAACTINIGC CONGGIACA CITATIGCIN TICNACACCG TOCTONAAAA ANTGIGNITT	780
5 <b>5</b>	GITACGATTA ACTOGITITOC TIGATIGAGO AACTITIGNI TITTATOATA G	831
<b>55</b>	(2) INFORMATION FOR SEQ ID NO:363:	

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 841 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1279UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:	
15	GATCAAGAGT ACAGTTGATG AAAAGGAGTT CCATGATGAA ATATGTAAGA TOGACTTGCT	60
	TAAGAAATTG ATAATATAAA AGGCTACGAG CTTCAATATT ATAATACGCA TTGCATAATT	120
	TATTACATTA AATTGATATA GGTATATTIT TCTTOGAAGA ATTAATTCTA ATCATTTCCA	180
20	TOTGAAGATA TOOCCCTCTG TOTTACCTOC GGATATTTCG ACTOTTAGTA TATCTACATA	240
	TTTTOOCGAG CCATTATTTA AACTOOCCAG CTTGACTCTG GACCCAAGAG CCGTAATGGC	300
	AGCAGCTCTT CCTGAGCGCA ATTTCTTCAA GCAATTGAGG CACCATGTGC CGTTCTTTAA	360
25	TICAAGCACA TATAAACAGA COGTOCOGIC AATAAACCCT AGCACAATTA TATCCTTTIC	420
	TITOCAATAC ATGTGCCGAT ACCTGGACAT TTCCTGAGAT GCAAAGITAA CAAAGCTTAT	480
	AGCAGIGATA TCTTGCGTTA GAGACATGCT TGCAAATTTC GAACCGTTGA GGTCATAAAC	540
30	ATGAACGITA TITGAGAATA TCAACCACCC ATTAAATGAA CTGTACCTGT TTGAAACCGC	600
	AATGCACTGG NIVININCTINGA AATATTCINCC AACCCINCCCT TAAAAGNGTC CCCCTTTATT	660
	NNONCCINGC TATTCCCAAA AACNIACCCG NITCNITGIG NCNCCAAGGN NITTINNONI	720
35	TNITIGGCAGC CITTTAGAGN TITTAAANAIN TITCCAANCCC CAAATCCANT TTTTAAAGCN	780
	CTCCCCTINAA AANIVICNIGA ATGANCAGEN GAATTGGTTT GOCNITTAAC TICCCAGTINA	840
40	G	841
40	(2) INFORMATION FOR SEQ ID NO:364:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 826 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1280RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:	
55	GATCATCAGA CCTGTCGGAG CGTTCCGTAG TGGAACCTCT TGGTAGGGGG GAGCCGCTGT	60

	TETERACCTIT GRACCOCTET GERGACOCCG GOCTOGRACTG ARACCGRACT CETATOGOCG	120
	ATCOCCAGAT GTACTOGOGC GACCTTAATG CAATTITICTT CTCGAAGGAC TITIGTOGOGA	180
5	COGREGARAG TOTTTCARAT ATTGROCOCAG ACCOCCOCTT TGRGATTTGG CTCTGCARAG	240
	ACCORPORTE CAACCOCCC GOCACCITET CICCOGICCT TOCACCCCIT CCCCCACGIG	300
	CAAGCACGGC CGCCTTCGCA AGAACGGGAC TCTGCTTCAG TAGGCTTGTC TTGGTCATCA	360
10	TOGOCTOCAC CACCAGOGGA TOTTIGITICG GCAGOGGCAC AAACATGITIG GACCGCOGGA	420
	COCTICCOCTIC ACCOCTICCOC CCAATICACCG CTCCCCGTCCCG AAACCTICAAC CTCTTCTCCCC	480
	COCTOTTOGA CATOGAAACO TICGTOTCTCT TGATGCGACT TCTCCGAGTC CACCTCCTGT	5 <b>4</b> 0
15	ACCETICETET GETECCOCTIC CTECCTICCOC TCCCOCCTCCN CNCCNCCNCT TCCTGCCTCC	600
	CIGACINFIC CCCCCCTTT AGGGGAACAC GGGAACAAAA NAANINCCCT TICINNCCCG	660
	OCCCCTTGIG TOOCCCCCIN NAMOCCCCCIN CCCTINAIAN NAMOCANANIN INCCNNCNIN	720
20	NNNNAAAAT NTAGGGGNGG GAAAAATGNG GITTAGNGTCC CCCCACCNGAA CCCCCAAAAAA	780
	AACCNCCCAT GINIOCAGGG NCTINATGAN CANCTICNON NIGGGA	826
	(2) INFORMATION FOR SEQ ID NO:365:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 840 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1280UP	
35		
33		
33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:	
33	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:  GATCATAATG CGACTATOOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT	60
40		60 120
	GATCATAATG CGACTATCGC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT	
	GATCATAATG CGACTATCGC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT GACCGTTCCA TTCTCCGCGA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTGCAGGG	120
	GATCATAATG CGACTATCOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT CACCGTTCCA TICTCCGCGA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT	120 180
40	GATCATAATG CGACTATOOC CCATAAGCAG GOCAATACOC CTATCCACAT CAAAGTCCCT GACCGTTCCA TICTCCGCCA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCCAG	120 180 240
40	GATCATAATG CGACTATOOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT GACCGTTCCA TICTCCGCGA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCGAG GGGCGGCAGA TTACCAATTT AACTCAGGGT GTACCAGGCG ATGTCCCGAT TTCTATTCTA	120 180 240 300
40	GATCATAATG CGACTATOOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT GACCGTTCCA TICTCCGCGA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCGAG GGGGGGCAGA TTACCAATTT AACTCAGGGT GTACCAGGG ATGTCCCGAT TTCTATTCTA	120 180 240 300 360
40 45	GATCATAATG CGACTATOOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT GACCGTTCCA TICTCCGCCA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCGAG GGGCGGCAGA TTACCAATTT AACTCAGGGT GTACCAGGC ATGTCCCGAT TTCTATTCTA	120 180 240 300 360 420
40 45	GATCATAATG CGACTATOOC CCATAAGCAG GGCAATACGC CTATCCACAT CAAAGTCCCT GACCGTTCCA TICTCCGCGA CCGTGACGTG CCTGTGTACA AAGGCTCAGC GCTCCAGGCG CGCGATGTCA TCCCGTATCA CGAACTATCA AACTCGAACT ATTTCACTGT GAATCCTGGT GAAACACTAA CACTTCCTGT GTATGAACCG GAGTTAAACA TCCAAGGCAA CATTGTCGAG GGGGGGCAGA TTACCAATTT AACTCAGGGT GTACCAGGG ATGTCCCGAT TTCTATTCTA	120 180 240 300 360 420 480

	TICANCICON NONVITCAON TITICCONAGO COCCAATINON GANCICCINA GOCCCIGNAA	720
	CACCATTNAN CNICGACCTA CTCAAAAGIN TICIATCCCC CAAINICNIT TCCAACACAA	780
5	CGATCTOCTA ATTONOCONC CAACCATCAC TINNTOCATC ATTTTOCCAC AACAATONGA	840
	(2) INFORMATION FOR SEQ ID NO:366:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 833 base pairs  (B) TYPE: mucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1281RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:	
	GATCCGACGT TCAGTGGACT CTTCCCATTT AAGGTTTTCA ACAAATTCCA AACTCATGTG	60
25	TITAATOCCT TGTACCATAC CGATGAAAAT GTATTTATTG GAOCTIGTAA GGGCTCGGGT	120
	AAAACTOCAA TOOCAGAATT AOCTITIATTG AGTCACTOGA GAGATOGTIAA GOGACGTOCC	180
	GICTATATAT GICCATCTCA OGAGAAAATT GATTTTCTOG TGAAGGATTG GOGAAACAGA	240
30	TITITIAAATG TOOCAGGTOG AAAGGITATT AATAAACTCA CATTOGAATT AACTAACAAT	300
	CITCGAACGC TAGCCCAGTC GCATTTAATC TTAGCGACTC CAGAGCAGTT TGACCTGCTT	360
	TCTCGTCCCT GGAAAAGAAG AAAAAACATT CAGACATTAG ACCTGTTGAT TCTAGATGAT	420
35	CTTCATATGA TCAGTAGTGA CTTGCCTGGC GCAAGGTATG AAAATATAAT ATCCAGAATG	480
	CIGITCATTC GOGGICAACT TGAAACGGCC TIGCGIATAG TCGGITTATC TACCICCCTC	540
	GCTAATGGTC GCGACTTTGG AGAGTTGGCT CCGAGCTAAA AAGCTACATT TTTATTTCTC	600
40	CITICACGAA GOGITATOCC CITACAGATC CNCTTACATC CGITCCTAGA NOCATGAAAN	660
	TOTTANTIC AACTATOGOO AATOCOITOO TGACGNACAA CTOTGIGATA CTOCCANINT	720
	TANCTITIGT TOCATTAGAA ATGITICAAT TOTGTONOTG CACGOCGOGO GGANGAAATO	780
45	CTOGTICNOCIN ATTAGTTOGA ACCATTOTAG GINAAAAGAC TOTTATOCTA ACN	833
	(2) INFORMATION FOR SEQ ID NO:367:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 853 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1281UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:	
	GATCTGAACG TATGAGAGCG GGTTTTTACT AATTATAGAA CCATATGAGA TAGAAAATOC	60
5	GGCAGTTCCA AATCCAATAA TGCGATTCAC GTGCCTTGAT GCCTCCATTG CAATCAAACC	120
	AGIGITICAG AAGITTIOGT CAGITATTAT TACATOGGG ACCATTICIC COCTIGACAT	180
	GTACCCTCGA ATCCTGAATT TTGAGACAGT TCTTCAAAAA TCTTACTCCA TGACCCTCCC	240
10	OCAGAAGTOC TTOCTOCCAA TGATTATAAC CAAGGGGTCA GACCAGGTAG CCATCTCTTC	3.00
	TOGGITTGAG ATCAGGAATG ATCCCTCAAT TGTCAGGAAT TATGGTTCCA TATTGGTTGA	360
15	ATTIGCCAAG ATTACTCCTG ATGGTATGGT AGIGITCTTC CCCTCATATT TATATATGGA	420
15	ATCCATTATT TCAACTTOOC AGACAATOOG GATCTAGACG AGGITTOGAA ATACAAGCTC	480
	ATCCCTCCTC GAAACACCAG ACCCCACAGG AAACCTCCTC TACCTTTAAA AACTNACCNA	540
20	AGGCCNGCCC NNAATGGCNC GGGCCANITA ATTTCNGTGG COGNGGGAAA ATTCTNAGGA	600
20	ATOGATTING ACNOCCIOGG NEOGAGIGIT TGAAAATOGA TOOCTOOCTT NACOGANAAC	660
	GITINITITAG OGAGOGITINI NICCIVINANA AAANATOCAA ACCOOGAATA CITITITICCIT	720
25	NNAGCATGAA NCCCCCCCCT TTTGGGAAAA TTCAGGGGTG AGGAANATAT GCTTAATGIN	780
	CCCCCCANCN CHUNCCHNAA AAAAANCACT CCCAATGTCC CAGGNCCTTN NGNACCACTT	840
	CINNINATIC GAT	853
30	(2) INFORMATION FOR SEQ ID NO:368:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 598 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1282RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:	
45	GATCCOGAAT TATAGAATCG ATGAGCATTT CATTTAGCAA CCTTCTTCCA ATTCGTAATG	60
	GTICATATAT AAACTCCCTA GCTTCCTCTT GATAAATCCT TTCAAGAACA GCACOGTCGC	120
	AGICTOGGIT TATCTTTATA TTATTTCTTG TTATGCAACT CGCATGGICT ATGAGGICCC	180
50	TACATACATT TAGGICGCCC ATCAGTACCA CCCTCTTCCC CAGATTCTCT ATGITCCTCA	240
	CACGITIGAA TAGAGITTIC AGGAAACGCA GCCTAAAAAC TICACCCTCC TCAGTGITCA	300
	TAGAATTAGC AGGGCAGTAT ACGGGAAATGA CCACCACCTT ACAGGCCAAT TOGACTAGAA	360
	GGCATCTCCC CTCACTGTCT AGTTCCTGTG CATTAGCATC ACTCCCATAG GGCAAGCCAT	420

55

	CHICARCOCC SHINCTHIC SICOPSICCL COCCULATION INCOMMONG CONTICULAL	480
	TTAATTTTT AGTCTOCCTG TAATACCTCC TCCCGCCTTC AATACTTGTA ATGATTATCG	540
5	CAACGATCGG CTGCTTCAGG GATTCTGTTC CACNCCCACN CCNATACCCT TCTCCTGN	598
	(2) INFORMATION FOR SEQ ID NO:369:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 622 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1282UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:	
	CATCTGCGCA AACACCCCCA CTCTGTGTAC CTCCTCGATG CTGTCAATGG AGTCCTTGTC	60
	CATGCTTCTA TCCTTCAGCA GGAACGCGCC TAGGTACGGG ATGTTCCGGC GCAGCAGCCC	120
25	OCAGATAGOT TOGATGACOG COGGGTOGTA CACGGTCACO GACTTGTAGT ACCOGGGGAA	180
	GAGCGGCCGG TTGCTCATCG GTAGCACCAT CAGCTCCTCG TACTTGCGCG GCACCTCGCC	240
	CTCGCTCGGC GGGTTCGACC GGCCGCCGCC GCCCGCAA GACGCCGAAC GGCCGCTGCC	300
30	CCGCGAAGAA CTAGCCTCCG ACGACCGATT CGCCTGCTCT TCCCGTGGCT GCCGCTCCGC	360
	CTCCTCGTCG CGCACCGCTT CCTCGTCGCG CCCCTCCTCC GCGCGCGCGG GCACCTTTTT	420
	GTCGTCGCTC TGGTCCGGCT CCCCGGTCCT GCTTCAGTAT GCAACTGCCC GCCGCGTGTA	480
35	TOOOGGACTG CTGCCCCAAG GCCACTCTTT TTGGGGGGGG GGGGGGANAG MANACCCCAC	540
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	600
	CCATCCCCC CIMPITTIC CT	622
40	(2) INFORMATION FOR SEQ ID NO:370:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 798 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1283RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:	
	GATCAGGAAA TCGACGGGAC TGGCTGATTG TCTTTATAGT CAAGCATATT AAACACACGT	60
55	CACTIAAACT AGATTIACAC GIGACATOCA ATTGIGIOGI TICTITITITA TITIGAAAAAC	120

	CTOCATOGAG CTATTAGATG CTCATOGACA CTAGTGTACA AACCAGTCAA GOCTTAAAAG	180
_	CTCTGCAGCA TGGACCAGTC GAATAAGGAG CATCGTCCTA AAAAGGAGAA GOCGACAGCT	240
5	AAAAAGAAGC TOCACTCCCA GOOCCACAAT OCGAAGOCAT TCOCOGTGOC COCTCCGGGA	300
	AAGATGOOCA AGCAGATGCA GCGCAGCAGC GATAAGCGGG AGCGCCGCCT GCACGTTCCG	360
10	ATGGTGGACC GGACGCCGGA CGACGACCCG CCGCCACTCA TTGTTGCCGT TGTAGGTCCC	420
10	CCGGGGACGG GTAAGACAAC NCTGATCAAT CGCTGGTGCG GCGGTTGACC AAGACGACCC	<b>4</b> 80
	TCCCCCAGAT TAACCCTCCC ATCACCCTCC TCTCCCCCCAA GCCCCCCCT CTGACCTTCA	540
15	TTGAGACOCC COCOGACGAT CTGAACTCCG ATGTOGACAT TGCGAAGGTT GCAGATTTGG	600
15	TOCTOCTOCT CATOGACOGT ACTITOGITIC CACATGAGAC ATGAGTTCCC TGACCTGGCN	660
	CACNCCACOG ATNOCCTTTT NOTOGATTAC AANONONCAT TITTCATTING NAGOCONCTC	720
20	CNOCTONAAA ACTITINACC TOGTTOTGAC NATTITINOON GGGGNNONNI COCCTTOGTN	780
20	TTTTTTATGN NGNNCCNI	798
	(2) INFORMATION FOR SEQ ID NO:371:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 829 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1283UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:	
	GATCCOCTOG CCCATCOCCG AGAGCTATGT OCATCOCCTC ATAGTOCCCT TGATACGTGT	60
	CTCAACCAAG ATTIGTIGGAAG ACACCGTIGCA CTCCCACGAG TATTITCAGCA AGGICTIGCGG	120
40	CATATOGAAG AAGCTCTTGA TOCOCCTOGA OCTAGCCCTC ATACTOGTCC TOCOCGOCGA	180
	COSTITURATE STCACOCCTE CACCICTAAA COCTOCCTCA AACGCACGTG CTCCCCTTCG	240
	CGAGCAGTCT GCGCTGCCAG CCGCTGCTGC TCAGTGATAA TCGCCCACTTC TAGGCCCACA	300
45	ATTCOGTIAT TTAATAACCA ATAAATACTC CAACACTAAT AGTATACACC GTTTOCGAGA	360
	GTAAGCACGC AGCAGGAGGT GGCAGCTTTT CTGGTACCAC CTCAAGCCCC TTGCCATTGC	420
	TOCCTATICTIC GITTAGOCAT GAOCAACCTT AGTCAGTITTC GAACCCGTGA TATATGTTTC	480
50	GAACACGITA CCTITTCOGT GAAAAGAAAA AGCCTAAAGG CGAAATGITT TCCATGITAA	540
	CACAGCAGAT TAGAGGTACC TIGIACTGGA TATTCTGTAG GATCACGGGC TACGAGCATT	600
	CATCCAGAAG CTTTGAACTT ANOGTGTTTC NGGATGOCAG TINGGGACTT ATNCCGTGGN	660
55	TNTAAAANAA TACTTOGTOO TAGTOTTTOG AACAAACNIG CATTTGITGT TOTTNGTTTG	720

	GAINMICOGN AMGHEANCCI ITGCCCTGCT AMNAMGHEING TIGGGAMEING MUGCENNIGN	780
5	CCCONCTICCEA GNONICAACN GOCCCONTIN CONTITIONICN GOCGONNINC	829
	(2) INFORMATION FOR SEQ ID NO:372:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 817 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1284RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:	
20	GATCGATCTG GTCAGGTCTA TTTGTGGCAC CGATGACAAA AACATTTTTC TTTGCATTCA	60
	TACCATCCAT TICAGITAAC AATTOGITAA CGACTCTATC AGAGOCGCCA CCAGCATCAC	120
	CCATTGAGCC ACCICIAGCC TITISCAATOG AATCTAGITC ATCCAAAAAG ACAACOGITG	180
25	GCGCTGCGGC TCTAGCTTTA TCAAAAATAT CACGAATGTT GGACTCAGAC TCACCATACC	240
	ACATOCTTAG CAACTCTOGA CCCTTCACAG AAATGAAATT AOCAGATACT TCAGTTOCGA	300
30	CTGCCTTTGC CAACAACGTC TTACCAGTAC CTGGAGGACC GTAAAACAAC ACACCTTTCG	360
30	ATGCCCATAG ACCAAACTTA ATGTATTGGT CAGGATGCAA GACGGGATAC TCAACGGTTT	420
	CCTTCAACTC CCGCTTTATG TCATCCAACC CACCAACATC GTCCCAAGTA ACGTTAACCG	480
35	ATTCAACCAC GGTTTCACGT AGCGCGGATG GATTGGAGTT CCCAAGTGCG AATCTAAAGT	540
	TATCCATTGT AACTCCTAAG GAATCCAAGC ACTTCAGCGT CGATTTCATC CCTCGTCCCA	600
	ATCAATTAGA CTCATCTTCT CTCTAATCTG TTGCATTGCA	660
40	ATATCAGCAC CCACATACCA TGGTTTCAGC AGCTAGCACT TCCAATCAGC TCATCAGCCA	720
•	TCTCANFTCT TGNTGTGGAT GITTAAATTC CCACCCTCCA GTGCTCTGGA NACCANFTTA	780
	TINNIGICAA TITACCAACT TITAGNOOGN TINATOG	817
45	(2) INFORMATION FOR SEQ ID NO:373:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1284UP	
55	(	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:	
_	CATCAACCTG ATATGTATTC TCGGGCTACT GGTCGTATCC GTGGTAATCT TCTTCGGCGG	60
5	COCTCCCAAC CACGACCGTA CTGGCTTCCG CTACTGGAAG AACCCGGGGG CCTTTGCGAT	120
	GACCCTCCCC CCACCAACCA CCCCCCTTT CTTCCACCTC TCCCCCCCC	180
	GOCCITCOCC TICATCCTAT CACCAGAACT TATAGOCATT GCATGCGTCG AGOCGCAGGA	240
10	CACCOGGGG AACACTGAGA AGGCATCGAG ACGTTTCATA TACCGTATTA TCTTTTTTCTA	300
	TGTGA9CT9C GCOCTCATGA TCG9CGTCAT CTTATCAAGA ACTGATCCGA AACTCATAGA	360
	GOCCOCTOGAG ACAGOCCOCC CAGGOGCTICC CTCTTCTCCC TTCGTGCAGG GGATTGCCAA	420
15	COCAGOGATT CCCGTOCTOG ACCACGTCAT CAACGTCGCG ATCTTGTCTT CTGCGTGGTC	480
	GOCAGOCAAC TOOTTCATGT ATOCATOCAC GOGCATOGTG CTAGOGCTTG COCOCCAGOG	540
	AAATGCGCCA AAGTTCCTCA CCAAGATCAA CAGATATGTG TGCCCTACAA CGCGGTCATC	600
20	GICTOCACOC TOGICOCCTG TOTTOCCTAC CTGAACGTCA AGACGACTCC GCAATGTGTT	660
	CCAGTOSCTG TOGAACATAT GCACCATCTC COCTTCATCC OCTTGTTCGC CATGGCTCCC	720
	TTATATCCCT TCCCNGCCGT TCTTTTCACA CTCCNANCCN INCCCINCCA GITCCCTGCA	780
25	CONTITIONOC ACTATICCONT INTAATGINF CITITINGAC AATGITCOCT C	831
	(2) INFORMATION FOR SEQ ID NO:374:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 817 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1285RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:	
	CATCOGGGTC CGCCACAAGC TGCTGGTCCA CATCGTGCTG CTGCGCGGGCC CCCCCGACGC	60
	OCCOGGAAAG AAAACOGGAAA TCAAGGCCAG CATTCOGGTT ATGCTCTACA TATCGCCGCT	120
45	CGTACCTGTG CAGGGCCGCA COGTOCTGGT TGATAACGCT GGCCGCTTCC ACATCCGTCC	180
	COOCCIOCIO ACAGACCIAT ICCOGRACOCO GAGCOCOGRAC ICACTICCOGA GCIOGGRACOC	240
	SCCGCCGTCC TACGAGTCGC SCGTGCACGA TCGGCTGTAC GATGGCGACG TAGGCTCGCT	300
50	TOCTTCOOOC AGGGGGGCC COCCCGATTIC COCCCGCCC CCCCCCCCC CCCCCACATTIC	360
	OCCACIOGGI CICCITCOGC CCCITCACGC CITGIOGITG GATGATCIAA GCAGGGTCCC	420
	CACGIACCAA CAGCAGCACG ATGGACACIC CCTGCCATTG CATCACCTCT CCCCGGCGIA	480
55	TECCECCACE ECOCCACONS COORDECCA ACAGORCACN TEACAATCAC TINTECESTE	540

	CGICGCGGCC CCCCGGACCC CCIIGCGCCC TIATICIGCC CCCCCCAAAC CWACCWIGCN	600
	COCAATAGGG TCAAACCGCG GNETTEGNAA TTTNCTTGNT CNGNNNONG NNCNGETTTT	660
5	COCCCCCC GCTTNCCCCC CNVANTTNCC CCAANCOGAA NCCCCCCCCC GCTTNNNCTCN	720
	NNCNETAAAA ACTINTACOC OCCONCTITE GETINOCINESC COGNEGETTI TITTTITTOCC	780
	COCCOUNCES ACCIVITINGS NACIVATT	817
10	(2) INFORMATION FOR SEQ ID NO:375:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1285UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:	
	GATCTTCTTC ATGACGCTAC TGTAGACAGT TTCACAACCG ATAGCCTGAA GACACAGTAC	60
25	AACCAGACCA AAAGATATCA ACTGTTTCGG ATTCCGTATT CGGAGCATTC CAGCTTTAAG	120
	GACCTAAGTA TTTTCCCAAC CACGATCCAG ATGAACGCCA TTCGATCTAC AGTGAACCTG	180
30	OCCICITIOS AGAIOCATOS CATGIOSTIC GACACTIOST CIOSTATIAS AAACGAAAAA	240
30	TACCTOCCTA AATTATGATT ACATGITATA TATAGIAAAA GATAACACOC CACTCAGTGT	300
	TARATOGTOC ATCATOCCIC TAGGACTOGT TGTOGTTOCT CGACAGAACT CCAGTOCCCA	360
35	TITOCCIOGI AGGITTTIGI GAGGCITITT TCTAATTGIC TAATTIAAAG TCCTGAATAT	420
	TATOCTOCAA TROTOGAATG AAAGACACAT GTACCACTAG AGGTTCAGCC CGATGGCTGC	480
	AAAACGGCAT ATTTGTCATC CAAATCATGC COCTOGTCCA ACAGTTTAAT AATGTCTCTG	540
40	GAACTICGAC TACGICCOGA ACTOGICIAT CATCIOGAAT ACCINCTICCT GITAIGONIT	600
	ACCATANICC CCTCCCTTGG TGGCCNAATT CTTAANCAAT TTTTGNITAA AINCCCCCNT	660
	OCTINNCIAA GGINAATTOC NWTTGGCCCC CCCCTTCGGG TTINTCCGTT CTTTGGAATG	720
45	GAGGAAGCCC AGGCTTGNCC CCCAATACNC GCCCTCCGGG AAGNGTCCTC CTTNGCCTTN	780
	CCCANTIGGEN THETITIGGETT NEWNGCAAAN CHACHNENGE CCCTCCTINCN C	831
	(2) INFORMATION FOR SEQ ID NO:376:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 802 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1286RP

3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:	
	GATCOCACCT ATAATGAAGA CCOGFFTTTT TITATGAGAA ATAGCAGCCC TCCAGGGGFT	60
	ACTTATIANA TAGCTACAGI NAGATTAGGT TATTCGITIG CANATTCATT GGIAGATCAN	120
10	CTTGTACACT TCAAATAATG CTTCCCTCCC ACCGTCATAA AACATGTTAT CCCCCGGTGTT	180
	GACAACTACT CTGAAGCTAT AGTCAGGGTA GTGGGTGGCA TTAGCTGGAC ACACCTTATC	240
	TICACIOCCE ACCAAGACAT COOCTETOCA COCCCIGIOG ACCAAAGGIG GOCCGITAAT	300
15	TAGGICTICC CAGCCTAGAA GATACTCAGT GATGGATTIG GTOGAAACTG CTACACOGTC	360
	GIAGAAGIGA TITIACCITCC TGIACITGIT CCCCATGITG GAGAAAAAGA ACTIAATTICC	420
	GCACCIGITC AACCCITCAT CIGGICGAAA TIGGICCITA TGAATTIGAG AACCATGATC	480
20	AAGAAGOOCT TGAAGAATGT TAGTGAAAGG TITAGATATG OCTOGAGGAT ATOCAACTIT	540
	CATTICACAC TICTACCIOC COCCOCCC AATACAATCA TCTTTCTCCC TICAATTCTT	600
	CACOCCOTAT CCTCAACOCT AATOCCAACC CAAATGCACC CCATCNATTG CCCAAAAACTC	660
25	CCACNGACAT TATTATGGTT GGCNCGTAGA CCATGAATCT AAACCCCCTA TCACNCACCC	720
	CCCCCACANG GITACCATCG CCCATGTCCC TTCCCCANCC TGAGNTCNAC CCCATTNTCC	780
	CCCTATTING CACATATONT CC	802
30	(2) INFORMATION FOR SEQ ID NO:377:	
35	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 835 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1286UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:	
45	GATCTICGCA GCCAGCGGT AGICCACCGG CGICAGICCC TCGCAGAACG CCCCGCCGIG	60
	CACGTACAGC ACCACCOGGT CGTCTGGGTG CCGCTTGTCG GGCCGCCACA CATACACCGC	120
	GOGCOCAGIC COCTCOGCCG CCCCCAGCOCCC AGCTCGCAACA GGTCGCTAIC	180
50	CTGCACAACG TACGTCTCCT CCAGCACCTC GCCGCCGCCC TCGAACGACC GCCGCGCGCTC	240
	CCACCACGGC ACGCACGTCC CGACGGACGC CCGGCAGGGCG CCGGGGTCCGC	300
	GTGCCGCGGG GCCTCTACGC CCAGCAGTCC CAGCAGCATG CGCCGCCGG GGGGCGGCAC	360
55	CACCGAGIAT ACCAGGGGG CCAGGGGTGC CGGCAGGCC AACCCATAGA ACTICAGCAG	420

	AAACOCCAGT ACOCTCCACG TITTGTTTGG ACATCCCATG ATGCCCGGCCC GAGGGACGTC	480
	GACOCCCOCC ACCTGACOOG OCCOCTACTT ATACACCACA AGATTCTATA GAAAAAGGAAT	540
5	OCCACCAACG ACGAACGGIG TATCGITTIGG GAAAAAAAAGG AGICCCCCAA CTAAAGCTIG	600
	CTIOCIOOCT ACGAGITIGI GITICAGGIT TCTICATAGC ATCCCAGTIG TITTIGITTIGI	660
	TIGOCAAATC OCATATGAAC CATAAAANAT CAAANNITGI ACAATTOCTG COGACCGITG	720
10	CCCCATCCNC CGGCGAAANA TCCAGAAATC GAGANAATTT CAGACGCCGG GTTTGCCAAA	780
	NICCOGARAC COCARANICO CARCATTOCT GNOACATTIG ATTOTONNO NINCA	835
	(2) INFORMATION FOR SEQ ID NO:378:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 799 base pairs  (B) TYPE: mucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1287RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:	
	GATCCCACTG GTATTAGGTG TCTGAACACG GCCAAATAAA ATACGCAAAA TGAAGGCCAT	60
30	TAATAATCIT TCATCAGTGI TGACAATAAC CCTTGACTCA TTCTGACCAA ATAACTTTGT	120
	TACTICGICG TICAATAACG TGICATCIAA TAAGITCIIC ACATIGICCC TATATITCAC	180
	AGCTACTOGA TOCTTGTATG CTAACAACOC ATCTAGOGOC AGTTTCTGCA CTTCCAGOGT	240
35	TCCACTACCC AATAATTCCA TCAACCTTTG GCGCACATCT TCGGATTTGT AAATAGCTTT	300
	GATATTOTTG AACTTOCCCA ATAATTTCAA AATTAGATTC CTATCOGTCT CAGACCATGT	360
	ATCCCCAGAG TOCACTOCTA ACTCACCCAG ATGGTCTTCA TCTTGGTTGG CATCGAATTG	420
40	ATCATTOCGI TITIAAGACAA AAGGIACAAT GAATCTOCIA TITTOCTCCC GOCAGCIGIN	480
	GCAGCGCGAT TAATATCTIC AATGCTIGIT TCTAATCATA CCGCATATCC CAGTGAACCG	540
	CGANCCCCTT TAAGGITTIC CAACCAAGGA TITTICGAAA NCAACAINCN TTINGAACNI	600
45	TCCNAANNCA AATAATINAT CCTAAAAAAT TINIGCCCNA NICCAAAAAN TCCCCNAGGG	660
	GINVAAAGAG TOOCCCCAAA TICNAAATNA GNOVITTIIN GOGNITINOO NAAAAAAAAAT	720
50	CCCINCCCINAC CINCONNTTTA ANAATTTTTIG GGAANCCCAT TCCCCCCCCA AGGGGAAAAA	780
50	AGNGTONNOC CNATTTINA	799
	(2) INFORMATION FOR SEQ ID NO:379:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 817 base pairs  (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1287UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:	
	CATCACCTICG TCTTCCCCCA TACCCCTCACC CAAATCCATC TCCTCCCCAT CCCCCACATA	60
	CATTICCTOC ACACAACCTC CTCCTCGAAG GGCCTGATGC GGCGAGAGGC CTCAATGGAG	120
15	AGGCACGTAC AGGGCGCGAA CACGGTCACA GACCCATGGG ACATGTCTTT GGAAGTGGGG	180
	AGAAGATACG CCCCTGACGA CGACCTGGAG CAACAGACGT CGCTACTGGA CCTCAACTTT	240
	GAACTCAGTG ACATGCAGAA CTCCAAATCT TGGGGTGAAG GGACGCACAA TTCCGAAGAG	300
20	ATCAGTGCCA ATGTGCTTGC AGAGTCGCAA CGCCAGGAGC TGCCCGGGAA CGAGGCATT	360
	GAGOGTGAAG AGGATCTTGA TTGGAATCTG GGATTCACGG AACCAGCAAT TGTAGTCCCT	420
	TCAAGCGATT TTGAACACGA TAACAGCATA GAAGTGGGCC GGAGAGCAGT CCCCGAATGC	480
25	OGACCTTCAG GAAACTGTOG ATTTOOGATT OGACTTOGAT ATTOOCAGOG TTGACATTGA	540
	GOCTACAGOC GGCGAGCAGA TOCTGGCAGT TTGCATCTGA GCTTTCCGGA AGTATAGTAC	600
	GTCTTCCTGG AACACTGTINC ACANCCAAAA CAAGAAAGGC ACCTGGTTAT CAATTCTACA	660
30	TTCACCCCCA CCGGATTACT GAAAGGTGNT CNAAAAACCCC CCCNACANTG CTCCNTGANT	720
	ACCCATCCON NOCCCATTON NOCCNAAAAC GONINICGAC CCITINAAAT GATCCINCAA	780
	TITTOCNIGA CATCCIOCIC MITTOCAACG ACNOCCA	817
35	(2) INFORMATION FOR SEQ ID NO:380:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 787 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:	
50	GATCOOGATT GACCGIAATA TITCAGCTTT ITGATGIGAA TTGCCCAAGAG GACCAGCGAT	60
	TIGAATCICG CIGACTCIGI TGIGAGIAAT TAGTACAAGA ACCIGIOGCC TGICACAATT	120
	AAGCCCTGGG AATAGGACTT CAACTTCAGA AGCCCAGGAT CGTCAAGCGA TGATACAAGT	180
5 <b>5</b>	GCCTACCAAC ATTGACTTAA CATGAAAATT GATAGCATTT TTATAACAAT GGAAGCAAAG	240

	GACTAAGTOC TICACGTOGT COCCAATOCA GCCTGTTAGC AGGTTTCGGC ATATTCCTGG	300
	AAGATGTCAA CCTTCCAAAA ATATTCCTCA GAGCATTAAT TATCATTACA CAAGCCCTTG	360
5	GTGTGAGACA GAATCTTGAG AGGTOCTOCG ATAAAACTCA AAATCOCAGT GCTTGGATTA	420
	TAGOCCITAT ATACTGATIT AAGTGGTGGT GGTTATCTAT TCAGGGTTGT ATAAATTAAA	480
	ATATCACAGT COGTATACTC TTACACACTA ATTATAATCA CGTGATATTT GACTATTTAT	5 <b>4</b> 0
10	TACACCAGGA CACCTCGCTA TGAAAATAGC AACAGGCTGA TGGTATTAAC ATCTGAAGAT	600
	ATCOCCAACA TTAGAACACA CTACTGACAC AACOOCCAGC CATTCGAGAC TATGOCTCGT	660
	ACTACTOCAN TACTOTICATO CTTATICTOAC NOCTOACONO TOATTOTTOC OGAAATCONT	720
15	TIGATONGCA AAATCATNIC GNIGACONCA ANITOTACIN TATTAACCCC CCCACCGCCA	780
	ACCITIG	787
	(2) INFORMATION FOR SEQ ID NO:381:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 788 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1289UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:	
	GATCCCAGGC TGCCCCAGGA TGACGGAAAG TTGCATGTTC TTTTCGGCGC TACAGGCTCG	60
35	CTPICOGTAC TGAAGATTAA ATGGATGATC AAAAAACTOG AAGAGATTTA TGGTTGGGAC	120
	CATATATCCA TICAAGICAT ATTAACTCAA CCCCCTCCCC AATTCTTTCC TAATAAAAAC	180
	CCCAAGAAGA AGAACCTTIA CGIGICTAGC GAAACAAACT CATICICAAA CICCGIGOCT	240
40	CACCAGGGGA AACTIGCAAC AGAACAACTC AGACGCATCC TACACTGGGG TAAATAGGGT	300
	CTCCAATACC CCTGCAGTTG GGGGGCAC ACCAACGCCA GCAGATCTTC TCCAGGGCGC	360
	ASCOCCOCAA GOCGGGGCT CCGGTGTAAG CCAGGGGGCA GCTGCGGGGA AGATTGAGCT	420
45	CCCTCCACAC ATACAAGTCT GGACGGATCA AGACGAGTGG GACGTGTGGA AGCAAAGAAC	480
	AGATOCGTAC TOCATATTGA ATTACOCAGE TOCOCGATAT CCTTGTCGTC GCCCCACTTA	5 <b>4</b> 0
	COCCAATACA CTICCAAATT GCCCTGGGCC TIGITAAAAC CCGCGAACAT GTICNICCGG	600
50	NAIGNAACCA MITTICCAAT TCTMCNCCCA NCCGNGTTIN GNGMINITINA ACCCCCCCCC	660
	TACCCCCCNA AAAANAANAA NAAAAACCCC GTTNTCNGTG TTTCACCNCC CANAAAANAG	720
	GGINCCCCGG GAAAACGAAC TGGGGGGAGA GAGAGGNANN AAATINCNAN AATCCTTTTA	780
55	NCCCNCCC	788

	(2) INFORMATION FOR SEQ ID NO:382:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 761 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1290RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:	
	CATCOCTAGA TOCCCAGGAT GAGACTOTTIC AGGTTAGGCA GGTGTTGTAT GCCCCCCAG	60
	AGGGAAACCC AATGACTTTG CATAGAACAA ACCCGCCATC ACCCATGTCT TGGGCTGTAT	120
20	AGAGACTAAG GIATCTGACG ATCCCTIAGC GACTCTCTCC ACCCCTCGAC GAGGCCAITIG	180
	AGCTCTTACG AACTGCACAA ACCTACTCGA ACTCTGTTTC CAGACTTCTT TCTGTTTGTC	240
	TICAACTOCT TICGCATGAA GTACCCCCCA GOCTATTITT CITACCCGCC TGGTGTTTGT	300
25	CINTATACCC GGTIGTATIT TIGATAAAAA ACTCAGCTCT TCCTCTACGG CAGAAATATA	360
	TATOCAGICC TYAGOGOCAT GOGAAAATCT GOCTITYTAC GGCTGITTCT COCAGICTYA	420
	GCACTGGCAG AAAAAACATG TATGGCGTAT AGGCGCTGGC CCCGCGCAAA AAAAAAAAAA	480
30	ATAGAAAAAT AGAAAAAATAA AAAGACGTOG OCCOCCCOC OCCCAGACGA AGAAAAAATA	540
	GCCCCCACC CCTCCAAGCA GACGACAGGC GAGACATAAT AAATCCCACA CCAAGGGAAG	600
	AAGTETTGTG CACCCTCCCG OCTCATACGC CTCCCATTCT GTTCCATCCC GCTTGCAACC	660
35	CAGTATGCAT GTCAAGCATG MTCCGAGCTC COCTGCTTGG AGTCGAATCT CTTCCTACCC	720
35	AGCCGAATCC CATACTTGCC TTCACATACA TACCTTTCAT T	761
	(2) INFORMATION FOR SEQ ID NO:383:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 639 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1290UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:	
	GATCAGACAT OGTGTTTTOC OGCCCTCOCT CCTTGTGGGT GGGGTCACCG CAGTTCACTG	60
	GOCCAGCATC AGTITIGGIG GCAGCAGAAA CCCTTAGGAA TGTGACTITC TCTTCGGAGG	120
55	AAGTGTTATA GCCTAAGGTT ATACTGCCAA CCGGGACTGA GGACTGCGGC TTCGGCCAAG	180

	GATOCTOCCA TAATCETTAA ATOCCOCCCG TCTTGAAACA COGACCAAGG AGTCTAACGT	240
	CTATGCGAGT GTTTGCGTGT AAAACCCGTA CGCGTAATGA AAGTGAACGT AGGTGAGGGC	300
5	CICITIAGAG GIOCATCAIC GACCGATCCT GAIGICTICG GATOGATTIG AGTAAGACCA	360
	TAGCTGTTGG GACCCGAAAG ATOGTGAACT ATGCCTGAAT AGGGTGAAGC CCNANGAAAC	420
	TCTGGTGGAG GCTCGTAGCG GTTCTGACGT GCAAATCGAT CGTCGAATTT GGGTATAGGG	480
10	GCGAAAGACT AATCGAACCA TCTAGTAGCT GGTCCTGCCG AAGTTCCCTC CAGATACAGA	540
	ACTOCTATOA TITTATGAGT TAAACNAATG ATAAGTTACO GGGTTGAAAT GAOOTGACTA	600
	TCCCCACTTT AATAGTTAGA ATCCCTGTTG CTTATTGAC	639
15	(2) INFORMATION FOR SEQ ID NO:384:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 813 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1291UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:	
30	GATCGTGCAC GGCAAGACGT CGGAGCTGCG TCACCACGGG CGCGGGCTCT TCCAGGGGGT	60
	ACCCCAGGCC GTGGCAGTGA CACGGTACCA CTCGCTGGCT GCACTGGCGT CAACGTTGCC	120
	GOCCERACTE GAGETGACCE COCCECACGGA CACAGOCGTG GTTATGGGGC TGCCGGCACCG	180
35	CAAGTACACC GTGGAGGGTG TGCAGTTGCA CCCGGAGTCG ATTICTGACGG ACCACGGGCA	240
	OCTAATOCTC COCAACATOC TACCOCTOGA ACCOCTACG TOCOCTGAGA ACCACAACCT	300
	CCAGCTGCGG GCAGGCGGG GCTCTGTGCT GAGCGAGATA TACGCTCAAC GACAGGAGGA	360
40	CATGGCAGCG CACATGGCTA TGCCGGGAAC TGGTATGGCG GACCTGGAGG CGAGCTTTGG	420
	ATTGGGGGTT CTGCCGGGGG TGGTGGACTT CCATGAGCGG CTGGCGCGGG ACGCCGGGG	480
	CTGGCTGTGG TAGCCGAGAT AAAAGTGCGT CTCCGTCGCG TGGCAATATT AGCGAGGCGC	540
45	TIGOCNICCAN AANANOCOCT INCININITOC OGAAGOCOGA ATTITICCOCC AICICCOGGIG	600
	CTITIACCGAA CCCACTGTTC TAAAGGGACC CGCNAGANCN NAATTATINC CCGACCCNCC	660
50	CTITGANAAA AACNANACTG CCCAAANACC GCCGGTTTG CTNCTTTANG ANATCTTTAT	720
50	TNICCNITCC AATMITTGAA GCCCGNITNC GGCCNACAAT TTCCCTTATT TINAAATTIT	780
	NAACCACCCC CCCCCAGACC NITITITIIN CCC	813
55	(2) INFORMATION FOR SEQ ID NO:385:	
22	(i) SEQUENCE CHARACTERISTICS:	

	<ul><li>(A) LENGTH: 773 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEINESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1292RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:	
	GATCCGIGTA TITTITATIT ACATTATITA ATTAAAAATA ATGATTIAAA TAAAIAITIT	60
15	TTATAAAAA TAATTAGTOC ATTGITACAT GITCATTAAA CAATCATTAT TATCAAAACC	120
	ATCAACTAAT TGTTATATAT TTATTAAATA TTAATTTCAC TTAATTAAGA ATTAGGAACT	180
	TTATCTATTA GICTOCCTG TTTCCCTTTT GATTATTAAC CTTATCCCTA ATAATCTGAA	240
20	ATATTIAATT TTAGATTAAT AATATATICT GAGATTIAAT ATTITTAATA AAATAAATAA	300
	TIATICCCIA AATAATATIA ATAACIATAC CATATATATC TAATATITAA ATAATCATAC	360
	TAACATATGT TICGTAGAAA ACCAGCTATT TOCAAATCAG ATTIGACTIT CICTACTTAC	420
25	CATTATICAT CAGATAATAT TOCTACATTA ACCTGITCAA TOGTITTIAT ATTITATTAT	480
	ATTITAAATA TAATAAATAT ATATTITAAT CATTIGATAA TAGIAAGATC ATCIGCTFIC	540
	CGPTTAATTA ATATTAACTA AATTTAATTT ATTTTAATTA ATTTTACATN GITAAANATT	600
30	TAAATTAATT TTAAAACCAN TITTATITIN AAATTITCNC AAATTAATAC TOOOCC	660
	CTTTCCAAGG GOCCINININ NATTTTTINA AAAAAATAAA AAAGGCININ ANAAACCTTT	720
	TAAAANITCC CONGGCCCC NNAANANINA AANATTINAC CONAAAGGIC CON	<i>7</i> 73
35	(2) INFORMATION FOR SEQ ID NO:386:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 798 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1292UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:	
50	GATCCAGITA CITAGTAGAA TGATAAAATT AATAAATATT ATTTATTAAT ATTTGGITAA	60
	CAATAAATT CAATAATTTA TITAAATAAT GATTAAATAA TCTCAATATA AAATTATTAA	120
	TATAATGAGA TATATATTIT TAAAAAGAAT ATATAATTAA ATAATCCCAA CCAAAATTIG	180
5 <b>5</b>	TOCCACCACC TOCCOGTAAGA CAAAGOGGET TAGCGTTAAT CGTAATGGCT TAAAGGGTTC	240

	GTAGAATGAT TATTTAAAAT AATAATTAGA ATTAATAAAA ATAATTTAAG AATTATTCAA	300
	GTAAAGATGA AATAATAATT ATATGAATAA GACTTATAAA GTGAAAATTT AAATTATATA	360
5	TTAATTGACA TTGAGGAACG AAGGCTAAAG TAGCAAATCG GATTCGATAC CCGAGTAGTT	420
	TTAGCAGTAA ACAATGAATA CCTATTTATT TTTTATTAAT TAAAGAATAA ATTAAATGAA	480
	AATTAAAGTA TTCCCCCTGA TGACTACGTT TGCAATAATA AAAATCAAAA CAATAGACGG	540
10	TTCCGACTTA AGCAGTGGAA CATGITTTTT AATTCGATAA CCNCCCANAA ACCTTACCAN	600
	TTTINGAATA TITAATTATA ATAATTINIA ATIATTACOG NGIOCATATT NICTICCCTC	660
	COOCCOOCNA GITITINAAT TATONINAAC GAACAAACNO COATITITIT TITINANAAAA	720
15	ATTATTTATT TITIGAATAT TNAAAAAAA TAAANATOCT TINICCTITIT TAATOCNICA	780
	GINITITIT TINITON	798
	(2) INFORMATION FOR SEQ ID NO:387:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 762 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1293RP	
30	(A) ORGANISM: PAG1293RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	
30		60
<i>30</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:	60 120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387: GATCACCGAG CAGCTGGTTG GCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG GCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT	120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG OCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTGG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC	120 180
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG COCTCGGCAT AAGCCCCCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTGG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCGC CCAGTATGCG TCTAGTTGGA TGGCATCATC GGGGTCTACA CCCGTGGCGA	120 180 2 <b>4</b> 0
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTOGTTG OCCTCGGCAT AAGCCCCCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTGG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCGC CCAGTATGCG TCTAGTTGGA TGGCATGATC GGGGTGTACA CCGGTCGCCA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA	120 180 240 300
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG GCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTCG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCGC CCAGTATGCG TCTAGTTCGA TCGCATGATC GGGGTCTACA CCCGTGGCGA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGCCATTGG ACCATTGATG	120 180 240 300 360
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG GCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTCG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCGC CCAGTATGCG TCTAGTTCGA TCGCATCATC GGGGTCTACA CCCGTCGCGA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGCCATTGG ACCATTGATG  CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG	120 180 240 300 360 420
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG OCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTGG GGGCCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCCC CCAGTATGCG TCTAGTTCGA TCGCATGATC GGGGTCTACA CCCGTGGCGA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGCATTGG ACCATTGATG  CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG  CCCTGATGGA GCCAATCAGT AGCTTTGCTG CACCGGGCTT CATGGTGCCG GCCATATCTT	120 180 240 300 360 420 480
35 40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG GCCTCGGCAT AAGCGCGCTT GGTCTCTGCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTGG GGGCCCTTGA GGTCCGCTTC GAAGCATGAG TACAACAGTC  TCATCTCCGC CCAGTATGCG TCTAGTTCGA TCGCATCATC GGGGTCTACA CCCGTCGCGA  TATCGCCACC CAATGAGGCC TGCAAAACCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCCCATTGG ACCATTGATG  CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG  CCCTGATCGA GCCAATCAGT AGCTTTGCTG CACCGGGCTT CATGGTGCCG GCCATATCTT  TAATACCCCAA GATATGTGTG CCCCATGCCA ACAATCTTTT CAGTCAATCC AGTAGTAATC	120 180 240 300 360 420 480 540
35 40 45	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCGAG CAGCTGGTTG GOCTCGGCAT AAGCGCCCTT GGTCTCTCCC CACTGTTCTC  CAAGACCAAG CTGCTGTGCC TGGAACAACA GGTTTGTGAG CTGACCACCA GGAATTTCAT  GTTTGTACAC CTCTGGGTCG GGGCCCTTGA GGTCCGCTTC GAAGCATCAG TACAACAGTC  TCATCTCCCC CCAGTATGCG TCTAGTTCGA TCGCATCATC GGGGTCTTACA CCCGTCGCGA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGACAT GGCGCATTTCG ACCATTGATG  CGACACCTGT GCCTGCACAA TCATGTGTAT GCACATCAAT TCGCAGGTCT GGATACTTTG  CCCTGATCGA GCCAATCAGT AGCTTTGCTG CACCGGGCTT CATGGTGCCG GCCATATCTT  TAATACCCAA GATATGTGTG CCCCATGCCA ACAATCTTTT CAGTCAATCC AGTAGTAATC  AAGGTTGTAC TTCTTGCCTG CTGTAGCATA TCACCTGAGT TACAGATAGT GCTCAACCAC	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:387:  GATCACCAGE CAGCIGGITE GOCTOGGCAT AAGCGCCCTT GGICTCTGCC CACTGITICTC  CAAGACCAAG CIGCIGIGCC TGGAACAACA GGITTGTGAG CTGACCACCA GGAATTTCAT  GITTGTACAC CICTGGGTGG GGGCCCTTGA GGTCCCCTTC GAAGCATGAG TACAACAGTC  TCATCTCCCC CCAGTATGCG TCTAGTTCGA TGGCATGATC GGGGTCTACA CCCGTCGCGA  TATCGCCACC CAATGAGGCC TGCAAAGCCG TAATGGAGGG CTGGGACGTT AAGCCAGACA  TCGAGTTGGT GGCGACGTCC ACAACATCGG CGCCAGAGAT GGCGCATTGG ACCATTGATG  CGACACCTGT GCCTGCAGAA TCATGTGTAT GCACATGAAT TGGGAGGTCT GGATACTTTG  CCCTGATCGA GCCAATCAGT AGCTTTGCTG CACCGGGCTT CATGGTGCCG GCCATATCTT  TAATACCCCAA GATATGTGTG CCCCATGGCA ACAATCTTTT CAGTCAATCC AGTAGTAATC  AAGGTTGTAC TTCTTGCCTG CTGTAGCATA TCACCTGAGT TACAGATAGT GCTCAACCAC  CCTCCCCGCTT TCTTCACGGG TNNAAACCCA CTTCACTGTT CTAGTCNTCA CCCNTCNAAN	120 180 240 300 360 420 480 540 600

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 805 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1293UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:	
15	GATCITACAT CTGACAACAA TACGCTGGGG GCAGATGAGC TGCATTGATG GAAATTTTAA	60
	CACAGCTCGG GCAACCAGCT ACACGGGATA TATAAACTCA ATGCACGCGG CTCTTTACTG	120
	ACACAGTOCA TOAGCATOAG CACCACOCOC AAAAATGAAG ACTACACACA TOOTATOOCT	180
20	AGCAACACTT GOOGCCTGOG CACCTGTTCA GCCCGCACCT GTTCAGCCCA CGGACCTCGC	240
	CGCAGCGGCA AACGTCCCCCG AGAAAGCTGT TCTCGGCTTC TTCCAACTGT ACAATGTGGG	300
	CGATGTGGAG CTGCTCCCAG TGGACGACGG CGCACACTCC GGGATCCTTT TCGTGAACCG	360
25	CACACTAGCG GACGTGGACT ACTCCTCCGA GCATGTGGTT CAAAAATGGT TCCGTCTGTC	420
	TCTCCACCAT GOGCAAAGTA TGTAAGGCCG GACCAGAGAC AGTTTGCGTT GAGATATGTA	480
	AGTITACTIG GIGICCTACA CCATGCATTA IGACACGGC TIACGTACCT GCTTCTATAA	540
30	GCTAGITTAA ATGITTICTA TOCGTATIAT ATGGTTTACC CGCGCCGATA GTTCGCAGAG	600
	GCTGCTGINT TAAGGCCNAA CTTTATTCCT AANANGGTGG ATTACCCGGT NGAAANAATG	660
	AATCTGAATT GOOGAAATTC COOCTGGNCT ATTANCTCCC CNINCCOGTCC NAATAAATGG	720
35	AANATGGTGG GGTTTAATAC AAAANGGNCC GVTGCCGGCA ATGNACTGGA TTAATTTCAA	780
	AAACCTCCAA NIACCCCCAA NIGGN	805
	(2) INFORMATION FOR SEQ ID NO:389:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 764 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1294RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:	
	CATOCOGAAT GTOOCTCAAG CTOCOCTOCT TTCOOCTOOC CTOOCTGTTC TCTGTGGAAT	60
EE	CGITICIOGI GGICICCTIC TCCCATGIIG ACCTIOGGIT CAGOGICIIC ACCIOGIACA	120
55	CCTCGAGAAG CTTCGAGTTA TCGAATGCAA ATGGGTTTAG CATCTCGACC ATATTCGCTG	180

	COCCACCTOC CTOCCCCTTT COCCTTACAT COOCAGTCCA ACTICAACCT AATOCTATAG	240
5	AAAACGCCAT TGGCCTCGCC GTCTTATCAC GTGACTGTTC ATTCAGCTCG ACAGCTACTC	300
	CACTAGGACT OCTOCTOCTT TAACTGGGCT ATACACTTTA TATCGTTACA TTACTTTCTC	360
	CETECTICESC ECATERSTICS TOCTORCTIC TETECACACT CACTETICAA CACACCACC	420
10	TTCTTAAACA TGTCTGGTAC GACAAAGAAC CTTACGTGCG AGCCTCCGCA CGAATACATG	480
	GICCATATGT GTCACCTGGC CGTTCCGTGC CGTCGCTGTC ACGTCTCTTA GCTGGCAGTC	540
	AUGITIGICCT COCTOCCAC CAACTTOCCC CGATAGTITC GOOGGICGIT ACTOCAGCAN	600
15	ACCORDINGE TINGGETTEE TICACACTTA CAGGAATICOG GAANIGOCAG ATCNIACTITI	660
,,,	TROSTITIOSC CONTROCTOR CONCACANAA ANTOCTITIAT ATTITICOOG AAAACNITITA	720
	ATTITIACATT TICHAAACAA CATANGITIGC NITTITIACHN AACC	764
20	(2) INFORMATION FOR SEQ ID NO:390;	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 800 base pairs  (B) TYPE: nucleic acid  (C) STRANDERNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (A) Organism: Pagl294UP	
30		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390: GATCIOGAAC TOCAAGITOC TGATGIOCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA	60
<i>30</i>		60 120
	GATCTOGAAC TOCAAGITOC TGATGTCCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA	
	GATCTOGAAC TOCAAGITOC TGATGTCCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTCCGA	120
	GATCTOGRAC TOCARGITICO TGATGTOCTG CTTACGCTTC TCTCGCTGCT CATGRATICGA CTGCTGCTTC CACCGRATICA ACGRCCGCTT GTCCACATTA GCATGTACCT CGATGTCCGA GTCATCCCAC ATTTCTATCT TGTCCCCACTT TCAGTACTCG ATTGCCCATTG CACTACCTTG	120 180
35	GATCTOGAAC TOCAAGITICC TGATGTCCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA CTGCTGCTTC CACCGAATCA ACGACCGCTT GTCCACATTA GCATGTACCT CGATGTCCCA GTCATCCCAC ATTTCTATCT TGTCCCCACTT TCAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTC GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT	120 180 240
35	GATCTOGAAC TOCAAGITIC TGATGTCCTG CTTACOCTTC TCTCOCTOCT CATGAATCGA CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GCATGTACCT CGATGTCCCA GTCATCCCAG ATTTCTATCT TGTCCCCACTT TGAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA ACGACCAAGG	120 180 240 300
35	GATCTOGRAC TOCRAGITICO TGATGTOCTG CTTACGCTTC TCTCGCTGCT CATGRATICGA CTGCTGCTTC CACCGRATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTOCGA GTCATCCCGAC ATTTCTATCT TGTCCCCACTT TGAGTARTCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TRACTGATAT CARAGATTCA TATATGCARA CGTCCARCTA RATRATGTTA CACATARGGA AGGACCARG CARCGCCTGC CCAGTTCTAG CARCTTCTGT GTGTCACTCT CARCGATAGA AGTCTGCTCT	120 180 240 300 360
35	GATCTOGAAC TOCAAGTTOC TGATGTOCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA CTGCTGCTTC CACCGAATGA ACGACCGCTT GTCCACATTA GCATGTACCT CGATGTCCGA GTCATCCCAG ATTTCTATCT TGTCCCCACTT TCAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAAGG CAACGCCTGC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGGCCACAGC GCTGCTGAGG TCGTTGACGG TCAAGGTGAC	120 180 240 300 360 420
35	GATCTOGAAC TOCAAGTICC TGATGTCCTG CTTACGCTTC TCTCGCTGCT CATGAATCGA CTGCTGCTTC CACCGAATCA ACGACCGCTT GTCCACATTA GCATGTACCT CGATGTCCGA GTCATCCCAG ATTTCTATCT TGTCCCCACTT TCAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA AGACCAAGG CAACGCCTGC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGGCCACAGC GCTGCTGAGG TCGTTGACGG TCAAGGTGAC CTTGTTCGCA TTGGTCTTTT CGTTTTGTTG GTGCTGCTGC TGGCTGATCT GCTGTGTGCC	120 180 240 300 360 420 480
35	GATCTOGRAC TOCARGITICE TGATGICCTG CTTACGCTTC TCTCGCTGCT CATGRATICGA CTGCTGCTTC CACCGARTGA ACGACCGCTT GTCCACATTA GGATGIACCT CGATGICCGA GTCATCCCAC ATTTCTATCT TGTCCCACTT TGAGTARTCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCARA CGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAAGG CAACGCCTCC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGCCCACACC CCTGCTGAGG TCGTTGACGG TCAAGGTGAC CTTGTTCGCA TTGGTCTTTT CGTTTTTGTTG GTGCTGCTCC TGGCTGATCT GCTGTGTGCC GGGCTGCTGC TGACCGAGCA TCAGTTGTGG GCCGCGGGCC TGGCCGTTGT TGGAGGTTATG	120 180 240 300 360 420 480 540
35 40 45	GATCTOGRAC TOCRAGITICO TGATGTOCTG CTTACGCTTC TCTCGCTGCT CATGRATICGA CTGCTGCTTC CACCGRATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTOCGA GTCATCCCGAC ATTTCTATCT TGTCCCCACTT TGAGTAATCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TAACTGATAT CAAAGATTCA TATATGCAAA CGTCCAACTA AATAATGTTA CACATAAGGA AGGACCAAGG CAACGCCTGC CCAGTTCTAG CAACTTCTGT GTGTCACTCT CAACGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CCCCCACACC GCTGCTGAGG TCCATGACGG TCCAAGGTGAC CTTGTTCGCA TTGGTCTTTT CGTTTTGTTG GTGCTGCTGC TGGCTGATCT GCTGTGTGCC GGGCTGCTGC TGACCGACCA TCAGTTGTGG GCCGCGGGCC TGGCCGGTTGT TGGAGTTATG GACGCGAATG AGGAGCGGAT ACGGAATACT CGTAGGCGTT CGGCCGCNAT GTCGCTAACG	120 180 240 300 360 420 480 540 600
35 40 45	GATCTOGRAC TOCRAGITICO TGATGTOCTG CTTACGCTTC TCTCGCTGCT CATGRATICGA CTGCTGCTTC CACCGRATGA ACGACCGCTT GTCCACATTA GGATGTACCT CGATGTCCGA GTCATCCCAG ATTTCTATCT TGTCCCACTT TCAGTARTCG ATTCCCATTG CACTACCTTG TTTCGTTCTG GCTTCACTAC TGTTGTCCTT AGATCTTCTG GATCCACCAA TRACTGATAT CARAGATTCA TATATGCARA CGTCCARCTA RATRATGTTA CACATARAGA AGGACCARGG CARCGCTCC CCAGTTCTAG CARCTTCTGT GTGTCACTCT CARCGATAGA AGTCTGGTCT CGAGATGTTG AGACCGTACT CGCCCACAGC GCTGCTGAGG TCGTTGACGG TCARAGGTGAC CTTGTTCCCA TTGGTCTTTT CGTTTTGTTG GTGCTGCTGC TGGCCTGATCT GCTGTGTGCC GGCCTGCTGC TGACCGACCA TCAGTTGTGG GCCGCGGGCC TGGCCGTTGT TGGAGTTATG GACGCGAATG AGGACCGGA ACGAGCCTT CGTGAGGGTT CGGCCGCATAC GTCGCTAACG AACTCTGGTT GCCAACGCGA AGAAGGCCTT GACCGGANAT CNGTGCACNC CGAACCGTCC	120 180 240 300 360 420 480 540 600 660

	(2) INFORMATION FOR SEQ ID NO:391:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 796 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1295RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:	
	CATCHITCCT TCAAATHOOG ACCAGGIOCT TAAGTCATOC TGATCCTOCA CAATCACGTC	60
	CATATTOCCG GACATCAGTG CCGGTTTGCC ACCAGAATCG CTGCCCGGCC AGGTGACTAG	120
20	CAATCCCACC TCGTTCACAG TTTCCACCTT TAGCTTACAC CAAACCAGAG GAAAGTCCCG	180
	CGACAGCTGC TCGTGCAACC GTTTGAACTG CTTGTATGTC TCCGTGTCGG ACTTCACCGC	240
	TOTOCACCAG TOCOCTOCAT CCACCACCCA TOCOCAGGGG ATCTOCACTG CACCCTGTAG	300
25	CITICIOGACA GIGAGATICO TGACOGIOGA GITGIOCAGA ATITOCIOGA GGIOGICIOC	360
	AAAGCCCCC TGAGGITTGG ACACGTCCCA GCACGATGGC AGTGACGCCC CAGTCACCTC	420
	CGAAGAAACA ACAGCACTCC GCGCTGTCTG AGCAGAAAAG CAGGCCAGCA ACGCCAGCGC	480
30	CGITGCAAAG GATATCOGIT GCCCCAAAGG CCAAGCTOCA AACATCATTC TOGTOGTCAG	540
	CGACTOCTIT TOCCACCAGA TOCCTICGGGA CCATGCGCCA GATGGCGCCC TTAATATAAG	600
	CCCCTCCTCG CCAGCATGAC TTCTGCCAAC TCCCGAACAT TCTAAATGGC CAGCTGCTGC	660
35	TITGATGGTA CCINCCOCNG CINGCOCCAA AATINATATA CCATAATCCC CNICCTAAAT	720
	ATINCTITACAT ACCACGOCCC AAAGCGCTCC CCGNAGCINCN CCCGAGCCCC CACTITICNCC	780
	NIVAACIVANCC CIVICIVG	796
40	(2) INFORMATION FOR SEQ ID NO:392:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1295UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:	
55	CATCAACTIC ACTICIOCOC CITTICICOCA TOCACOCCCC CCAACOCCAG ATACCTICIC	60

	ARTIGIOSES GIACCIGEN COSSICIENT GREEKING CASICIANAL CETOMINAL	120
	GITICITIGGIG TAGIGCTIGA AGIACTOCAA AGACCACACG AATGCGAGGC CIGOGAGGAT	180
5	ATAGAAAACC AGCGTCCCGT ACCTACCGAT TGCCATGGTT GAAGCAAGGA TTCCACTGCC	240
	GIRAGIACIC AATTATIGAG TOCTACCAAG CIGATGIIGA TIGIGIGATA TCAACGGIAA	300
	TOOGTOGTTA AGGAACCTTT TCAAGAAACG CAAAAGAAAT GOGTOOGTAG GTOGAGCAGG	360
10	TGACAACCTC ATATTACTCA TAACAGITAT CTATCTAAGA AGCGGCACTA TGGATATACT	420
	ATCAGCTTCG TATACACATA TATATCOGAG GITTATAATC GCAAGTTAGC TATAATTGCC	480
	ATCGAGGTGT AATACATCGA AGATTGTCTA CGAAACTACT CTGTCACCAA CACATCAGCG	540
15	TATGAACAAT AACAGCAATA TTATGACAGG CAATTOCATA AAAGTATTCA AAGAGGGTTA	600
	AACAGITAAA TICOGTAAAG GITCAGNGAN TATTCOCTGA CACCCCATAC CGAATCGCCC	660
	TOCACCAATT GTTCACATGT TCANAGATTC TCCGGGACTT CATATONACC ATGTTGCCGC	720
20	COCNAACTON CATTATGINA ATOCTTGINT TOCTGACTOC CCCCCTTGTC CCAAATGCCA	780
	TCCCAGGGTG ANAGGTGCTC GTGATCTC	808
	(2) INFORMATION FOR SEQ ID NO:393:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 779 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1296RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:	
	CATCCATTGT GCGTTTCCAG GTCACCCCAC GGACGTCGAC ATGTACGTGA TGAGCTTCGA	60
40	CGGGCAGCTC TTCATTCGTG CGGCACGCAA GAAGCTTCAG TTCCCGACGT CTCCGCGGCA	120
	CACTICOCCC TACCTICCCT ATTACACCCC ATACAAATTC GACCCCATGC CCCTCCTGGA	180
	CCGTCCCGTG GCCGAAACTC CGCGCGAGGT TCTGGAGAGC CGCGGCAAAC AGGTCGTCCG	240
45	CAACOGTICCG CAATACAGGA CTGTGATGAG AACOGGGGTC GGGGAGCACA AGCTGGTGCT	300
	COGROCTIGAG ATCIGACOSCA TCATTIGACTT CCGCGAGCCT ACGGGCGACA ACCTGAAGCA	360
	CTACGTOGAG CTGAAGGTGT GTCAGAAGAA CCGGAACTTC TCAGAGAAAC TTTTCTCTTC	420
50	THOCHOCAL TOCTHICTOG TOSOCATALA CAGOGITATT ATTOGATICC GOGATGAGAA	480
	ATTCCTCCTG AAGAGCGTCG AGGAGTTCAG TACGTCAGAG ATCCCACACC TGTTTAAAGG	540
	OCACOGAATA TICCATOTAT GITGIOGACG CCATAGATTG TATOGTOCTC CTTACAAATT	600
55	OCTATIVICAC TOCCOCOOOC COTGAAAANA NITCAACTOT TACAGTOTCC TOCNICATOG	660

	TOCTTACTIT TOCCCCACTG CCCAACAAAA ACCCCCAATG CCANAAATIN TOCCTNGTTG	720
	GICCCCAAIT GONGNOCC CCANATANAA AAITCCGNAT TAITCCCTIG TITCCTTAN	779
5	(2) INFORMATION FOR SEQ ID NO:394:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 815 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	•
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1296UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:	
20	GATOGIACOG TITOSCIOCIG COGITITACOG ATATOCATOG GITGITTIOCA GITGOCGAGA	60
	GCACGGIGGT COGIGICICT GOCGACGICT COGACATOCA ATACCTACAG COCCIGCTCC	120
	AGGACATOGA GATOGAGAAC AACTACGACA ACAGGCCACGC AGACGGCGCG GAAGGGCTCA	180
25	AGCCGAGCTA TATTTTTGAG TACCTTGCCT CGCTCATGTA CCAGCGCCGC TCAAAGCTGA	240
	ACCCOCTCTG GAACOCCATC ATCGTCOCCG GCGTCGAGGA CGGCCAGGCC TTCCTGCGTT	300
	ATGTGGACCT CAAGGGGTC AAGTACTCCG CCCCAAGCTT GGCTACTGGC TTTGGGGCCC	360
30	ATATOCCCAT TOCTICTCATG COTAAACTICG CAGATOCCCA AAAAGACTICG CCCCCCTCCA	420
	CCTCTCAATT GCGCGAGCGA CTATCCTGGA GTCCATGAAG GTGTTATTCT ACCGCCATGC	480
	COGTAGTICO COTOCCTICT COCTTOCCAT CATOGACAAT GATOCOOGTIC TICAGCATOG	540
35	AGCAACTOGA AGTOGAAAAC ATGACCTOOG GTTTOOCCCA AGGATATTOC GOOCTATOOC	600
	NCCCAAATINT TITGAATTIAC CNGGGCCGCA ACGCCGCACC CTGTTTACTA TCTTGTTCGC	660
	GENTETICNOC CARCOGOTING GIVIATCOCAT ACIVITICARAR INSCINIARICA TOTOCOCTIGA	720
40	ACCCONCIGI TITINGINGAN ACCITICNOCO CITITICINGA TITICCOGGAT TIGNOAAAAAC	780
	CCTTIGAAAA AACATINCCC NITGGNAAAT CGATG	815
	(2) INFORMATION FOR SEQ ID NO:395:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 766 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1297RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:	

	GATCTCCTCG ACCCTGGTGA CCTTGCCGGC CTTCACAAGA CGGCCCAACT TGGTCACTGG	60
5	CACCCAGOCC TICTOCTOGA CCTCTCTTCT GCCCTTGCGG CCCTGACGGC CCTTGTTTCT	120
3	GCCGCCGAAG CCGCCTCCTTC TTTGTTCTGG AGCTGACATC TTGCTATCGT CGGAATGGAA	180
	CACGGAAAGC TOOOGGAGTA ACTITICGATC GACGCTOCTG ATGIRGTTAC GATACACCTC	240
10	CGGCCGCGCG CTTGCGTGCT GAAAACCTGC CCACGGTCTG CGTCACCACA AAGGAGGTCT	300
	GOGTGCTACC GCTGTTTCCG GCCTCACGAC GTGTCTGGGT TTCACACTGA AACCCACACA	360
	TCAGACAAAC GCAGTCCCGG ACGGCTCGAA AGCAAAACCC GCCTGAAGGA GCAACGCGGA	420
15	ACCIGCOGCG TCCGTGCCGA ATCTCGTCAA AAACAGGGGT CACAAAGGGA TTGGCGCTGC	480
13	COCCAGGACTI OCTIACODOGG CATTOGCCCCC GOCGGCAGCC CCCAGCAATIG GAGCAACCCC	540
	CTTCCCCACG TACCCCTCAC ACTCCCCTAT AAAGGCCCCC AGAGCCCTCG AAGCAGACAG	600
20	TCACACACA CAGAGGACAG ATGTCGGACN NCAAAATGAC AATCCTATCA ANAGGNGCGT	660
20	COCCCCAAA CTATCAANAG NITOGAAGIT CCAAACINGC CAGATCAAAA GGCCCCAAAG	720
	GCAAAAAACT TOOCCCCCAC GACCCTTTCN CATTITITAAC COOCING	766
25	(2) INFORMATION FOR SEQ ID NO:396:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 795 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1297UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:	
	GATOCAAAAA CAATGAACTG TTTACAATGT GGAAGCCGTG ACACAAGTGA ATGGCGCTCA	60
40	GCACCOCTAG GAAGGAAGIC TATGIGCAAT GCATGCGGIA TCTGGIACAT GAAATTAAAG	120
	CACCOGTTIG GOGACGAGGA TOCTOCOGTIG ATTATOGAAT ACCOGAGATT AACTAATAGG	180
	CACGATGATC GCAGGGTGCC CAAGAAATTT GAGGTGCCAT TGCCTGAGGT CGAAAAAGTG	240
45	AAGAGACCCA TAAGACCTCG TGTTGTCGAG TATTTGAATG ATGTTGAAAT CCCCGGTTAAA	300
	ACGAGGAGOC GOGOGITATT ACATAAAGOC AAGCOGGGCA GTGOGTTAAA AACAGAGATG	360
	AAAACCCCTG CCGCATGAAG CACTGGAAGG ATGAAACCAG TITGTCAGCC GGAAGGACAA	420
50	TACCOGCOGG TAGGAAGGTA GAGACTATIGC TGTGCCATGT AAGGAACGTA CTTTTATTTA	480
	TCTAACATAA CTAGGGTTCT TTTGACCTGN TACCTTTGTA TTATCCTTTG AANAACTGAA	540
	CCCCCNCCTT TTAAAAANTT TTCNNNTTGN AAATAAATCC CCTTTAAAGA ACCCCCCCCN	600
55	NAANCAAACC CTTNINCCCT TNOCCCAAAC CCACCCAGAA ATTTTCCCINC CNITINCCGAN	660

	ACANONGTIN OGAGATICCC CONTITNOOC ONAAAAAANC ICCCCCCGAN INININCCAN	720
5	AGNOCCETT INCHETECCE NECEVANAATE CECAAATTAG AAGGOGTINTT CINCECNIGET	780
	CCCCCGACATC CAAAA	795
	(2) INFORMATION FOR SEQ ID NO:397:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 601 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	·
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1298UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:	
	GATCTTCCTA CTGGACTGGC TGCTAGACGA TAAACGATTA TGGCTACGTC AACTGCGGAA	60
25	CTOSTOSSCC OCCUTOGAGG AAGCOCAGGT GOCACCCTTT CCAGGTOSCG CTGTGGTGGT	120
25	GCTCCTCAAC CCCACTCACG TGACACAACT GGAACGAAAC ACCATGGTTT GGAACTCCCG	180
	COGTICTOGAC CTOGTACACC AGACACTOCG AGCTOCATOC CTCAACACOCG GCTOGOCOCT	240
30	AGITACACTT GATCCTAATA CTGCGCGCGA AGACGTCATG CACATATGTG CGCTGCTTGC	300
	GGGGCTGCCT ACATCCCGTC CCGTCGCGAT GCTAAGCCTG CAAAGTCTAT TCATCCCCCA	360
	COGTOCAGAT TOCATOGOCA AGATOTOCAC CATOGOCCC GAGTICCCTG TITIGCTACOG	420
35	TGITCGACAA CGATTTTGIT GAGCTCGACA TICGAGGCCG CAATTGCTCC AGAACTTACT	480
	CCAAGAACAC TIGIGOCAIC IGAOCACCCC AIGGCTAACA GACCTACCAA CCCCCCTTCN	540
	GAAGCAACCG CITCHATTIC NATCIOCNAG GICNCTCCCT ACCTATACCG CICTIGIGAN	600
40	A	601
	(2) INFORMATION FOR SEQ ID NO:398:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 753 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1299RP	
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:398:	
55	GATCTCCCAC ATTGAGACOG TAGCAGCCCA CATATTGCGC TTGAACGCCA TTAAACGGCG	60

CCATTOCTCC CATAGAGCTT TCAGATTTCC TGTTAGGCTC CAACTCAACG TCATACTGGA 120

_	GPTTAAATCG AGTGGGTGCT GPTGATATCC AACTTGGAGG CGPTCFTTTT GTCCTCGTAT	180
5	COCTTIGAATA OCCOCCCAGG TCCCCGTGGCG AAAATCCATA TATATCCATA TTGGCCACCC	240
	AGCTTIGTICAC ACATAGAGGC AATAGTGCCA GTAATGCCTC GAGCCGAAAAC CATGCAGCTC	300
	CCCCCCCCAACCCCC CACCCTCCCC TTCCCATACAC GCCAACCCCC GCCAACTCCCCC	360
10	COCACOCTICA OCACOCAGTT OCTOCCTOTIC ACOGTIATOTIC COCAGCOGGC OGTIGCOCACA	420
	CCCAGATACT AACACAGCAC AGACGCTGTA TCAGCTGATT GTCCAACCGG CGTACTATTT	480
	CACCITICIG COGAATGICC TACTOCACCC CITCOCCCAG COCCCCCAG TOCCCATACC	540
15	ACTOCCCTTC TOCATGTCCA COGTOCCCCT CCCCATTICCC CCCCCCCCTG CCATTIGTCC	600
	TOCCOCACOC OCTICTOSCAG OCTICTICTOC TOOCTOCOCT CTOCTOCOCC AACTACCACC	660
	TOCACTACAT OCACACCTAC ATTOCCACCC TOCTCGTCAC COCACACCCC CACTCCTGTT	720
20	THENCOGAIG COCTECCOCC CGICCOCCCT TCC	753
	(2) INFORMATION FOR SEQ ID NO:399:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 751 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1299UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:	
	ACCCITITGG TITTCCCCCT GATGGTGCGT CGTGGTATAG ACGATGTGAT CTCCCCCTGC	60
	AATTGTAAGC CTTCTCCTCC GCAGATATCC CGCACGGAGA AGTCGTCTAA ATTTAACATT	120
40	ACGITCATGI AATCACAGGG CACCITITICA AAGACACAGA CGATCATGCC ATTCTTACGC	180
	TTTCCCCACA TCCACCCCA AATGAATTTC TGTGTATCCG ACGATCCTGA CGATCCACCT	240
	GAACCACCAC ACCACACCA TETCACCCCT OCTTGTATGA COCCTACTAT TICACCTGTG	300
45	AATACTIGIT CTIGGCCCTC IGTAGACATA AICTIGITAA GGACAAAGCT CCTGCTGTCG	360
	GIGIGIATCA GGICAAGIAA AGIAAGCGCC TIAAATGCCA ATTIGGAGAT ACCGAAGAIT	<b>4</b> 20
	AAGCATGOON AATOGITAGO COCOCTAAAC TGOCATGOGT GATGCTGOGA ACAGGTAAAT	480
50	ATGGCCTGAG GTGCTGTGTA CTTACCTGAT ATAAAAGTAT GCAGTATGCG GGGCGCTTCG	540
	TACCITICTOC TGIACTCTAT COCATCCIOC ATACATGITA GITCATCOCT AAATGCITIGC	600
	AGATAATITT COTOCTOA GOOCTOTATA GTAGITICIG TOTTGAATAT TOATGAAAATG	660
	GITGOCCTAA OCTITICAACC ACCIOCTICT TIAGITICITIC CICATTACTG ACTITICITICG	720

	CAGGATCTAC GCCATCCGCG TTGGTGCTGA C	751
	(2) INFORMATION FOR SEQ ID NO:400:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 777 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1300RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:	
	GATCTCTCTC COCCGTGCAC AAATGACGCA GAAACAGGCA TTCACGGAAT TGAAGAGGCC	60
20	TCAACTOCCE CCEATCOCTA CACGOCCAET COCACGACAT CCTTTCTTTE GTGCGTATCA	120
	GGATACCTAA ATAAGCACAT ACAAAACGTT AAATATGCAT AAGGAGATAT ATGCGAAAGT	180
	TAAAGTGTTT TTAGTGGCCC TCGGCCACAG TTGCGTGTTT CAGCGATAAT GGGAGACCAG	240
25	CCCOGCACGI GATCAGATAC GGITGTAGIG GCCATACOGG CITIGCOGCACG AATCTACOGG	300
	GTATOGTOCC TGACOCTOCG CCGOCGOCGT CTTACOCTGA GTTCCCCACA GCCGTTCCTC	360
	GIACIGGITG ACGICTICGI CGIGCACAGC CCCTCGITIG CCGIAGCGGC CCCGACIGCC	420
30	CCCCCCCTTC TOCOCCTOGA GATOGTAAGA CTCGTTOCTG CTOCTOGAAA AGCCCTTCTT	480
	9090T090TG TAGTACTOGT CCTT900GTA GTAC090GGG 900T0009GG TTACTAC99G	540
	CTOGTATACC ACTIGIOGOG COGAGCATAT ACTIGIOCAC OCTOCTICIC CIOCOCCCG	600
35	CCGCTGGCGG TGCCGTCTAT AGCAGCAGCA CGGCCAGCAC AAGAGTCGCA GATTCCNCTC	660
	ACCCCCCCAT AAACNCCGAN TTACACCCCC TATCCNATAC CCAATTGACG CTACNCATCC	720
	CNCTATACOC CATCNITIGCA CNOGGTACCT ACTITITCOCN AANTGACOCC CACNING	777
40	(2) INFORMATION FOR SEQ ID NO:401:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 812 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1300UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:	
	GATTGAGGAG TITTCCACTOG AGGTGGCGCG CTACATGAGG CTGCTGCGCG AGATAGACGC	60
55	CAAGTOCGTG CACACGGTOC COGAGCTTAA COCGCAGATA GGGCCCTTCC TGGCTGCCTC	120

	GCGGCAGCCG GGAAGCCCGC AGCTGCAGAC CATCAACCGG CTCTTCCAGG ACCTGATGCC	180
_	GICOCTOGAG GAGAAGATOC ACGICTOGTIC CATTOCGTTC GAGACOCTCG ACCOGCTCGT	240
5	COCCCCCTC GACCTCCCCT ACCACCTCCC CCTCAACAAC CACCACATCC CCCAACAACCT	300
	CCCCCCCCCC AACCACAACC ACCCTCCCAT CCACCTCCAC CACGACCTTA TCAAGAAGAT	360
	CGAGTCCAAG CAGCAGAGCA AGTICOCAGCA GGCGCTTGCGC TCCGAGTCCC GCCGCGAGCC	420
10	GATGOCOCCC AAGAAAATOC ACCTGGACCC GCCGGCGCCG CGCCTGCTCT CAAAGGCCCC	480
	COCCOCCOOR COCCCCCCCC COCCCAACCC CCCCCCCCCC	540
	COCCCOCCOC CONAGCOCAA GAACCCCAGG AACAANTACT CCCCCCCCCC CONAAACAAC	600
15	AATTICGGGA AGGCCICITA CIGCTACTGC AACCATTCNC CCTACGGGAA AATGICGGIT	660
	GOGAANGGGA AAAATGOCINC TONATGGTOC CTCCCCTGGA TCACTONAAA CCTTACCGAN	720
	GOGAAATGIT CTGCAANAAT GCAAAAAAAC CCTACATACA GNCCGGITAC TANNICCCCC	780
20	CCCNCCTINCN TGCCTINCAA TGGGTTCCNC NT	812
	(2) INFORMATION FOR SEQ ID NO:402:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 786 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1301RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:	
	GATICOGOGAG ATTICATOGTIG GACCOGOCAC AGGCAATTIAC TATAACAACA TOCTGOGGTIG	60
	TTANAGGACC TANCTCACGC TCANGTATTT CAGGATGATA TCCTAGATGA AGAGCTGCGC	120
40	CACACGCTGG TTCGGTTACA ATATTGCTCT CTTCCGCAAA ATTTAAACAT GTCTGTACTA	180
	CACCGAGCTG GTCAACCACA ACAGATTITG TCCTGTATTT TTCCCCGTAA CTCAGAGTAA	240
	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT	300
45	TOCTOCCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACCC CTCTGTTTCC ACTGCTACAA	360
	CAGOGATAGA GICTOCCAAA CCATGTTTCT CCAGCCCATA TACAATCCCA TTATATAACC	420
	CCCCCCCACC TACCCTCCAG ACCATACCTT TCACCCTCTC CAATTGCACG CCTTGGAGAT	480
50	OCAGIGCTIC TACTACTICA TCTACCATTG TTOCATOCCC TTCCCAGATG AGTOGITGIC	540
	GAATGGATGT GCATATATCG GACCGACTTT TTCTAATTCA CATTCCCCAT CAACTCCGGA	600
	COGTAAGITA TOATOSCTOT CTTTCAATAC ACTTCCCATT GANATCACAT CNGCCCCCGT	660
55	TGANCGGTTC CGCTCTACCT CCNCCGCCAA TINTTTCNCN CCTACNCGGG CAGGINICCT	720

	MINNOGICA COCGIGGIGC IGCACCONIG CNIGONCOCA CICCONAAAC NITIOGNIGC	780
5	GNGAAG	786
5	(2) INFORMATION FOR SEQ ID NO:403:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 782 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1301UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:	
20	CATCATCTOC GTGCCATACT GOCAAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT	60
	AAGATATTOC ATGATATAAG CACAGGOGG TITCGTCGAA GAGGAAAGGG TGCACTTGAT	120
05	CTGGAAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA	180
25	CTITICAAAC AAAACATATI OGAAAAATOGI GATACTAOCA AOCTOGIATO TAACCOCAAG	240
	TCATACOCCT TTTTTCAGAC GATGGTGGAC GATGTTACTG AAGCATCATT TOGAAATACA	300
30	TTTGATGCCA ATATAGATGA AAAAACAGAT CCATCTGCTG CAGGTCGGAA AATTGTCATA	360
30	TCAGAACAAT TIGIAAAGGA AACCCIGICA TICTIGICGA GCAAGAGIGG CGACICAGAA	420
	ATCCCTCCAG AAACTAAATC TATTTCATCC ACCACAGTTG AACGTGAAGA AATTCAAGAC	480
35	TICATACATT GAAGCAAAAT AGTAACATTA ACATTIGAAA GGAGTCTAGA CTICCTGCTC	540
~~	AGATGOCTGA CTCAGCAGTG AGATAGAGGT GATTACNOCT TTCTTTANAT ANATTCCNCN	600
	GCCGCNAAAT TTTTATATGA ACTACTTCAC AANANITITA AAGTTGGCCC CAGGGGGGCN	660
40	ATCITIAAGGG AATAAANATN GOGICCAAGC CCAATACTIT TNINGGAAAN NGINGNGGIC	720
	CCCCCNAAG GATTTAAATT CNACCAACTT NICCNCCANN ACCCCCCCC TINITITICNG	780
	NG	782
45	(2) INFORMATION FOR SEQ ID NO:404:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 785 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1302RP	

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	(xa) SEQUENCE DESCRIPTION: SEQ ID NO:404:	
	CATCGAAGAG CITICTCCCTIG ACTITCCAACG CCACAAGGTA CCCAAGCTCC TGTAAAGAGT	60
5	TATGAAACTC CGTAGCGGAA AGCGTGAACG AACCGTTAAT ATCATTGTCC ACATATATCA	120
	TOCGCCACTT CITICACGCGC TIGITATAACG AAGITAAACTC AGACAAGTTT ACGGTACCAA	180
	ACCOCCTICOC GCCAAACAGG CTAATTIAGCG CGTCCACCGA ACTCATGCAG AACTGCGAAT	240
10	TGTCATCATT CTGTAGCAGA TGCTGTAGCT CCTCTGCTGT GAGACGCTCC ATCTTCCGGA	300
	CGICGICATT CATGAATAAT TICTTTOCTG TTATACCATC COCGICTICA TTACCAACCG	360
15	TOCCOCCUT COCTICOGIA TOGITCOCGI GACCCICCIG ACCIGOCICC COCCITOCAG	<b>4</b> 20
15	GCAAATTATA GCTCTGTGGG CTCGGTGGTA TTGGCTTCCC GTGGCCCGGC AGGCCAGGCG	480
	COCCTIGUICA ACCICAGGAG GATTITCCCTG AACCTCCCCA ACCICATICCG CAGGCAACTA	540
20	CTATGTGTAC AAAAATTOCC GTGNTCCTGC AAAACCTTTG GTCTGTACAG AACCCANCCC	600
20	ATOCCCATG GAACOCANTG CANTITITICC CCAAATTAAN CCCTGGAAAA MTOCCAAATT	660
	TITICOCCATIN TITITCCNATT AAAAANCONG COGINNAACT CONACCONC CCATININGGG	720
25	GOGNAAANIC COCCCCTTIT TMITTINCAT AANGGNCONC NITGANNINCC GCCCCINNINC	780
	cccac	785
	(2) INFORMATION FOR SEQ ID NO:405:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 803 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
<i>35</i>	(ii) MOLECULE TYPE: DNA (genamic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1302UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:	
	GATCAACAAC ATACTTCTAA AGACATCAAT ATACGCCCGC ATGTCTCCGG ATGAAAAAACA	60
	TGAATTOGIT GAGAGGITOC AGICCATTOG ATACCAGGIT GOCITICTOCG OCGATOGIOC	120
45	GAATGACTGT GGTGCCCTTA AAGCGGCCGA CATTGGTATA TCTCTATCCG AAGCGCAGGC	180
	ATCTGTTGCT GCGCCATTTA CATCCCGCTT GTTTGAAATC AGCTGTGTTT TGGACGTAAT	240
	GAAAGAAGOC CGTGCCGCGT TOCTCACGTC CTTCGCCTGT TTCCAATACA TGAGCTTATA	300
50	TTCTGCCACA CAGTTTGTTA CAATATTGAT CTTGTACAGC CGTGGATCTA ACTTAGGGGA	360
	CTICCAGTIT TIGIACATOG ACCTOTICIT GATOGIOCOG CIAGOGGIGT TOATGIOCIG	420
	GTCGAAGCCC TATGAAGTAT TGGCCAAAAA GCGGCCAACG CCAATTTGGT TTCTCCGAAG	480
55	ATATICATIC CITIOCICOT OCACATOGIC ATTICITOGI CITICACCIT CICCOGICOC	540

	TCOCACTCCA GCATATGAAG TOGTACCOOC AGCCACTCGT COCGACGACG AACATGTTGC	600
5	TICCCANGAN NACNCAACCC TITICTINGTC TOCACTICCA TAAACCCTGG TCCCAATONT	660
3	OCTIOCOGIN GIOCOLOCCON NOCONONAACO NAANITOGAA AATTITOGIT TATOOCANIT	720
	CCCCCTTCCC TGNCCCTCCC GGTGGANNAT TTCCCCCCCC CGAAACAACT TGGCNNCTTT	780
10	CNCTCCCGAA GITINCTCCAT MIC	803
10	(2) INFORMATION FOR SEQ ID NO: 406:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 773 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1303RP	
	<b>,.,</b>	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:	
25	GATCAGGICG CCTTTATGGC CATACTTGTT GGACTCATAG TATATCTCGG CGACTGCACT	60
	ATTACTOGAC TOCTTOTICAA GATCTTOCOC ACCCATCACO COCACTATAC TACATOTICTC	120
	GITGGGCTIT GCGTCGCTAA CCGGCAGAAA AGATACCTIT ATACTITATA ATACCAGTGA	180
<i>30</i>	GOCGOCCATA CCACGTAATC CATCTTTGTT GOCAAATAAT TACAATATTC CTTTTAGCTA	240
	CTGGAATTGG GCTTATCCTT ACAGTGTCAC ATCAATTTTC TATCGTAATT CGCTATCTCC	300
	OCTOOCAATC ACTOCACTOC AAACCATTAT CGTCCTGATA GATAAAGATT ATAGGGTAGC	360
35	GATCAATAGT ACCGGTAAAG GCGTGACCAA TATTCTGCTG GGCGTGTTTA GATGGCCGAG	420
	ACCCTAGAAT GTCCCACCAT CCTCGTTTAG CGATATCCCA ACCCTTCACT AGAACCCTCC	480
	CACTAGTAGA GCACAGAACG TIGAGACTTA CAGCTGTTOG AAGTATAAGT TGTAAATTTC	540
40	CAAGGGTGGC AAGTAATATC AATTGATTON AAATGACTTA CCCCTACGTT GAACTGCTTA	600
	CITTAANITG GGTCGGGCCC ATCAAGCCCT GACACTCTTG ACTITCCCCC ATGAAAAAAC	660
	TCCCGGGTGG GTTCNANCCC CATTNCCCAA ATACANTCCA TANGTCCTGG CCCTTAACCA	720
45	CTICNICCOG ACGATITITT TINCCAANAAG ANNINACTIT TINAATTINGC CAC	<b>77</b> 3
	(2) INFORMATION FOR SEQ ID NO:407:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 807 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1303UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:	
5	GATCTAAGTC CTCTCCCCCA AGCGGTGACG CAAGTGGACT GTCTGTCGCT CGGTTAATAA	60
	AGITATOGAG ATOGTOCACA AOCTOATOCA COTOGGATAT ATGTOGOCTG TGAGTAGOOG	120
	CAGAGTCACG TOCOGTIGTCG AACGTGACAT CAGACTTTCG GGACGGGCTT CCTAGCTCAG	180
10	OGTOCAAATC AATOGACACC TTTTCCAOCT CTOCCAOCGA OCOCAAGAAC TTTTTGTCTA	240
	ATATATAGIC GITAGTITGG ACCACGCAAG AAACCGGICG TTCGIGGCCT CCTGACGCTC	300
	TCCCGTGTAC CTCGGCTGCG CTGATGACTT TGCCAGTGCA TGGGTCAGGG CTCTTGGAGA	360
15	TGACTTGATC GOOGGACTOC CACTITIOCCA ATCGAGGATC GICTACAGTT GTAAACGGGC	420
	SCACITICIT TICIGIAGGI SCICOCOCIG CIGGIACIOG ACICCICCIG GACIGICIGG	480
	OCCITACTOG ACCIOCTOCT OCTOCTGITA CTOGAACOGA AAAAGAAAAA TGACTTCCCC	540
20	TOTTITICATA TGACATTOCC NGITGIGANA CNIACTATIG OCCCCNAGAA AATAANITAG	600
	GENGARATAC ACTONOTATG TITGCCTATA TITCCCNTAC CATATACAGC CTGCTGATTC	660
	CCAGITTTAN AANITTAAGI GCGITACCIT ATATGITGAA NCCCGITATA TGAAGAATAA	720
25	CCCCCCAANT TIGCAANGAA CCCCCANAGGC ATTGNCTCCT TCANCANNAT TAAGNACATT	780
	TIGICCITIC AAGNACITIA TAAGNCC	807
	(2) INFORMATION FOR SEQ ID NO:408:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 778 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1304RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:	
	GATCAATGAG CGTGGCTACT ACTGCAGTGC TGTGTCAATA TTACATATCG	60
45	GIOGATAGCT AGATAAAAAT GCTATACATA TATCTGTCGC CATTGTGCCA ATCTATATCT	120
	ATTIGIOCCG ACGITIOCOGA CCAGTAGGAG GITIGIGITICC OCOCOGTIOCG CAAATTICCOC	180
	TGAGATCAAG CCATTOCCTG TOCTCTTOCC CTCCCCTAGA TOGTAGGTOC CACTTGTAAT	240
50	AAAACCGACG ACATCTTGTA COCOCOOCAG ACOCTGATCG GCGTCATGGG TCCGTTTGCC	300
	COCADCATTG TATTTCCTGG AAGCGACTGC CTGCCAATGG GCGAGATGCT TGACAGGCAC	360
	TOCATACAAG COOGCATTGT CCCTGAAATG GCCGCGTTCG AGGGCTGTAC AGACAACGGC	420
5 <b>5</b>	GATCACGOGA AGTTGOCTOG TCACAACAOC CAGTTGGACG GOCAAGCCTG TGTCCATTAGG	480

	ACCITITICCA AAAAGAGACA ACTOOCITAT TOTNAAOGTC CCCCCGANCT NCNAAAANAA	540
	TCTTGGTGGC AATACCAACN CCTAAGGATT TCANCGNGTT CCCCAACTIN ATININFTIN	600
5	TNOCNCCCGT TTCAAATTCA TATNOGTOOG TTOCNOOCGN GAATMITCTT TTCNATTTCA	660
	AACCAACGNG GOOGNOCCNT TIGAGATTIG GANACNCCCC TCNAAANANA MTIGTCCCCT	720
	TICNOCNNAA AACAAAATIN NOGAGGAAGA GGITTTIANOO ONNIATATINO OOOONOON	778
10	(2) INFORMATION FOR SEQ ID NO:409:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 792 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1305RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:	
25	GATCAATGTA TCCATTATAC CCAGCTTTCG CAGCGACATA ATATATTGAC TIGATTITAA	60
	AGCGGTAGAA CTTTACGGGG CTAGGGCCCC TAGGTATCCA AGGTTTAGCA TCAGGATGCA	120
	CGTCTGCAAA GCACTTCTGC AAGGCTGGAA TGGGCTGGAG TACTTCGAGC TCACCCGGGA	180
30	AGITTOCACG AGGIGCTTTC ATGGGGGTCTT CAATGGATAT AGACGCAACT GAGAAAGACA	240
	CGITGITATT GITTITAGCG TITACTIGIT GIAGIGICGI GICGACCATC AAAAAAAIGG	300
	OCTOOCCGTC ATOCTCTACT CCCTCACATC TGTCGGGAGA AATATAGTAC ATTCTAATAC	360
35	CATATOGAGT ACCOUNTINGA TIGATIGHTG TCAACTOGAA AGAACTITOG TCTTTAATTA	420
	ATTICCTGAG TIGCACTGCT GCTTGTTGTT CCTCCTGCGA CGCTTGCGCG AAAGCCGAAG	480
	TAACTAGIGC CAAAAAACAT GIAACIAATG AAAAAATGGA CITCATTGTT GCTATTGAGT	540
40	OCCAATAGGC GAGACTCATC CATATGINAT GAAAGCGTTT ATANATCNIT GITNIGGCTT	600
	GAAAGAATTA TIATACIIIT CONGOCGGIT ACATTATCIT CCAACCAAAT TGITTCCTTT	660
	TNGANAGGNA ATCCCCCAAAA TTTTTINAAAT TAATTNGTCN NOGCANCOGT TTTTTTCCCCCG	720
45	GNGOGGAAAA NAAAGCNGGN NACCCGCCAA ANCCGAATAA AGGATTTCCA TNAAAACCCA	780
	ATTMICCNAA AC	792
5 <i>0</i>	(2) INFORMATION FOR SEQ ID NO:410:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 812 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

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(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1305UP

5		
3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:	
	GATCCCCAAG AAGAACATCA AGATCCACOG GTTCTAGOCG CTATGTACTT TGTGTAACTC	60
10	AATACATATC CTCCTCCTCC TCCACCACCA CCACCTCCTC CTCCACGTCC CTCTGCGCCT	120
	CCGCATAGTA CCTCACACAG TACGGCAACA GCTCCTGGCT GAACAGCCTG GCCAGCTGGT	180
	COCCUTTODE AAACTECTEG COCCOCCOCT COCCTGTCCA COCCAACCAC GCAAACCAAC	240
15	TCCCGTCGTA GCGCTTCGGC CACTCCATCT CCACGGCGCC GCTCCGCACT TCCCCGTCCT	300
	COCCUACOST GAACIGCTTC CTCACGCTCT GOGCCOGCAG CCTGCCCTCC ACCTCCCCGA	360
	ACTICCACCOT GATICGCAAAG TCCCACGCCC CCGCCCCCCC CCACTCCACC TCCACCCCCCC	420
20	SCATOSCCIC CACGI'ACCCC CAGI'CCCCCG CCCGCACGTA GTTCGCGAAA ATCCCCGTGC	<b>4</b> 80
	TOCGTCAGCA CGAATCCCCCC AGAACCCCGC GATCCCCTCG ATCGCCTTGC TGCGCCGGCC	5 <b>4</b> 0
	GTATACCOOC COCAGOGCOG CTOCCOGCTCC ACCTCCAGOG CCCOGCTCCTC CCGCTCCCCC	600
25	NCCCCTNCCA NTCCCCCAAGN CCTCCACCNG CCCCCTCCCN CCCCTTAGTC CCCTCCCCCC	660
	CATTIAGANG GOGNNOOGCC TINNVITGITT NINNGAAGGNA GNGICCCGNI TCCNOGGCCG	720
	GNINNGITTI TOOGNNOGAG NACOGNGITT TTOGANCNOC CANTONOGGA MICCTOGNOC	780
30	GAANGGNACT TACCACCOANN TTGAGCCCCC CT	812
	(2) INFORMATION FOR SEQ ID NO:411:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 778 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1306RP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:	
	GATCTGATAT TOOGTAATTG CAACCTTTGC ACCOCTTTGA AAAGTACTTT AGGAAGTGGT	60
	ATTTOCAATA TAGTTCATCA TIGTAGTOGA AGCACGAGGA TACCTTACAC TTOGTACCGC	120
50	AAACCGTGCA GCAGAAGTGT TCCTCGTCAT ATAGCTTACC AAATGTATTG TAATACACGC	180
	COCTCAGTOG CTTATTOCAC ACATAACACA ATAGCTTGTT CCGCGTGAAA TAATCCTGCT	240

300

360

GCCATAGCAG TACCACTICA GACGTATCCG GGAGCTCATA AGGGAAGAAC TICCGCCGAC

ACAAAGCTCC ACAATCGTGA CAAACCAGAC AGTTTTCATG GTAGTAATCA CCAAGCGCCT

55

	TCAGGGAGIT CTGCGTGATA ACCCCCTTGC ATTGTTTACA GATTTTGGCC GTTTTTTGAG	420
	ATGAGGTGCC GGTTTATGCT CCCCAGACGT TCGCATTACT TGCTCCGACG CACTGTGTCT	480
5	ATGGTTGATA TGGTCACTAT ACGTCCAGCA ATAGCTGTGC TTCTGTATAT TAGTCATGAA	540
	AAACAGTAGC ACTOCCTATO TTACCCTTGC NGATOGTATT GGTACCGCCA AATNGTTAAC	600
	CCATTITICCA AGAACATTON ACCINCTICCG TITTITGCCCA AAGAGAGGIN TOCTATATIT	660
10	OCCAACAAAA OCCCAACTGA AATTNAANAA ACCCTTTTTT CCCCCTTTTN TTTCTCCCGA	720
	GGAACCITIT COOCAANITT CNCCCTAAAT TGTNTGGGGG NTGANANCCN AGAAAANC	778
	(2) INFORMATION FOR SEQ ID NO:412:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 806 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1306UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:	
	GATCATTICA GIOGATOGOG ACATICATAT GGATATCAGT TOGACTITIG TITOCAGICT	60
30	TATTCCACIG ATTITCAGGT TACAAGAATT GOGAAGGGT CTCCATTITG TAGGGACGAA	120
	CAATTGTAAG ATGTCTCAGG AATTCAAGAC TCAGGTTGAA ACGAAAACTA TTATCTTATC	180
	CCTTCCTGIA GOGGACGATA CCCTACAGAT GATTATCCAA CCCATCTCTT ACGAACTGTC	240
35	ACTACATACA GITTICACTG ATTITIATITC CATATCTAAG GTACAAACCT COGAAACTAG	300
	OGATATOGCA ATTATTOGGG AAATTAAAAT TOGATATOAA ACAGOCCAATT TTCAAGTGAA	360
	ATCGIACAAC TIGAAATIGI COGAGACOCT GCTAACATCA AAGCIACOGG GGAGTIGITC	420
40	TOGAGCOGIT GAACTITATT GITCIGATAG TGACATCAAG TIGCTITITIG ACGAATGICC	480
	CCCCCCCCA AATGAATACC CGCNATNINC ATTCCINAAC CGAATTCCCA AAACCCNTIN	540
	TNAANTAATC CCTTTAAAAA TINATTITIC CCNAAGNITT ACNOCCOGNA ATTITTITICC	600
45	CAAATOOOCC CCTTANATGA AAAAANACTN CACCCCCCCN NOGAAAANAA ATTTCNCTTT	660
	GGAAANINNIN AAACGAATTA TTCNCNCCCT TINICCCCCC CCCGAAANAC ANINITTCCT	720
	CCCCCCCTTT AGGAAAANIG TTTICCCCNA TTINANANIN TCCNCCCNCC CCCNNAACNA	780
50	AAATNITAAA NCACCCONIN TINING	806
	(2) INFORMATION FOR SEQ ID NO:413:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 753 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	
	· · · · · · · · · · · · · · · · · · ·	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1307RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:	
	GATCCCTTTA TCTCATATTA TAGTCCATAG TACCCCGTGG ATGCCTACCA CACAGAGGTC	60
	CCTCTTCTCG ACCTCAGACC TAGATATCTT CCCATATCAT TCAAAATATC GTTCAATTCC	120
15	TOCTOCGIGA GOOGCITAAC TICOGOCTOG ATATCAGCAT COOGTGITTC CGAGATGTOG	180
	AAGTICICAA CITTOCCCTC CAAAAACTCC TCAAACTICT CITGITCTCT CAGTGTCGGT	240
	OCCAACAACT CATAAAATTT COCAAGCTTA TACAGCTTCA CATTGTCTAG ACTTTCGAAG	300
20	TOGOCCAACG TGAGAGGGAA TACGOCGTOC TTCACGTOCG GAATCTCACC GTCGGGGTTC	360
	GECANTEGAG CCAAGAAGTC CTTCTCCTCC GACTTCGTCG AATTCACTAA GCGCCGCACC	420
	GACCOCTICTT CCATCGTGTC AAGCTGGCCC TGAAGCTCCC CCACTAGCTG CACTAAGTCC	480
25	TCATTCGTCG CGAAATCCGT TGTATCAAAC TTCCCCCCCCCC	540
	TOGTCTAAGT TTGCCATGTC ATGCTTTTGC TTGCTGACCT GTAGCTCCAG CACCGACTGT	600
	CCTGTCTTGG TGATTAGGAC GCTCTGCCGT TTAACTAGCG CCTGTAGCTC CTCAACTGTT	660
30	TOTICAATGO CTOGTOTGAC ATAACGCACT TOAAATTTAG TAGAACGOTT CTGAATATTO	720
	CTACACCAAA CGCCGCAGAG AGAATGGTAA AGA	753
	(2) INFORMATION FOR SEQ ID NO:414:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 811 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1307UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:	
	GATCCACCAA AGGGTATTIT ACTATATGGG CCTCCGGGGA CAGGTAAGAC ACTTTGTGCC	60
	CGTGCCGTGG CCAACAGGAC CGATGCTACA TITIATCAGAG TCATTGGCTC CGAATTAGTA	120
50	CAGAAGTAGG TOGGTGAAGG TOCTAGAATG GTTAGAGAGT TGTTTGAAAT GOCCAGAACA	180
	AAAAAGGCAT GTATTATTTT CTTCGACGAA GTGGACGCAA TTGGCGGTGC TCGTTTTGAC	240
	GATGGAGCGG GTGGTGACAA TGAGGTCCAA AGAACTATGT TGGAACTCAT TACGCAACTA	300
5 <b>5</b>	GACGGATTCG ATCCACGTOG TAATATCAAG GTGATGTTTG CTACCAATAG OCCGAACACC	360

420

TTAGACCCAG CATTGTTGAG ACCCCGTAGA ATAGACCGTA AGGTTAGAAT TCTCTCTTCC

_	GGATTTGGAA GOCCGTGCCA ATATTTTCCC GCATTCACAC AAAGTCCATG AGTGTTGAGC	480
5	GIGGINTIAG ATGGAATIGA TICCCAGITG GIGICCAACT CCACCGOCGC TGACTANATC	540
	TNGTTTGGCC CGAGOCTGGC ATTTTTGCAA TCCAATTCCC GACCCAGGTT ACCTACAGAA	600
	ANGACTICCT TAAACCNGIG GATACGICCT CCACCCCTAT AAAAATICAC NCCCCTICCC	660
10	CGTTTINIGC AAACCCNAAN CNNICNCCCC CCTTGNGGCG TTTTTTTAAA GGNITATTTA	720
	TCCCAAANNG TNITCCITIT ACNATACTAN TGITCCAATT TCTATNAAAT NITNICCCCC	780
45	CCGTCAAANC CTNCCCCGTT NGCACCCCTA T	811
15	(2) INFORMATION FOR SEQ ID NO:415:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 791 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1308RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:	
30	GATCTGTCTG CTGGTACACC GATGAACGAA ATAATTGTGA CCGTCACGGA CTTCCACGAAT	60
	GCACTICGGA AGATAAAGCC TICGGTCAGC GATAAAGATA GAATGAAATA CAATAAGCTA	120
	AACAAAAAA TOOOCTOGAA TGACGAAGCA GOOGTOCAAG TOCGAAGAAGA AGCATAGAGC	180
35	AGCAAGTTAA ATAGGCACAG CTATGTACAA ATAACCAATT TCAACTTGTT CAAAGTCGTC	240
	COCGICTTAC AGATITICACA CATOGAGAGG GCOGAATTIA CITUITATAA TOCCCICTOC	300
	TOCCAACGIT TITTICCAATC TICCAGACAT ATTOCGTATT TCTTCCTTTT CCAGAAAGAA	360
40	ACATATOGIA TITCTCTATT CCTGTAACTT GAGCTTAGCA ATTTCTGTGG ATATAGTTCC	420
	GCAAAGAGT AGATCCGTGG CACCTCTGAC AAGAACGAAG TIATTCTTCA GAGAATGAAC	480
	ACGOCCOGAT ACATOCCCAG AATGTATATG TTCATAAACT TGCGCTCCAA CATCAATGGA	540
<b>4</b> 5	ATGGATAAGA GOCAGOGTAA CAAGTOOCAT ACTAGTATAG TOCAGOGGAA TGCTTCAACA	600
	TIGGAATACC COCACAIGIC ATAICCOGAG CICTTIGATT GATATAACAA CCCCCNCCCT	660
	NITINIGOCNO AAAATIOCOCO CIGAIGGIAC COCTAANGGI ICIIGCAAAA GOGGAACOCT	720
50	ATCCCCTGGG AGCCNAAACC CTTTACGACN AACNNATTAT GGCCCGGINT TTNACGICCC	780
	TNNCCIGICN N	791
	(2) INFORMATION FOR SEQ ID NO:416:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 817 base pairs

5	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1308UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:	
	CATCACCTOG CCCCTAAGTC CCAGAGAAAC TTGCAACTGA ACTGCCACTG CCCCTCATGC	60
15	ACCACCAAGA COGTTAAGOG CGACCATATC ACCTCCCACC TGCGTGTGCA TGTTCCCCTG	120
	AAACCCTTCA GCTGCTCCAC ATGCACCGT AAGTTTAAAC GCCCGCAAGA CTTGAAGAAA	180
	CACCTGAAAG TGCACATGGA GGACACCATG AAAGAGGGTT GGCGTGCGGC GCCGGGCTCG	240
20	CGTGGTGTTC GCAAGACAGG CGTTAACAAG GGCTCTGCGC TACAAGAGAA GGCGCGCACG	300
	TTACCCAACC TGACTGTGGA GAGCTTTGTC AGCCAGGAGA TGCAAAATTA CTACCCCTAC	360
	TACAAAACCA GACAGCACCT AGACGAAACA CTGTCGCACA TTATTCTCCC GCCCCCCAGC	420
25	COCTOTAGET TOGTACTITG COCTOCGAAC COCCAAGOTA CACACOGAAA COAGTGTCTT	480
	CTTCACGACG CTGTCGCAGG ACATGTCTCG TCGCTTGCCT TCTCTTGCTC CTTGCAACAG	540
	CCCCCGGCCT GCGGTTAAGA TGGTAATGCT TCCCCCGGCCC CAGAACAGCA ATATGCACGC	600
30	CGTGCCCTAG ATATCCCAGC GATGCCCCGGA CTCCCCTCCC	660
	AATCCCANCC TITTGCCCGAG ANACACTICC GACCCNCTCC ATATCCCTGC TCTANCTGCC	720
	CNCCTCACCG CTTTCTCATA AAATOCCATT GTTGCCGCAN CCTATCCTCA TCAAGCCCCC	780
35	TGATANACCC TGAAAAAGAC TGANTCCCCC CCAAACC	817
	(2) INFORMATION FOR SEQ ID NO:417:	01,
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 795 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:	
	GATCAATTAT TAGAGGCAAT ATCAAAGAAG TCCCATATTA CTGAGGAGAA CAGGGAACAG	60
	CCTGGAGAAA GAATGCCGCA GACGTACAGA TACACGCTGG AAAATCAGCT TGCCCAGTGA	120
55	GIOCTOGAAC AGCOGATAAG AGTATTGACA GIGGTAGOGT OCAAGAGICA ACGACAAAAT	180

	GAACAGAACA TCATACTICG COCCCGAGAT GTIGAAGCTC GACTIGGTCC GCCCGTGGAC	240
5	CTTTTTTGAA GAAGTTGCGC CAGGATCCCA CGGCGGCCTT GCGCGACGCA GCAGGGACTG	300
J	GTCTCCAGCG CGCCAGCAGC AGGGAGCTTG TCACCACGCT CACAGAGCTC ATCCCCATAC	360
	CCCCCCCCCCC ASCCATGCCC CCCAATTICTA TCCCCCACCC AATGACCACC CCCATGCTCA	420
10	CTTOCCACCO ATCACACAAT TOTACACCAC TOCCCACAAA ATCITCACCT TCACCCCGTT	480
,,,	AACGTGGCGC GCGCGAGATT CGATGGCATA CAGAATGCGG TTTAGCGGCG GCGCCCGAGG	540
	AATGICCCAA ACCACGATIC CCGCGCGTTC CGCACGAAGT CACTGTTGCC GGACAGGGAA	600
15	ATACCCAGIT CNCTTTCACA ATTOCCACAA TTTCTTTGAN GCCGTCTCCC GATAAGGCAC	660
	ATATINGTIN TETTTOCCOC ACTOCCOCAA NGINCCACTT GCCCCCCTGG TACTITCCCT	720
	GAACATTITG ACGGATNOCC AANOGTGCAA ACTOTOCONC COCGTGTINN COCATACCAT	780
20	CCANTITITG GCCNC	795
-	(2) INFORMATION FOR SEQ ID NO:418:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 797 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP	
30	(vi) ORIGINAL SOURCE:	
30	(vi) ORIGINAL SOURCE:	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP	60
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:	60 120
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GOGGICNOTG ATTOGATTOG COATGAGTTT AAGTATGACC CAGAGGGCCG	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCGGTCNCTG ATTGGATTGG CCATGAGTTT AAGTATGACC CAGAGGGCCG  CCCTGGTGTA TCTAATCTGA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATGGCGGC	120
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCGGTCNCTG ATTOGATTGG CCATGAGTTT AAGTATGACC CAGAGGGCCG  CCCTGGTGTA TCTAATCTGA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGCCGC  GGTGGAGGCA GATATTGCTG GATTTAAGGA CCACGCAACT TTTAAAAAACT ATGTTACAGA	120 180
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GOGGICNOIG ATTOGATIGG COATGAGTIT AAGTATGACC CAGAGGOOOG  COCTOGTGTA TOTAATOTGA TIVACATOGT AGCTGGCATO CAGAAGAAGA CIVATOGCGGC  GGTGGAGGCA GATATTGCTG GATTTAAGGA COACGCAACT TITVAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTCA GOOGGCCCAG AGAGGAGTTT GCCCCCCTATA TGAATGATAA	120 180 240
35	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GOGGICNCTG ATTOGATTICG CCATGAGTITT AAGTATGACC CAGAGGCCCG  CCCTGGTGTA TCTAATCTGA TTAACCATCGT AGCTGCCATC CAGAAGAAGA CTATCGCCGC  GGTGGAGCCA GATATTGCTG GATTTAACGA CCACGCAACT TTTAAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTGA GGGGGCCCAG AGAGGAGTTT GCCCGCTATA TGAATGATAA  ATCATACATA TACGAGGTTG ACCGCAATGG GCCTGAGCGA GCAGGTGCCA TAGCTGCTAA	120 180 240 300
35 40	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCGGTCNCTG ATTCGATTGG CCATGAGTTT AAGTATGACC CAGAGGGCCG  CCCTGGTGTA TCTAATCTGA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGCGGC  GGTGGAGCCA GATATTGCTG GATTTAAGGA CCACGCAACT TTTAAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTGA GGGGGCCCAG AGAGGAGTTT GCCCGCTATA TGAATGATAA  ATCATACATA TACGAGGTTG AGGGCAATGG GCCTGAGCGA GCAGGTGCCA TAGCTGCTAA  AACCCTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT	120 180 240 300 360
35 40 45	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAGI309UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCGGTCNCTG ATTICGATTGG CCATGAGTTT AAGTATGACC CAGAGGCCCG  CCCTGGTGTA TCTAATCTGA TTIAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGCGCC  GGTGGAGCCA GATATTGCTG GATTTAAGGA CCACGCAACT TTTIAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTGA GCCCCCCAG AGAGGAGTTT GCCCCCTATA TGAATGATAA  ATCATACATA TACGAGGTTG AGCCCAATGG GCCTGAGCGA GCAGGTGCCA TAGCTGCTAA  AACCCTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT  CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGACCAGA TGCGTAACTG	120 180 240 300 360 420
35 40	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAGI309UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCOGTONCTG ATTICGATTICG COATGAGTITT AAGTIATGACC CAGAGGGCCG  CCCTGGTGTA TCTAATCTCA TTAACATCGT ACCTGCCATC CAGAAGAAGA CTATCGCGCC  GGTGGAGGCA GATATTGCTG GATTTAAGGA CCACGCAACT TTTAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTGA GGGGGCCCCAG AGAGGAGTTT GCCCGCTATA TGAATGATAA  ATCATACATA TACGAGGTTG AGGGCAATGG GCCTGAGCGA GCAGGTGCCA TAGCTGCTAA  AACCCTGCCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT  CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAGCAGA TGCGTAACTG  GTTGTCACTC TTTGGACCTG CCGGATATCA GCACATGCAA CCAATATCTG CTTCAGCAGT	120 180 240 300 360 420 480
35 40 45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GOGGICINCTIG ATTOGATTIGG CCATGAGTITT AAGTATGACC CAGAGGOCCG  CCCTGGTIGTA TCTAATCTCA TTAACATCGT AGCTGGCATC CAGAAGAAGA CTATCGCGGC  GGTGGAGGCA GATATTOCTIG GATTTAAGGA CCACGCAACT TTTAAAAACT ATGTTACAGA  CATCCTAGTA GCTGAGCTGA GOGGGCCCAG AGAGGAGTITT GCCCGCTATA TGAATGATAA  ATCATACATA TACGAGGTTG AGGGCCCAG GCAGGTGCCA TAGCTGCTAA  AACCCTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT  CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAGCAGA TGCGTAACTG  GTTGTCACTC TTTGGACCTG CCGGATATCA GCACATGCAA CCAATATCTG CTTCAGCAGC  CCTCCCGCTT CTCGTTAGCT ATTGTGCCAC CTTGTATTCT CCATCCGTTA TACAGCCAGC	120 180 240 300 360 420 480 540
35 40 45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1309UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:  GATCAGGACC GCOGTONCTG ATTCGATTGG CCATGAGTTT AAGTATGACC CAGAGGCCGG CCCTGGTGTA TCTAATCTGA TTAACATCGT AGCTGCCATC CAGAAGAAGA CTATGCCGGC GGTGGAGCCA GATATTGCTG GATTTAAGGA CCACGCAACT TTTAAAAACT ATGTTACAGA CATCCTAGTA GCTGAGCTGA GCCGGCCCAG AGAGGAGTTT GCCCCCTATA TGAATGATAA ATCATACATA TACGAGGTTG ACCGCAATGG GCCTGAGCGA GCAGGTGCCA TAGCTGCTAA AACCCTGGCA GAAGTCAGAG CGATAATGGG TTATTAGTTA TATTCAGATT CCAACTTTGT CTATAGACTA GCAATAATTA TAAAGATACA TCAAGAAGAC CAAGAACAGA TGCGTAACTG GTTGTCACTC TTTGGACCTG CCGGATATCA GCACATGCAA CCAATATCTG CTTCAGCAGT CCTCCCCCTT CTCGTTAGCT ATTGTGCCCAC CTTGTATTCT CCATCCGTTA TACAGCCAGC TCAGCACATC ATCCATCTAT TTTGAGCCCA TTCTGCTAGG CTGATGCAAT AGACTTCCAT	120 180 240 300 360 420 480 540

	CTCCCCCCTC ATMAANC	797
	(2) INFORMATION FOR SEQ ID NO:419:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 830 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1310UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:	
	GATCCAAAAA AATITTIAATA CIGAAAAAGA AATGCCACAA CITAAGCTCAG CTACCITIAAA	60
20	GAATCOOGAC CAAAGCIGIA AGGCAACAGC ICTICCAATG ITCOCTGCAG AACCTITGGAC	120
	CCGTCGGCGT TCATCATAAT CACCGTGAGC TTCTTCGGAT CAACGAACTC GCCCAGGACC	180
	TOCCOCCAAA TCCCACACOC GCTCACGACG TCGCACGACT CCCCACTCAA TGCCATGCAG	240
25	ACCCAATTCG TATGCCCCCC TGTTACCGCC TTTACGACCG CTGTGCGTTC CGCGCAAATA	300
	CCGGCTGGCT AACTGGCATT CTCGACGTTA GCGCCGACAA TATACTCGCC TGACGCTGTC	360
	AAGATOCAGC AGCCCACOGG GAACTTOGAG TIATOGOCTG TIACGAGAGCT CCTTCGCGGC	<b>42</b> 0
30	TAGTOCTOGA GCAACOGOOC COTGATATOG CTCTOCCTGT GTOCTTGOCA TTGGCTTCOG	480
<b>J</b> 0	TGGCGTCCCC TCCTAGGTAT TGGGGTTCCC CTAAGTACTG GCTGCGAACC CTTATGTTTT	540
	TTOCAGOGGA ACGAATTOCG COCGAACCOG GTGAATCCCG GGAACATNCA ANTACCCNCT	600
	TITICEVIENC GEGNAAACCG INVANVITCON INCITINECIC COCCUCGAAN AAANAATGIT	660
35	AACCATGIGG ANTAAACCIT TAANATGANN CCTATGGCCN GTTTAACTIT ATCCCCCCNC	720
	CCCCCCTTT AAANGINNNA NOCCCGCCNT TNIACCTCTA NNCONGCGG GGNGCNNANC	780
	CCACAAATAN TATGTTGNOC GONGNOCGIN NCTAATATGG AGCCTNOGGN	830
40	(2) INFORMATION FOR SEQ ID NO:420:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 799 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(V.) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1311RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:	
55	GATCITATOS TICACOSTAC OSTOTOCAAG AATOTGAGAC ATAAACTIGO GOTOOGACGA	60

	CITCHIGGIA AATICHIGGI AGIACIGIGC GHIGICCGCT TCCAACGCIT CCHICCCCCG	120
	CTIGIACAGE AGCTCCACCT TITICOGTOGA GAGOGGCTCT TOCTCGCCAG AAGCCTCCGC	180
5	GTCTAGCGGC ACCTCGTGCC AGGGCATGTC CGCAGGCACC AGAAGGTTGC CGCTGCGAAC	240
	CGACCOCACC TCATCGACCA TOCCOCCCC AGETTCCTCC CCCCCCGACT CCCCATCGAA	300
	CCCCCCATCG GACTCCCCCG CCTCTCCCCCC GCACTCCCCC GCATCCCTCT CCTCCTCCCC	360
10	TIGGICITICG OCTIOCICCI COOCTIOCIC CICOOCTIOC TOCTICIOCIT OCTICCICOCC	420
	TIGOTOCTOC ACCGAATOCT COGGCTOGCT GCTCTCTGCT GCTGCCGCTG CCGCTGCTGC	480
	CCCCCCCACC CCATGITCCC ACCACCCCCC TGACGTCGIT CTGCAGCCCG GCATCGCCGT	540
15	CICCTICGIC GCCGCICAAT GCCIGITICGC TGAGCICGIC TGCGTTCCCT CAGCCCTTCC	600
	ACAGCOCCAA GITGITCTTT CINAACCCCC CANNOCCAAT NGITCINCOGG CIVICATCCCC	660
20	CALIMITICS CLOSILLOSS CLLLOSINGN COCCUSONAN YCLLILLIGGG LOGGLINGIN	720
20	CAATTCCTTT TTCATTIGGT TTTCCCCCCCA AAATTTINAN ANNOGGITAN CINNICANIN	780
	NGCCNGNINIA GAGAAACCT	799
<b>2</b> 5	(2) INFORMATION FOR SEQ ID NO:421:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 790 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source: (a) Organism: Pagl311UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:	
	GATCTICTGA TOCATATTIC COCTCTCACC TICOCCGITA AGTITTTCCA TGTAGATAGC	60
40	TCAAAGICAT CATCCCCGIC ATCITTTICA GIGIATAGAT TCIGIGATAC TICICCTICT	120
	TOCTOTTOCT CITCTICCIC TTCTTCCTCG TCIATATGAT CITCGCCTGT CAGITCATTG	180
	TCTATTCCAT AATTGGGTTC AACTTTCGGC TTGGGGCTCCT TTTGCTGGCT ATGATCTTCC	240
45	TOGATACCTT TCTGTCCATC TGCCAATCCC GTTTTCTCAT CAGTACCTTG CGAACCGGC	300
	ACAGTATOGA TITGITTIGA GCTAATTOCA TIACTACOGT CACCATOTIC AACAGGTOCT	360
	TIGOCASCAT GACTITICOGA AGATITICGAG CGITTACCIG CAGSCGCACT CITACCCCGT	420
50	TTATCTOCAG GAATGTAGTC CTCATCGTCT TCATCTTCCT GTATCGTCTG TATGCCTCTC	480
	CICACGATGC CGCCCTTACG CTGTCCCTAC ACTCTTCATC ATCCTCCTCC TCATATCTAC	540
	CICTITICCA GICTICICCA CICATACTAT CICTACCACA TATCAGGATA ACGIATAATG	600
55	CHERCACTUTE TUTICCATACE ATCNETGOCE CHACGAANGE INCOGTICOG AATATAATTI	660

	AACATCTICC CAATCACAAA TINCICAGIA ACNGIGGIAA ATINAAACGN AANITIITAA	720
5	CTITICCATAC OCTITANCIAC CCATOOCTCT TGAAANCOGA AAAATCCOOG OCCCCCCTTN	780
	GAACTIGITT	790
	(2) INFORMATION FOR SEQ ID NO:422:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 788 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1312RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:	•
	GATCATTCTC ACCAGTACAA ATGTATATTT ATATGTAATT GTCTCTCTCT GCTTTTGCCA	60
25	TATTITITIA TITTITIGIGG TGACAGOGIG CACTGACGCT GACGCGCAAG CCGCAGGCGC	120
25	GATTCTTCCC AACTTTTCCT CAACCCCCGA CAGACAGTCA GAAAGTAATA CGAAACAATT	180
	AAATACGITG TTATGITATA TGAAGTTATA CATAAGTGGC TGCCATCAGG TTATATATTG	240
30	CITTAAATAA CCCATTCGTC TOGAAACCTC CTCTGTGAAT GCCTCOCTCA AACCGGGATG	300
	GITCTGITCG ATCTCCCCCA AATATTACIG ATAATTGATC TACACCGICT TTTGTCTCTT	360
	GAGTICCGTGC TCTATCACGG ACGCGTCGTA ACTGTAGCGG ATAACATGTT TAAAGAAGTT	420
35	TAGITOCITC TGTGAAGGAG CAGCAGCTIT GAGTGCCTTT TCATCATAAT ATTGITCAAG	480
	GTAGGAGAGG AGGTAATGIT TGTCTCTOOG TTCTTTGAAG GGCTGGATAA TAATGACTTG	540
	ATTIGTICACTO CTOGTICATOG TACATTTAAC ATGCCAATCO CAGTICCCAA GITAGATTCT	600
40	TACCOGUITT GUTATACCIT GUTINATAAG OGUTACTITG CNCCCCNACT TOCCAAGAAA	660
	TCATCTTATC CCTTTGANAG GICACCTGTC CCTTAATTGT AAACCTACNC CCTTTACAAT	720
	CIATOCITAT ACCONSCCAT TOTOCCIGAA GGATTTINIT ATTAACCCTG CNCACATCCC	780
45	TIGGCTGG	788
	(2) INFORMATION FOR SEQ ID NO:423:	
50	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 769 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1312UP	

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:423:	
5	GATCAGOCAA AGGATTTCTA CICGTATGTT GOCAAGAACC TGTCACAGAA ATCCGACAGC	60
	AAGITGCTIC CICGGAGGAT TCAATTIGAA CITCAGAGGT TIGACIATIT TCACTCTCTA	120
	CICCAGTATG TIGTAGGATG TAACOCTOGT GATTITOCTG TGTCACTTOC GAGGITTCAA	180
10	TCTTCGATCG ACCCTAATAA TAAAAATACA AACATCCACC TCGTGAAGAA GTATCGTTCC	240
,,,	CATTICITAC CATITAACAA GATAAAGAGC CAACAGCGCA TAAGGCTITC TAAAGTGTCC	300
	AACTATICIG ACTIGAATGA CITICTACCAA CITICCATCAG CTACCTCAGA ACCAAATAAG	360
15	CCCCCAAAG AAGGACTCTT ATGGTCCTAC AGGAATAATG GATGGCATAA ACAGTGGGTG	420
, •	GTACTACAAG GATCACAGCT CTCAGAATAT TCCGATTGGA AGACGAAAGC TAAGGTGCTC	480
	ASCOGACCOG CCATTAATTT GACGITTIGTG TGTGTTAAAC GTTCGGAGAA AAAGCCTAAC	540
20	GGATTIGATA TCATAACTAC CGACGGGGGG GCTCGTTCTT TCCAAGCAGA GTCAGAGGAT	600
	GAAATGAACC AGTOCCTGTA TOCCCTTCAC TCTCCTGTCG GGATAATACC CATTCACGAG	660
	ACAGATGAGA ACAAAGATCC ATTGTCTATT GTCCGTAATG CGGATCCGTC AAATAGTGCA	720
25	TOCTGTGACT GTCGGAGGGA TAAGCAAGTG AATGGATATC TCTGAATAT	769
	(2) INFORMATION FOR SEQ ID NO:424:	
30	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 799 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEDNESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1313RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:	
40	GATCCTICT TOCTGACTTC CATGICTACC TCAGTTCTTT ATTACCCCCC TCATGTTGAA	60
	ATTITICCAGG AACCATCOCA CCAAATGTAC CGATGATATA GATTACATCT ACCCTTCCOC	120
45	AAGCCTGGAA GGAAGCTAGA CCTCTAATCT AGTAGCTTGC CATGTACATC CCGCCATCCG	180
	ACCCGCGAAG ACCAGCCAAG GTGACGGCCG GCCAGCTCTG CGAGCTGTGC CACGCGCCA	240
	AGGCCCCCT AAGAACTTGC AGAAAGTCTG TAAACTGTGC TTCTTCCATG	300
50	TATTOGAAAC CGAAATOCAC AATACCATTA TOGAGAACAA GCTATTOCAG COCGOGGAGC	360
	GGGGGCAGT TGGCGCGTCC GGTGGGAAAG ACTCCACGGT GCTTGCGTAC ATATTGAAGC	420
	TOCTCAACGA AAGACACGAC TATOCTCTOG AGATTGTOCT TOCTGAOCAT CGACGAAGOG	480
55	CATTIGTISSET ACCGAGACGA TITCOSCTAGE TACTIGTISAAG CSCAACOCAG AGCAATTACGG	540

	TITOCCCCIG AGATIGIGIT CCTACAGGAC CICTACGAAC TOGACGAATG ACGAATAGIG	600
	CCTGCGCCCN GGAATGCNCA ACACTGCNCC TTACTGCGGG TTTTTTTGGAC CCAGCGCCTG	660
5	ATTCCCCCCCC GAAAAAAATCCTT GAATCCACCN NTTTGTTAAN GCCCATACCC GAAAAAATCC	720
	CIVAAACINGCC CANAAATCCT GOCCGGGAAA TITTGGCNAAT CNAAATAACN CTTTTCCCCA	780
	AANAGGICCC GNIAANNIT	799
10	(2) INFORMATION FOR SEQ ID NO:425:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 819 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1313UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:	
25	GATCAAAAAA GATACOGATG TTATOCTTGT TAAAATATTA TATOCTATAG TACAACGTAT	60
	COCGTCAAAC ATAACOCATG AGGACTATAT TITTIAATTCA CTAACTTOGG CGAAGCATCT	120
	CCOGAAGAAA TAGCCTCCTG TATOGGGCTA AGTCCATAGG CGTCGGTTOG GCTCATCTCT	180
30	OCACACTITA AACAATTAAG TOOGAAGOOT AGOOTOOCAT ACCCCAAAGG OGAGTGGGCA	240
	CTTTGTTCGA GAGATCCTTC TGACATAGCC TTTCTTAGTG ACAGTGGCGG AACATGGGCG	300
	COGGAAGGAA TACTITIGTOC GTGCAATGAA COCTOGGATA AAGGCCTACT TAGCCCGTIT	360
35	TIGAAAAATG TGACAGTCTT GITCTTGATA TCTAGCTTGT ACCTCGTTGG AGTGGGTTCC	420
	THICCAAGAC CAGTOCGITT THOCGAAAAG CHTCGCGICT TCCCCGAATG AAHTCTGAGT	480
	CCTGGTAGGG AACATCCGAG ACTTCCCAAA AACCNITTCN CTNICCATTT TCNAAAAAAT	540
40	GGAAATCINIC CCGGCCATTA TINGATCTCTT CCCAAATTAC INCINCCNCCC TCACTTTGNG	600
	ACTIGGENAT ANAGANCOCC NICHNACCCC TOCAAANAAA AAAAATTOTO NINGIGCCCC	660
	MINATTOCCC CCCGOGGCCN NVITTTAATT CNGGGGAATT AAATTTIGTA TOCKNGCNGG	720
45	TNGAAGCANG TTATNGCCCC CCCTTGACCC ATNITINACT TNITAATTITI TCCCCNNNCG	780
	GNIGGAAACT TIGOCCNAAAG GCANGCTTIT TGAACCAGT	819
	(2) INFORMATION FOR SEQ ID NO: 426:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 791 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi)	ORIG	INAL SOURC	E:
	(A)	ORGANISM:	PAG1314RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:	
	GATCCATAAA CTATCTTCTC ACTCGCCGGA TGCAAAGTAT CAAGGAATAG GCGACAATCG	60
10	GUARICATUG GCICGAGCIC ACGCAGATAT TGGCGCACTI CUGATATCCG TGGGITGTTC	120
	GATOCATGAT GCACATGAAT AAAAGGAAGA AGCTTCGAAA GAGGTACACG GCCCGGGTAG	180
	OGIGIGATGA GAGCTGITAG TICOGCTICA ACATCAGCAA GITTICICTAT ACGGGACGCA	240
15	COGTOGTORA CATCATTTAT TAGACACTOC ACCAGTTTGT CTGAAAAAAAA CGTGTGCATG	300
	CACAACTOCA CCTCATOCTT TGAGATGOOG COGATAACGT COCTCAGOGA CGCCAGTCTC	360
	ATOGTOCAAC TOCGTCAGAA AACTCTTGAT TGATAGOGTA ATOCAGTCAG AAGAAGTOGT	420
20	TAAAAGCACT TTCGATCCCC CAGTGAAACC TAATCCTCGT COGATATAAA ATCGAACGTG	480
	THAGCAACAA TOTHOCATAT COGGAAAGIG TITHACAAGC THOTHACGAT THICCACTOC	540
	TOGATTGAAT ACTOCOGOCON AATTCTTTTA COATATACAC CONVINCNOG GOTTTTGCAC	600
25	GAATTONITA TITGITGAAG AACTGGACAC TITGAAACTT TOCACATTOC NGANTOCGAA	660
	ACNOTITICN CNOOGAACTA ATNINAACCO CAATOCTGAC CCAATACACT CCCCCCCAAA	720
	CATGACCCCG CACANGATIN TITTTICCCN AGAATTINIT NAACINITIG CCCCCINANA	780
30	CATINIAAAT C	791
	(2) INFORMATION FOR SEQ ID NO:427:	
35	(i) SPOUENCE CHARACTERISTICS:  (A) LENGTH: 833 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1314UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:	
45	GATCHTOCTG CAGACAGATG CCGCGGAGCT ACCCTTTCGA ATCCTTATAT AAACCCTTTT	60
	CCASCTIGIAC COCAGTAAAC TCCCCTTCCT TCAGGAGCTC CAGGCTGCCA COCACACTCG	120
	AGGCCTACAC GOGTGACTGC ATTGGCTTCT GTGCGCACAC GGAAGTCTTA AACGAACCTC	180
50	ANTOCCATCO ANOCAGITICT GOTALOGTAG CTACTTOTOG COALTOCTO AGCCCCATAC	240
	CGTOGAGGCA ATCTITICCAA GCCACATAAA CGAAACCTAC ACAGTTACTG CGCAAGGCAA	300
	GTOCCAAAAG ACCACAGGTT CCGCAGTACC AGACCAAAAA GCTTACCTGT CAACACTTCG	360
55	AACATTOOCG TOGCCTTAAC CATATOCCAC ATGAAGCAAT ACACCCTAA AATAGAAAACC	420

GATTGGCCCG CAACAGACAT TCCTGGTGTT GTACTTGGAA CTCACATAGG GGCTGCACAC	480
TECTTAAGT CCTCGCTTGC AGCTCAGGCC ATGTGCCCCT CATTAGTGAC CCACGTTGAT	540
CTCGAGCCCG CAAATGATCG TCAGCGTGCA TCCGACTTGG CATTGCAAGG GATGTTGATC	600
CCCTGANGGG AGGCTTGCAA CAGCGCCNCC CTTGTTTCNC ATCCATAGGC TGTCGAGGCC	660
GGAATGATCC NCTCTCCAGG GGAACNCCCT CCCCAACGCC CCATAGGGCC CNCCCTGGGN	720
THITTGCCCGG ANACTCCMAA NCHINGGITTA AANHTITITI ITAAANGNCC CAGIGGIHTC	780
AAGGCCCCCN NGCCTTTTC CANCCCGCAN TENCTHAATT TTTGNCNGCG GNA	833
(2) IMPORMATION FOR SEQ ID NO: 428:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 839 bese pairs  (B) TYPE: nucleic acid  (C) STRAMDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DEA (genomic)	
(vi) ORIGINAL BOURCE: (A) ORGANISM: PAG1315RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:	
GCGGCCGCTC MNCCAACTAG TGGATCTTCA TTTGTGGCCC GGCCGACAGG TTACCACCGC	60
TTTTCTCTCC CGTCAGCATC TCAACTAGCT GCTGTAGCTG GTACTCCCTG TCGCCGCGGA	120
ACACOTTOCA CTTGTCTATT GCTGTGCATG AAAGATCGTG CAGCTGAACT ACATTACCGT	180
ANGTOATCAG CCCAACAAGC GCGTTGGGGG GCAGCAACGA CAGAGAGGTG ATGATCGAAT	240
CCTTCAGCGC CTGGAGGTTC TCCTCCTCCG CGGTTACGTC CACGACGTAG AAGAAGATCG	300
GCGCCACCTG CACCGGCCGA TTTGTGATGT ACTCAACCGT CGTGGAGTTC AGTTCCGCGG	360
GCATCGCCTC CTGAGACATG TTCGCATAGT GCTGCGGAAG ATGGTTCCGC GTCCCCGCAC	420
AGAGGGCACG CCCACACGTT CGACCGCACG TCGATCTCGC AGTACGGGTT CAGCACCCGC	480
CTTACAGTGT TOGCCCCACC CACACACCAC CCGCTTTGTT ACGARAACCA CCGCCCACCT	540
CCCTCCAATC TCCTTCCACC GCGTTGTTAC AGCATCCCCH CCGGCNCCAC GTTCCTTGTT	600
CHCGTTCCCG TCCGGGAAGC CCGGGAAAAC ATTCCCACGA MAACCGCACC CCHTTTAGTT	660
CTTCCTTCCT ETTTCGAANC CACCCTTGAA COGNGANCCA CTTTTANNCC CCTTTACCCC	720
CTTTGATCCC CNCCGAACCC CCHAAATGGA ACCAANNAGC CCNTAACHBN TGCHAAAACC	780
CANTICCCCM TITCARGGIC CCATOCITIG CCCCCCGNGA ANAAAANING NCCGCCCHA	839
(2) INFORMATION FOR SEQ ID NO:429:	
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 518 base pairs  (B) TYPE: nucleic acid	

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1315UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:	
	CATCTTGCGC AATATCCGCT CCCAATCCGT ACCCATCCAC TTCGACACTA CCGACTGCAC	60
	COCCAGOGTIC TTCATCOGCA CAAGCTOCTC TCCTAGGCTC AGCACGGCG GCACCACAAA	120
15	GTAGAACCOC COCGTOGTICT CCAGCTOCTC CCGCTCGTTG CGGAACGACA CGTAGTAGCA	180
	ATACCACCC CCTACCTACA CATCCACATC CACCCACC	240
	CASCAGATGC TIGITAAAACT IGITCCCCTG GAACTICGTA TICCTTTCCCG GCGGCCAGIT	300
20	GETCCACACT AGCCCGTCCC GTGTCACAGG GGATCCGGGG GCTACCACCA ACCGCACCGG	360
	CAGOCCOCTG TOCTCCCCAG CGTCTCOCCC AACAGGTAAA CATGGCAACG TGAGCACACC	420
	CITICCAACC TCTCCTCTCA CCGCCTCCCC GITGTCGTCT AATCTCAACA GCACGGTTTT	480
25	CATCGCTGTT TGCGCCCTTT GCTGCGATCT AAAGGAAGCT TGGCTTGTCA TGCAGCTGCT	540
	ACCCTICOCA ACTOCCATAG TCCTTTCACC TTGACOCCGT GITAAATAGT GCATTTCAGT	600
	ATACACAATT TGACTTACGN NCTCCCNCNG TGCTAACTGA GGGANATTAC CCNAAACCCG	660
30	GANGOCANNA TAACNONINA NAATTINCCC GGINGCACNC MIGCONIATG NITCCNITIT	720
	TOGAAANAAA COCTNOOGNN GGINOGITIGN NAAAAATTIGA AAACOCNOON TNAATACTINC	780
	NITINACNI'IN TOGGAAAACA AAANINOGGC CCCCCCCON	818
<i>35</i>	(2) INFORMATION FOR SEQ ID NO: 430:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 798 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1316RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:	
50	CATOCAATAT ATGCCATGGT CTCAAGGGTT GTCCACGTCA GTAGCTTAGC CAATACTTTG	60
	CCAAGOCGIC TGCGACATCA AGAAGAGTCT CAAGATAATA ATAGTCCTTT TTGGGCAGTA	120
	ACCGAACATT GTTCCTCCCC TTTGTCATTT CTCCCCGGTC CCTGGACCCA TTTGGTCCGC	180
55	TGTTGAAAAA GCGCCAAAAG TACTTCAAAA TGACCGATTT TTCGACCTGG AAACCTGCCT	240

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

	GGAGAGAGA GTOGTGCAGC AACGTAAATT CACTGAGAGA CAGCAGTGTT TOGATAATTG	300
	CAGATTCTTG ATTCTCCTTC GTTAATTTTG GGTACAATTT AGATGAGCTT AATAAAAATT	360
5	GTAGTGTCTG GACAGATGOC GATTCAGCCA ATAAATAATG OCTGATOGAT TAAATGATGC	420
	CASCIGCOCC AACTCATCIG CATTOOCTAA GGAACOCATT GATTICAGAC TATAGITATT	480
	OSCASCATCC ATGIACTITG TIGIACTCGA TCAGGICCTT CACTGAGACA CCGTCAGAAA	540
10	GOSTCACOGT CTCGTCAATG AGTTAGAGCC ATCCATAGAT TTCCCCCGAGG CAGTTCCCGC	600
	CATGAATITC CACCCACTIC CCCCCCGGTC CATACCGCAA TITGAACATT CCCGGTCAAT	660
	ACCITICTICC TOCCOCOGNI NITOCNICAAN AGGGAAGITA NATICCIGNIC CITITITITIN	720
15	AAAACCCAAT TONCACCTTT TONCAGAANT TTTCCGGGTT GAGNAAAANT CONACNCCG	780
	GINGCOGGIT TAATINCC	798
	(2) INFORMATION FOR SEQ ID NO:431:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 820 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1316UP	
30	(A) ORGANISM: PAG1316UP	
30	(A) ORGANISM: PAG1316UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:	
30		60
30 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:	60 120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431: GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC	120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC  CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC  GGGCTCCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAGCAAT	120 180
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC  CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC  GGGCTCCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAGC GCGCAGCAAT  GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGCCAGC TGCAGCGTCC GGCATGTGTG	120 180 240
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC  CATTACATCGG CACCCATGCA CCCACATGAT GGTTTTTCTTG GCGGGGCCAG CGGGCTGGGC  GGGCTCCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCCGCT GGGCGGCCAG GCGCAGCAAT  GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGGCAGC TGGAGCGTCC GGCATGTGTG  GAAAATTTIGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT	120 180 240 300
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC  CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC  GGGCTCCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAG GCGGAGCAAT  GGGCGGAGGA ACAGCCAGCG CGCCAGCAGC GGTGCCGCAGC TGGAGCGTCC GGCATGTGTG  GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAACAG CACTTCCTGT  AGGTTTGAAC ATACTATACA AGCTCCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA	120 180 240 300 360
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431:  GATCAACACT CGTACAAACE AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCOG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCG GTCTACCCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCCGAGGG CGCCAGCAGC GGTGCGCAGC TGGAGCGTCC GCCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCATTC ACCAGAAAGG	120 180 240 300 360 420
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATTACATCGG CACCCATGCA CCCACATGAT GGTTTTTCTTG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCGGCT GGGCGGCCAG GCGGAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGGCAGC TGGAGCGTCC GCCATGTGTG GAAAATTTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTICAAC ATACTATACA AGCTCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCATTC ACCAGAAAGG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC	120 180 240 300 360 420 480
35 40	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATOGG CACCCATGCA CCCACATGAT GGTTTTCTTIG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGGCCAG GCGCAGCAAT GGGCGGAGGA ACAGCGAGCG CGCCAGCAGC GGTGCGGCAGC TGGAGCGTCC GGCATGTGTG GAAAATTTIGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAACAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCAAT CATCGACGAT GGCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAAGA AGAAGGTCGT TGACCCATTC ACCAGAAACG AATGGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC AACAGTCCAC CGTTTGAAGA ACGCAGCTNA CTTCTTGGAA GGGCNNTTTC TTCAAGGTNT	120 180 240 300 360 420 480 540
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO: 431:  GATCAACACT CGTACAAACG AATATAGTCA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATCGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCG GTCTACGCTG GGCGGTGTAG GCGGCCGGCT GGGCGGCCAG GCGGAGCAAT GGGCGGAGGA ACACCCAGCG CGCCAGCAGC GGTGCCGACC TGGAGCGTCC GGCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT AGGTTTGAAC ATACTATACA AGCTCCCAAT CATCGACGAT GCCTGTTGGT AAGAACAAGA GATTGTCAAA GCGCAAGAAG GGTTTGAACA AGAAGGTCGT TGACCCATTC ACCACAAAGG AATCGTACGA CATTAAGGC CATCCACCTT CGAGAACAGA AACGTCGGTA AGACCTTGTC AACAGTCCAC CGTTTGAAGA ACGCACCTNA CTTCTTGGAA GGCCNNTTTC TTCAAGGTNT NGCNTTGGCC AACCANCNGG TTCNTAGGAT TNNCNCTTCC NAAAGGTTCA ATTANAAATT	120 180 240 300 360 420 480 540 600
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:431:  GATCAACACT CGTACAAACG AATATAGICA CATGACCAGA TAATCGTCGT GACTGGCACC CATACATOGG CACCCATGCA CCCACATGAT GGTTTTCTTG GCGGGTGGGC CGTGCTGGGC GGGCTCCCCG GTCTACGCTG GCCGGTGTAG GCGGCCCACC GGGCGGCCAG GCGGAGCAAT GGGCGGAGGA ACACCGAGGG CGCCAGCAGC GGTGCGCCAGC TGGACCGTCC GCCATGTGTG GAAAATTTGT AGAATATAGC ACTGTTATAC TGAACAGTAT ATAGAAAGAG CACTTCCTGT ACGTTTGAAC ATACTATACA ACCTCCCAAT CATCGACGAT GCCTGTTGGT AAGAACAAGA GATTGTCAAA GGGCAAGAAG GGTTTGAACA AGAAGGTCGT TGACCCATTC ACCAGAAAGG AATCGTACGA CATTAAGGCC CATCCACCTT CGAGAACAGA AACGTCGGTA AGAACTTGTC AACAGTCCAC CGTTTGAAGA ACGCACCTNA CTTCTTGGAA GGGCNNTTTC TTCAAGGTNT NOCNTTGGCC AACCANCNGG TTCNTAGGAT TNNCNCTTCC NAAAGGTTCA ATTANAAATT TACAGGTCCC NGGGCAAAAAC CCTTTNGACA CCTTCCCCCG TTTGGGATTC CCCCCCCCNA	120 180 240 300 360 420 480 540 600 660

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	(2) INFORMATION FOR SEQ ID NO:432:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 807 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1317RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:	
	GATCTTTATC TTTCGATGAT ATCTTTCCTG AAGAATCGAC AAACACCTGG TCCAGCAAAT	60
	TOGAAOCTAA GTCTCTCCAA TOOGATOCAA AATAGTTGAC ATACOOCOCA TTTAACTTCA	120
20	CTAACCGGGC GGCACCAATA TOCTCCAGAA CTGTATTTAT TTCGCTACGC TGAACGATTT	180
	GITCAATCAG CGTAATATTC GICAATACAA AGAACCCAAT TCTCTGCATC TGAGGTATCC	240
	TITITATGIGG AGCTCCGACT TCGGGCTCTA AGTTTGGATT TAGAATCTTT TGGGCCTTGC	300
25	GCTCTAGAGA TATGGTTAAG TAATCTATAG CATCGCTGAA GAAGCAAGAG AGCAATTGCT	360
	GIGCATTCIT COGIGICATA GATATOGICC AAACATTTTT TGATTCATTG GOCAGCCATG	420
	ATTCGCGAGT CATCGATTGT ATAGTAGCAA GGCAACCAGA CTTGTATTCA CTAAACTTGC	480
30	GTAGTCTGGA CATAACATCA ACTGTGGCCT CCAGTTACAC CATTATCAGT GGTAACTGAG	540
	CCCAGAGAAG COGTTTTTGA CCGATGTACT TGINTCNATC TTTTTGAACA NOGACNOOGA	600
	AATTICATIT CANGICNOOC INCNONCICC CAAAACNGIT CONIGGITCI NGIAAAGGIT	660
35	TINOCCTARA ARTNOCCNIT COCNIGINAG NITOCCCCCC ARTICNARCN NAANACOCNA	720
	TTTTTIVIAAT TCCCCCCCA AAATTCAATT ATACCCCCCN TTTTIOGTAT TWIAAATTIN	780
	GGGGGNCNCN NITICCAAAAA GGNGCNG	807
40	(2) INFORMATION FOR SEQ ID NO:433:	
	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 835 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1317UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:	
	GATCGITCIT ATATTICTIA AAGAAGAGIT TICITCAAGC ACTITGAGCT GAATAATCIT	60
55	GTCAAACATA TIGICAGGGC TCCGCTGGTC GTTAACCGCG CGAAACCTCT TGAGGAACCC	120

	ATCTAAGATC ATAATTOCCT TTTCTGCCTC CGATAAAGCT TTAATAGATT GATGGTTGTC	180
5	CONTINUE COMMISSIONS ATTRIBUTAT THETETAMOR CATTOCACAT CONTINUAMEN	240
	CAAAAATGAT AAACACAGA CTTTGACTOC ACTGTTGTAC OGAATATAAT TCTCCTTCAT	300
	CTTTTCCAAC CATTCGAAAA GTTGTTTCCG CTCGAACGGC ATATGATTGT TTCTGTCCAC	360
10	AATTACAGCT CITIGAAGTAT CCTTTTIGTAG AAACTCTAGC GCGTCACGCA TCAATTTIGCT	420
	CTTATCCTTA GTAACAATAT TATCATTCTG TATGTGGCCC CAGGACTCTC CAAAAATATT	480
	CTTCAATGCC AGCGCGACTG TCGTCTTTCC ACAACCAACC GTGGCCACAG GGAATGAAAA	540
15	TGAACTTOGT ATCTCGTCCT ACCTTATCGA GCTCCAGATG CATACTGGTC CCCCCNAGCT	600
	CCTTTATATC CTCCCAATTT CCATAATATC CAATCCCAAA ATCCCCAAAT CWITCCTACG	660
	AANATTITOO NINACINGAA ATOOCOTTAC CITIGINIATA OCCOCTIONAA ATTINOGATN	720
20	TIGATICONG CCAGGGANIA CNATICCONA TITITINITIG IGANNAACAA NGCITITIGAA	780
	TTTTIGICCC CNCCCNCIGI GNANIACCON CCCICCICCC CCCCINITIN TIACN	835
	(2) INFORMATION FOR SEQ ID NO:434:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 748 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1318RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:	
	GATCGCCTCG TCGTTCGCCC GGCTCGTCAG GCTCTGCGCA AGGAACTGCC CGAACCGACC	60
	AACCAAATCT GGCATGTCCT TCGCGTAGAT GAAACCCTGC TGCTTGCTGT CCACCGCATC	120
40	CCACACGTTG TTCAGAATAC CCTCTGCCTC CGTCATGACT CCTGAGCGGT GAGTGCAGTT	180
	CCCAAGGCTT TIGTIGIGCT TGGCAGTTGA AACGACGCTC GCAGCGGCAA AACAACACCG	240
	GCCCCGCCGC AATTIGCTCAC GTGCCTCCTC GCGCCACATA AGCACGCACA CCCTGACCGC	300
45	ACACOCACCC TOCAAAGTAG GTCATCACCA AAGGGGCACC CCGCCTGACC GTTGCCTGCG	360
	TCGASCACC GCCCGCCACG CGCCAACGGC CACCAGCATG CGCGTTCTCC GTAGCCGCCG	420
		480
50	OCOCCUTTOG CCATCOCCGA AAATACCTCG GTTTGGCCCA CTGATGCCGT CTGCCGTCCG	
	CCCCCCTTGC CCATCCCCA AAATACCTGC GTTTGCCCCA CTCATGCCGT CTGCCCTCCCC	540
		5 <b>4</b> 0 600
	CCOCCCCCCC CCCCCCCCA COCACCCCCC CCCCCCCC	

	CTATTTACAG COCACTTAGG NGTTGACC	748
_	(2) INFORMATION FOR SEQ ID NO:435:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 758 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	,
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1318UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:	
	CCAAAAAATG AGGTCCGCCA TGCGCGGCGG CTGGGGGCGC TCCGGCGACCA AGCTCCGCGG	60
20	CCCCTCCCCC CCCCACAGCC ACCAGCTCGC GCCTGCGCGC TAGCTCGCGC CCATCGCGCA	120
	GICCOCCACC GCCCCCCCC CCCCCAAACGT CCACATIGICG CCCACCACCT TCTOGICGAG	180
	CACACOSCOC COSCACOTOG COCCOCCTOG COCCOCCOCC GOCACCTOGC GCTOTIGGGC	240
25	AGCCAACTOG CCTGTCATGA ACAACGCTGT AGGAATGCCC ATCTTTGCCC TTTCCGCTCG	300
	CTOCCOCTGT GIGTGTOCTA TACOCTGCCT TATATACCTG CCAGGAGAAA TGTCTGCTAC	360
	TATCCCCCCC AAAATATCCA TCCGATGCGA ACGGCGGAAC TCGCCGGAAA CCTGGAGCCC	420
30	COCCICTOTIC GATCOTATOG AGAAACAGCT AAAATCOCTC AGCTACTCAT CTCTOOCGCT	480
	GIGGITICACG GICGCCGCAA TGCCGGCGCAT GCCCCAAGICC GITTITITCIC TGIGGCCGGG	540
35	CCAGGGAGAG CGGGGCCAG ACGGCCAGAT TITIGIGCACG GCAGACCGCG TIGGCTGIGG	600
00	TAACOCCTAT CAAATACGGG CAAGCGGCGA TTACCAGTGG GTTTCGCTGT CAGGGGTGCC	660
	10000000G GAACCOOGTT ATGGTCTATA TTACAGAATG TGTACAAAGG AGTCACGTGG	720
40	GGGGGTCGC GGGCNGCACA GCTGCCTCTG TTTCTTCC	758
	(2) INFORMATION FOR SEQ ID NO:436:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 801 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1319RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:	
55	ولاحليكيان بالبالطالية وليابيان الماليان الإقالية الإيانية والمالية والمالية المالية ا	60

	GAATGICIGT TAGCAGITICC TCTICCTGTT TCGGTTICTT CCTGTTCCTC CTGCCAAGAT	120
	GCAGCATCGA GITTTGCTGG ATGGGCAAGA AATTAGAATT GATATCGCCG ATCCCTACGA	180
5	AGAAATOGTA CGGCACAACC TTAATGAGAT TCTCGCACCA GTTCCAGACA TCACCTCTAT	240
	COTCAATGAC TACGACCATC GACTOGTCCA TCCCGAACAG ACCCTCGAGT GATTTTTCCG	300
	TCAGCGAACC GITTICATCG CGIGACAAAA TICTATCOCC AAAGAGCITC CCATCCGGGT	360
10	CAATTATCTT GGCAATCTCT ACCOCATAGG CTCGAGTAGC CATGGTGTAT ATATGCAGCT	420
	CGAAATOCOG COCGATCITC OCAAAGAATT CCTTCAGOCC TOOCCGTAAT TICACGTTAG	480
	TACCAACACT TOCOCCOTTG GTTGOCTTTT GOCCCCCATA TAGAACGGCG GCAGCACAGC	540
15	TOCTOCATOC GANAGANAAA AACTOCNCAT COTTAGOOCC COGTATTOOG GITTIGTITING	600
	GITCCCTTTG ACCACTCCCC CATGGTGGGT TCACACCCGC NATINGATTCN COGTCTGGTT	660
	CAATITTACC CCCAGCATNG CTTGCGCNCN TCCNNNCAAC TTTGACTGCN CCNCTGACCA	720
20	AAATOCAACT TOCNITOGAC CCGATTIGIT TITTINITIG AAACGNNANT TOCINGICNN	780
	CITIGGENOCC CNCTITICCON A	801
	(2) INFORMATION FOR SEQ ID NO:437:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1319UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:	
	GATCATOGGC ATGCTGGAGA ACCCAATTIT CCAGTCTCAG ATGAACGAAA TOCTCAACAA	60
40	CCCGCAGATG ATCGACTICT TGATACAGCA GCACCCGCAC CTGCAGGCAA TGGGCCCGGC	120
	GGCGCGCAA ATGCTCCAGA GCCCCTTTTT CCGCCAGATG CTCACCAACC CCCACATCAT	180
	TOSCCAGATG TCTCGCCTGC AGATGGGCAT GGGCGGTGCG GGCGCCCAGC AGGGCACCGA	240
45	CTTTCCAGCC CCCGGCTCCG CCGCCACACC CGACGCCGCC GCCCCTGCGC CGAACCCGTT	300
	GOCTGCCATC CTAGGCTTGC AGCCCGGCGC TGCTAACCCG CTGGGCGCTG CGCCCGCAGA	360
	CCGCGGCCTT GCAATGCCCC CTCTAGACCC GGCTATGCTC TCTTCCCTCT TCGGCGCTGG	420
50	GCGCTGCCAG CCCTGCGCCC GCCGAATAAC AGGGCTNCCC AAGNANGNON TANCAAACAA	480
	ANATTOSCCC ANOCINAATN AATTNOOCCN TCTCCAACTT GAANAAANAT TTCCCCCTT	540
	NAAGCOCNOG AAGATGITCT NICHNOOCCG CCCTTNIATT CTTTNNIAAA GGNAAANTIN	600
55	TAGGICANGA NITNICTOCT NONVOCCOG NOGICCCCGT TITINITIAT TCCCCNI'INT	660

	TIGINITOTO CMINCIGNIT TOCNACCOCCA CNCAATITIT TITINOGTOOG GOCTINCOMIN	720
	TTTTCATININ TINCHANNAC CACCAVIRATT ATANTTGINI ATCACGICCT MITTINITITT	780
5	NNCCNACNON TROOGTTOCC CCTTINANNT GAGGNTGGTG TAGGGAAAGA AAAT	834
	(2) INFORMATION FOR SEQ ID NO:438:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 791 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
4.5	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1320RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:	
20	GATCTTTTCA AGAAGTTTAA CAATGACTTT AAAGCTAGCA TTGATAAAGT ACTCAAGAAA	60
	CCTAACAGAG COGAGATGTA TGATOCTCTT TTGTCAATTA ACGTCCATTC TAACAATATC	120
25	ACCITCOCCAT TGAATAGACC TATCTCCACT OCTAATTOCT COTTAAAGAG ATTTAAGATG	180
		240
	GAACGIGCIG GIGITACCCA TGICTIGAGT ACCCITICIT ATATTICIGC TCIGGGTAIG	
30	ATGACAAGAA TTTCTTCGCA GTTCGAAAAA TCTAGAAAGG TTTCTGGTCC TAGAGCTTTG	300
	CAACCCTCCC ACTICCCTAT CITCTCTACA TCCCATACCC CCCAACCTGA CCCCTCTCCT	360
	TOGTTAAGAA CTTAGCATTG ATGACACATA TTACCACOGA TGATGAAGAG GAGCCCAATA	420
35	AGAATCTTIG CTACTIACIG GOOGITGGAG AACATTACAT TGOCTAAANA ANGGCNCCCT	480
	TOCTTTTAAA TNINGGOGGI TITATITIGGA AAGGGIACIA COOCCOGINC ACAAAATCCC	540
	CCCCGNGITT TIGITCCCCC TTTTAAACIN TANAAAAAC GNGIAAATIT CCNNATITCT	600
40	TTTCCCNVIN TCCCAANINC CTCAAAACTT NITCTTTTGC AAGGAGGGG GAAATTININ	660
	ACCCCTTINI TTININGGAA GAGAATTTT GTCCCGGNGG CCCCCAAAAA TTTTTAAGGG	720
	GAANICNITA NATICCCNAN NGGGGVINNI AATTITIGGN TITTANAAAA AAANCCCCCC	780
45	CONCOGNIAA A	791
	(2) INFORMATION FOR SEQ ID NO:439:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 844 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1320UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:	
	GATCATIGNOG GAATCCTTIGG ANGAGGATGA CAAGAAGTICC GACGATIGAAG GTGACCTIGTC	60
5	TATTCCAGAT GCGCCTTCCT CTGAGGAGGA TTAGGCATAT AATGGGTCGT TTATATGTAC	120
	ATTAATTAAC ATTCCCCTTT ACCTTTTTTA CICTTATCCT TACCGTACCT CACCCATATC	180
	TGTAGCCCIG CTCAGTTATC ACTAAAACGA GTGCCAGGCC CTAGTACTAT ATAATCCCGA	240
10	GTTCGASCTG AGAAACAATG TCTGATTCGG CTGGTTTGCA TGGGAGTACC GCGATGCAAG	300
	ATCCAGATAG CACTITAGTC GAGGAAAGGT TGGCGGCTAC GCCAAAAGTT ATCAACAAGG	360
	TCAGCAAGAA AGGITCAAGC CCCCTTTCAG TGTTTAAGTT TAAAGAGGGG AGCCTATCCT	420
15	GCCNAAANIG CGCCAGOGIN CNIGAATTIN GGAGAAAAAA NIGCGTTTIT TCCGGAAAAG	480
	COCCCCNIGA NNCCAAAATT TATTNOOGAC OCNCNACACC NCGAGAAATT INNITNAAGN	540
	OCOCCCTITA AAATNOCCAA TNICTTONAA ANNATTIGAG GNOGAAAGAC ANITTNITTIN	600
20	AATINOOCOG GOOGINITIT TIGCCGCCCC GGNGNICNIC CONCCICCAC NANITINAAA	660
	NATAGGAGGA ANGOGNOGNG GCCANATTIC CACCITICINN AGITINGANING CCNGNAAANA	720
25	GNVIOGATON CCACCAATING OGGIGNINGA AAANANINGN NACIGOTIGI ACACAAATIT	780
25	TTTTGTOCCG CNOGTGACAG AAAAAAAGAN GGATTTTTTIN ACAACCINNAA AAANAAAAAA	840
	AAAA	844
30	(2) INFORMATION FOR SEQ ID NO:440:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 788 base pairs  (B) TYPE: mucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1321RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:	
	GATCACGICG TICCIOGACT TICTATOGIC GACOGIOCIG TICTICAGCC GOGAGGCGAT	60
45	ACGGCTGGCG ACGCTGCGCA TCAAGACGGG CGGGGACACGGC GGGCGGCGGCG GCGAGATGTC	120
	TOCOGAGCTG CAGACOCCCC TGAATTTTOC AAACATACCG ATGTGCATCG GOGCCCCCCT	180
	GOCGGTGGTG CTGOCGGTGT GOCAGTACTC GAACCTCAAC ACCTACTTCA CGCAGCTGCC	240
50	GITCTTCTCG TOGTCCATCT ACCTTGTOCT OCTGTCCATC CTGGCGCAGC TCGCCAGCCA	300
	GCCGCTGTAC GTGGTGAACC AGTTCATGCT GAACTACCGC AAGCGGTCGC AGTTCGAGGG	360
	TOCOSCOGTIA OCASCOSTOCT GOCTOGTGAA CTTCOCOGTIG ATCTIACTOGT ACCAGAACTIG	420
55	CITICAATOGG COCCOCACAC CICCACCACA CCTACACCCA CCACCCATCG COCTOCTTOC	480

	TITTINCCCCG GGGAAGGIIG CCCCCNCCAA AACTTINCCT GGCCCCAVICT ACTIGAANAA	540
	CTIOCONCIC TOOOCCCCCA AAAACITTIT TCCCITTNIT TNACAAGTIC CTITTCCOGN	600
5	NATITITIAC GOGNI'INITO CNOCCCONAAT TINITOCCCC TICCNAAGGI TITITOCCCC	660
	INITINITIA NOCONOCTIN NCAAGGGGGA AANNITITIN CITOCOCCINC COCGGGGAA	720
	ANDOSOGANT TICCTTITIT TITAAAAAN NCCCCCCCOA ANONITIINN CCCCCAAGAA	780
10	NATTITIT	788
	(2) INFORMATION FOR SEQ ID NO:441:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 815 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1321UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:	
	GATCGAATTC GATTTCCTTT COGTOCAAGG AAACAGAGCC TTCGTTAAAG TOOGATACGA	60
	AGACCGTGCC CAATITTCGT CGGCCCTTTC TACATACATC TCAAGCGAGG AACTTAICGG	120
30	CGTGCCATTA GTGGTCCATA TATTGCAAGA ATGTACAAAG TTAGAGAGGA TGAAGGTTGG	180
	GGAGGACGAT GAGCTATOCT TCAAAAGGAG TTTGCAGGAA NAAGTANOOG ATTCCAGTTG	240
	TAATTAGCTA CAAAAGCGGA ACGGGTCACA CTAAAATTCC ATGCGCTAAC TTTTCCACTG	300
35	AAAGAAGCCA CATGAAGCTT TTATATCTTC TGGGGCTCCT CTGGGACGCT TACACGTCCA	360
	GAACTGTTC CCAAAATTCC TCGACGTTTT CGAGGTTTTA AGAACCGATC GGTCTCCGTG	420
	CTTGCAGAGA GGTGCATTTG ATGGGGGGAA AAATGGTTTT TCAACCGCCG AGGGTGGTTG	480
40	TICAGGAGCT TIGITAGTIC GAAGITGGAG COCCATICCA TIGATIGCCC CITGCTCTIC	540
	CTCCCTNGCA CTTGCCGCTT GCTGCTATGT TTACTTACTA NAAGCACCGA NCCACACTTA	600
	TOTOGITTITI TITTICCTATO CIGANACICO CITGAATTAT TOCCIOCITT TGACTITICCO	660
45	CCTGTTCCAC GTTNGTTACA CNITTCCTTT GAATATCTTT CCTTTCCGAA GCACCCATNT	720
	TINIANTIAG TOCTATIGAC COCCCCACC TOGITTITIGI TITICCTOCCA ACANGITICTC	780
	TICTCCACTN AGNITTGTAT ACNGAATGTC NACCC	815
50	(2) INFORMATION FOR SEQ ID NO:442:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 773 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1322RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:	
10	GATICCAGGAA ATAGTACAAC OCCCTTGGAT AATGCCAGGG ATTCCTGACT CCTAACGAAA	60
	ASCUTUTOUT CITUTAATIT CTTATTAAAG TAGITAGCIG CAAACIGIAA CAAATCCCCC	120
	GOCCGICTIT GCTCCACTIC TTTCTGCAAT GCGTCCAGTA GGTCACGGTG TTCCTGTGAT	180
15	AAAACCATCG AGTAGTTTGT TGTGTGATGC AGAAAACCTG CCTATAGCGG AACCAAAATG	240
	CTCTAGTAGT GTGACGSCAC OGTTTTATOC AGTTTGCTAA GCAGCTGCCC TAGGTTAGGG	300
	AGAGTAGAAA GIGICATTOG ACCCGAATTT CCTTCTOCOC GCGGCGAACG ACGTTAAATG	360
20	TGATTCACGT GATCACCCTA CTGCCCCTAA CTACCAATTG AGACACCCTA GTTGTCCAAG	420
	CCTGAGGAGG TCTCCCGAAAA GCTTGATGTG AGGATACTCG TGTTCAGTTA TCTTGTATGC	480
	CTGTATTGAT CTGTCCGTGA GACCTCGAGC TCTTCGTCCG TCAATGCCCC GCGCCTAGAG	540
25	ASCTAGGITG ACTOCCAGIT CTACAAAATT TONAAACNOC TTGAAAATTC NCAACATTGT	600
	TNTOGACCAT CNANTICCCC NCCTTCGGAA NNAAGCCCTC CANCCTTTTT TNACGTTCCT	660
	NACTINECCN CIGAAAAAAC GITCNATTIA CCCINTINIA CNCGGCAGGA AACCCCCCAN	720
30	TTCTTTTTCC ATNAACCOGT ANCINAAAGA ATTTTCNNGC CATGNOGTTT ANG	773
	(2) INFORMATION FOR SEQ ID NO:443:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 817 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1322UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:	
	GATCITCACA ATCCACCCCA CGTCCATCCC CATGITCCCC CCCACTCCCG TCACTGTCAC	60
	ATATICGIAC GGAGAGACC GGIACGIGIT GATCATGAAG TIGCGCACAT CCTTGTACGC	120
50	TTTGGCCGTC TTGAACCGCA CCCAGTCGTT GAAAAAAGTCG GGCAACGCGC GACGCTCCAG	180
	CTCATGGATC TCGTTGAACT GGAACCAGGA GGCAAACGAC GGCACGATCA CCGGGTGCGC	240
	CTGCTTCGCT AAGAAGCGCG CCGCCTTGTC CTCCAATTTT TGCGCCTCCT GCTCGTAATC	300
55	GATCTIGGGT TGTTCCTCCT GCTGCTGCTG CTGTTGCAGA TGTGGCAGCA CAGGTACAGA	360

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	TOOLSTEALS CIRCLOSEST TOCCCOMEGA MARCETTICA TOCCCARGEST TESTCARTATT	420
	OCCATOCTOG ACATOCATTIC OCTOCCTCAT CGITATAAAG AGTATOCCAC OCTACTITICC	480
5	CCGITTAATA OCTTICAAAC OCGICITCOC TCIGCTACCC CGCTTAANIC CACACTGGTT	540
	TWIGHTICC NCCATACCCA AAMITITAAA ACCCATTIIT CCACATCAGC CCCATATCCT	600
	CCGITTOGIN GNOGARATTT GARACCCANC CCTCOCCTOG COGRARANNC INCITATOGA	660
10	CCCCCTTCCC MICTICAAT COGTCCCCTT NACCAAGNNT TTAGCCCCCC OGNANANGAC	720
	CAATINGGIC CTICCGICNC TITCCCTINI TAAATIGAAA AAGGIINCCC TITGAAAATT	780
	AACCONGCCC NONTCCCCCC GANAAATGGT TTTTTGT	817
15	(2) INFORMATION FOR SEQ ID NO:444:	
20	(i) SPQUENCE CHARACTERISTICS:  (A) LENGTH: 759 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1323RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:  GATCAGTITG CAGGGACCAT GAGCAGGGGG GGGGACGAAA GCAGCTCTCC TTGGTACACC	60
	TOOGTOCAGG GOCTICAACAC GOCCTOGCAG GOOGACGACG ACGAGGAAGA GGAAGATGOG	120
	OCACCETTIT ACATCCATCC AGATTIGAGE ACATCACAGC TCTACTITGA GAAGATGATC	180
35	CATCAACACC CCCTCCCCCC GCCTGTTAAG CCCGTGTTCT ACATTAATCC GTATGGAGAG	240
	GAAATTTTCC CTGTCGCGAA CTCTCGGTCT ATCCACCAGC TGAAGCGATG CGATATGCTT	300
	GIGIATICCA TOGGGICCIT AATTACCACC TATIGCCATG GIGATCCTCC GGIACITGCG	360
40	AGGIGGICGI CCAAGGGAAG AIGAAAAAAT GCTACIGGIC NCNCCAATCA AINNCNAACC	420
	TCCGATTAGG GOGGGGGVF TNITTTITTA ATTTIAACCC CCCTTTGGGG TGACCCGNC	480
	NAAAAAAAAG GOGOCTITICAN INNAITITITIT INCANCOCCOC CINCCINITICG GIVACANITITIT	<b>54</b> 0
45	TTTTCTGGNG GOGGGCCCC CCNNNCGGAA AATNITININC AAAAGGAAGN ATTINCCCCN	600
	NANGGGGANT TTTTTTNTTA MNAAATMNAA AAAAAATTINN TICCATTCCC MNAATTINNN	660
	NITTIINNIN CINIINCOGN TIIGNAANII NACCCCCCCCC NANAANIIIN NITTIIICCC	720
50	CCCCCCCCC CCCGGCNNN INCNITITIT TIMMGAIN	<b>7</b> 59
	(2) INFORMATION FOR SEQ ID NO:445:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	

(D) TOPOLOGY: linear

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1323UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:	
	GATCCGTTTT TCCAATATTT CACCGTCCTG TAAATCAACA GTTGAAAAAC AATCGCGTCC	60
	TTAATCGACG AACGCAGCAC AACCAGCAAT AGGCTTCGAA GCCGTTCCAG AGGTGATATC	120
15	OCAAAGITOC TOGAGCACTA GAACOGACTG GGTCATTATA TAGGTGGTAG TAAGAAGTGG	180
	CTAGAACGAA CCCCACTATG CTACACCCCC CCCCTCCACG CACCCACCCC CCACTCCCTC	240
	CCCCTCATOG CCATCCCCAT ATCCCCCAGT TGTACCAGTT CGTTTACAAC CCCCCCCCC	300
20	TOOGGACGTA GACGITTACT GCCGGACCTG CCGCGGCACG GGACGCTTGA CCCGAGCAAT	360
	GITGIGIGCA COCTAGIGGA GCIGITACCAC TCGATTCCGG GCGACATCCC GCTGATTAAG	420
	ACGCATTONA TOGOCOGTOG GIGINICIGA NONAAGITOG ACCONOGAAC CIGATIGITT	480
25	TGTGGCNAGA ACACATNOCO TTGTTGGTGG ACCCACCOGA NAATTAAACO GCCCCNOCAA	540
	GACIVACCOCC CCTCCCCCCN CNOCCTTTGG GTINNNOCCA TINGTCCCGGA CNTCCCAAGAA	600
	NITTACINGC ACCONCOGNE GCACCOCCON COGGOCACIT NITICAACNC CNITCCCCCC	660
30	CIVICESSEGGE NCCCCCCCTT TCAAAAANNE TGESSEGGAC CGGTTCGGGT CCCNTTCCCC	720
	CCATTCNATT TTINITTANA NANNACCAAC CCCCCTCCCT INNCCCCACN CAAANNINGT	780
	THEITAANCT NCCCCNITAT TCTNCCCCCC CGNCNCNTAT TCCCNACCCCCN CNET	834
35	(2) INFORMATION FOR SEQ ID NO:446:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 785 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1324RP	
45	(A) CAMILLY. PARTIENT	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:	
	GATCCTACCG GCATGCACGA COCATACAAG TATATCAGGG ACCTTGCCGA GGAAATGGGA	60
50	CATAAAATTG AAGGACCAGA TCACAATTGG TCGTTCCTTA TCATAGCCAA GATATATATA	120
	TATATCTOOG ATAATTACAG COCTTOGTAT GTATACCTCC TACATACAAA TACTTACATA	180
	CACATAAATA TAATACAOCT ACTIGTAAGG CGAGAAAGGI TACTICTOGA GAGCCATTAG	240
55	AGACOCAACG AATGTCAAAA TCAACCTCGG GCGGACTTCA TTGATATCTT CAGGAACCAA	300

	CCAGATTAAA GCACCAAGTT TTCTCGCGAT AGAAATTGCC AATTTAGCGT TTGCATACTT	360
_	CTCTTCCTCT GITACGCCCG GGAGTAACCA AGTCATAATC CACATATCCT GCAGCTAATC	420
5	CGTTCAATAC ATCCAATAGG AAATGGGCAT TOCTCAACGA AGCATCCCTG GAAAGACATA	480
	TOCTOCTOCA TITIOCCACCO TITOSCACITG COTTOCCCCC ACTITIAGATO TGACATOTGA	540
	ATNOTOTACO AAACAAACIN TGAGGANATN TGTTTGACAA GTTTTCTGCN CCTCACTGCC	600
10	AAACTAAACT AAGGTCACAC CINITIGONI COCCAATICG AACCCCCINN GCCCCCCAA	660
	AAAAACTINA ATICCCAAAT TCANNCCCIN TTIGGITICC CCCCCAATNA NCNINAATIT	720
	CINCCCUTINI CTGCICCCCC NNCAAACCCIN TGAAATAACC CCCCGAATAC CTNCIVITCCC	780
15	CCAAC	<b>78</b> 5
	(2) INFORMATION FOR SEQ ID NO:447:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 866 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1324UP	
<b>30</b> ·	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447;	
30 ·	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447; GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCCAGAA GAAGACAGGC TGGGCTTCGA	60
30 ·	•	60 120
30 ·	GATCTTAAAG AGGCTCAGTA TOCAGAGGCA GTTTCCAGAA GAAGACAGGC TOGGCTTCGA	
	GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCCAGAA GAAGACAGGC TGGGCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA	120
	GATCTTAAAG AGGCTCAGTA TGCAGAGGCA GTTTCCAGAA GAAGACAGGC TGGGCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGGC	120 180
	GATCTTAAAG AGOCTCAGTA TOCAGAGOCA GTTTCCAGAA GAAGACAGOC TOGOCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGOGCCA GCAAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGGC GTCGTCCACT GGTGCAGCCC AAAAACCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG	120 180 240
35	GATCTTAAAG AGOCTCAGTA TOCAGAGOCA GTTTTCCAGAA GAAGACAGOC TOGOCTTOGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGOCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGCC GTCGTCCACT GGTGCAGGCC AAAAGCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAACG	120 180 240 300
35	GATCTTAAAG AGGCTCAGTA TOCAGAGGCA GTTTCCAGAA GAAGACAGGC TOGGCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCCGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGGC GTCGTCCACT GGTGCAGGCC AAAAGCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTGC AGCCGCTCTG	120 180 240 300 360
35	GATCITAAAG AGOCTCAGTA TOCAGAGGCA GTITTOCAGAA GAAGACAGGC TOGOCTITOGA AATCOCTCAG CTCCCGCCGT GGAAGAGTOC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGCC GTCGTCCACT GGTGCAGGCC AAAAGCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTCC AGCCGCTCTG CTCCCGACAGC TCGGACGAAG GAAGGGAGAG CCCCGGGCGC CGCACGACGC CCCGTTTGAGA	120 180 240 300 360 420
35 40	GATCTTAAAG AGOCTCAGTA TOCAGAGGCA GTTTCCAGAA GAAGACAGGC TOGGCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGCC GTCGTCCACT GGTGCAGCCC AAAAGCCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTGC AGCCGCTCTG CTGCGACAGC TCGGACGAAG GAAGGGAGGG CCCCGGGGGC CGCAGAAGAA ANINITTCGA ACGCCCCGTT TGGTGGGTCN AGCATCCCCC GGANAINCNT CCCAGAAAAA ANINITTCGA	120 180 240 300 360 420 480
35 40	GATCTTAAAG AGOCTCAGTA TOCAGAGGCA GTTTCCAGAA GAAGACAGC TOGGCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATCAAC CGAGCAGGCC GTCGTCCACT GGTGCAGGCC AAAAGCCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTGC AGCCGCTCTG CTGCGACAGC TCGGACGAAG GAAGGGAGGA CCCCGGGCGC GCCGACAGACC GCCGTTGAGA ACGCCCCGTT TGGTGGGTCN AGCATCCCCC GGANAINCNT CCCAGAAAAA ANINITTCGA ACACGCCGCC CGCCCGCCCC CCNCAGAACC TCCCNTTAGC GAACNITNNA AGAAGAATNT	120 180 240 300 360 420 480 540
35 40	GATCTTAAAG AGOCTCAGTA TOCAGAGGCA GTTTTCCAGAA GAAGACAGGC TIGGGCTTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGCC GTCGTCCACT GGTGCAGGCC AAAAGCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAAACG CGTATTCCAC CGCGACCGTC CCCAAGAAGA CAGCTACCGC CCCGACTTGC AGCCGCTCTG CTCCGACAGC TCGGACGAAG GAAGGGAGAG CCCCGGGCGG CGCACAGAGC GCCGTTGAGA ACGCCCCGTT TGGTGGGTCN AGCATCCCCC GGANATNCNT CCCAGAAAAA ANINITTICGA ACACGCCGCC CGCCCGCCCC CCNCAGAACC TCCCNTTAGC GAACNITINNA AGAAGAATNT TNCCANTTTG CGNCCCTNCT TGGANAATGG TGGGCCNGCT TNACNAAACG CTAGGTTGNC	120 180 240 300 360 420 480 540
35 40 45	GATCTTAAAG AGOCTCAGTA TOCAGAGGCA GTTTCCAGAA GAAGACAGC TOGOCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGGCCA GCAAACGCCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGGCC GTCGTCCACT GGTGCAGGCC AAAACCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGGCCGCAA CGCACAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTCC AGCCGCTCTG CTGCGACAGC TCGGACGAAG GAAGGGAGGA CCCCGGGCGC CGCAGAGCGC GCCGTTGAGA ACACGCCCGTT TGGTGGGTCA AGCATCCCCC GGAAATACATCT CCCACAAAAAA ANINITTICGA ACACGCCCGCT CGCCCCCCC CCACGAACC TCCCATTAGC GAACATTANA AGAAGAATATT TNCCANTTTG CGACCCTACT TGGAAAATGG TGGGCCAGCA	120 180 240 300 360 420 480 540 600
35 40 45	GATCTTAAAG AGOCTCAGTA TOCAGAGOCA GTTTCCAGAA GAAGACAGOC TOGOCTTCGA AATCCCTCAG CTCCCGCCGT GGAAGAGTCC GCAGATGAAG CAACACACAC AACAGGOCCA GCAAACGOCG CTGCGGCGGC CGCGCTGCAT CCTCGGTGCC CCTTATGAAC CGAGCAGOGC GTCGTCCACT GGTGCAGOCC AAAAGCGCGA CTACGACTAC TCCGTGTTCA ATGAGAGCAG GCTCCTCACT GAGAGCAAGA TAGACCAGTA CTTGAAGAGC GAGCCCGCAA CGCACAAACG CGTATTCCAC CGCGACCGTC CCCACGACGA CAGCTACCGC CCCGACTTGC AGCCGCTCTG CTGCGACAGC TCGGACGAAG GAAGGGAGGG CCCCGGGGGC CGCAGAAGAC ACCTTGCAG ACCCCCGTT TGGTGCGTCN AGCATCCCCC GGANATNCNT CCCAGAAAAA ANINITTCGA ACACGCCGCCT CGCCCGCCC CCNCAGAACC TCCCNTTAGC GAACNITNNA AGAAGAATNT TNCCANTTTG CGNCCCTNCT TGGANAATGG TGGGCCNGCT TNACNAAACG CTAGGTTGNC GCGCCGAAAAA NCACTTTGCT TNACCGCATN CTCCCCNGAA AGANAGANAG NTCCCCNCAC TTTTTNCGCAA TTTTNICCCC CGCGANAAAG GTTCCCGTTN ANCCGANGGC NGGCGCANNA	120 180 240 300 360 420 480 540 600 660 720

	(2) INFORMATION FOR SEQ ID NO:448:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 749 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1325RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:	
	GATCAATGOG GGAGTGOCAA AAAGCGACTC AAGGTGAACG TGTTTCAGCA CTGTTCATGA	60
	TOOOCOGTOG TCATTITICCC CCACCCATCG TATCTCACCA ACCCATAGAT ATCAGTOCCA	120
20	ATOCCAAGAG OCATOGAGAA TOGTTACAOG AACAGOCOGT GCACTITTCTT GAGCACAAAA	180
	COTTTCACAG ATACACCACG AGOCGGAAAC AAGGAGGTTC ACAATCGGTT ATGGATAACG	240
	CCAAGGGGAA AGCAAATTICC GCAGGCTCTA CGCTACGTAG ATACAATGAG GCGGCATTIAC	300
25	GGAATGACGT TCAGGACCTG TTAAAGAAAT GGAGGCCATA CTTGGAACGC TGGGAACACA	360
	TATTTATTAG GOCCAAAAAT GITGCGGACA GGAGCGTATT CITTACGGAA AATACCCCAT	420
	TGACCAAGGT TAGACCOGAG GATTOGGACA TTCCCATTCA CAACCCGTAG ACCTACCACA	480
30	AATGAGCTAA GOOGAGCATG GTOOGAGATA ACATACTTGA AGAAGACATT GAAGCCCAGC	540
	CATCACATOG GAGCOGCATA CTCCTAAAGC GACAATGATC CACTGCCAAT AAGCGACGTT	600
	GTACOCAACT TAACCCCGNG GNAAACCTTA NCAGGAACOG CTTCTTTCTT TOGATTCNAG	660
35	GCCCCNNNVI ATTCCCTNIT CNAAAANCNI NITTCCCCAA CCICITIITA AACCCCCGGA	720
	AAAANVITIN AAACOONONC COCCOCCCA	749
	(2) INFORMATION FOR SEQ ID NO:449:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 801 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1325UP	
50		
	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:449:	
	GATOGIOCCA TGTCTGATGT GGTATTTCGA TGCGGGGGCG GGTGGGAGTG CCAGCTGGAC	60
55	TACGAAATCA AGGACGAACG TGAATTTTCA GCCGCCCTAG ATACTGTCAA GCGTGCGCTA	120

	CCCCCCGAAA AGAAGTCCCC CTCCCCCACG ACCGTCCAGC CTGCCCCTGG AGCAGGCCGG	180
	AACAACACOC CGACACOCGT ACCICTIGTICC AAGCTCTTTIG TAGGTGCGAA AAACACCAAG	240
5	TTCAAGCCAG TGATGCGCTC TGCGGATGCC GCTATGGCGG CAGGCAGTGC CGCTTGGGGC	300
	COCCACTOTIC COCTATICGA TRAGACACAG ATAGATGACC CACTOGICAT GAACAAAGCC	360
	OGTCACGACG AAGTCGAAGT TGTAGTCGAT CCTATTTTGT CAAAAAAGCT ACGCCAGCAT	420
10	CAGAGAACAG GTGTTGAATT CATGTATGAC TOCGTCCCCCG GOCTCGCAAG GTCCCAGAAG	480
	GACGATGATA GAACAGTGAT GATCTTOGAA TATGATAGTG ATGTCAAGGG TTGTCTGTTG	540
	OCOGNOCACA TOOGNITAGE GAAANCATOC ATGACGATTG CTCTGATCTG GACGCTACTG	600
15	AAGCAGCATC CCCAGGCCAT CGTCTGTTCC DATGCTCCGC AATTGGGGGG TTTGGTTTGC	660
	ACCEPTITIT COCANAAATT CICNIGGIAT COCCCCCIGA CICIGATICG CCACTCCCAA	720
	AANCATTION CONATNOONN GOOGANGAAT AAATTOGANC CINGAANCON ATTOONAANT	780
20	ACCCCCCAAA ANAAAAAATG N	801
	(2) INFORMATION FOR SEQ ID NO:450:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 774 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1326RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:	
33	GATCGAATTA AGTCAGATTT GATTOCCATG OCTACTAACG AACGTGCATT GTCAGACGGA	60
	COGNATICAGE TACACATTIGA ANCTOGTIGNE TOGCTNETICE AGACANTCAT ANATCANAGT	120
40	TGTGGCTGGA GCAAGGGAAC TGCGATGCCT TAACTTTCTC AAAACACTCA TGGGTGGTCA	180
40	AAAATCAATC TATTCAGTAT ATAGTATATC AAAACATTAA ACCAAACTAG GOGCCCAGAA	240
	TATTOCCAAA ACATTOCACT GGAGTATTAG TATOCAGAGA AGTAGCAATG GGCGGCTAGC	300
45	TOGTTACCTG OCATTCACCG ATGACTTATA GAAGCCCATT AATCATCTTT TAGTGACAGT	360
45	AAGATCAGAC ATTAAATAAC GTATCGAATT TTAGGGGAGA AGTCATCACA CTTGCATTAG	420
	TATACCOCAA TAATICOCOG ACCACATCAG TTAATACTOG OCATOGITTC TAAAAACCGA	480
50	AACTOGGITIC ACATTCAGIG TGITTTGCAA CATAGATGIC TCTCCTCATG CTGCTTCTCG	5 <b>4</b> 0
50	GITGAATAAC CATOCTICAG TAGOCACCGT TCCCAGTATT TOGTAATTAG TTGCCACACT	600
	CCTTTATAAA OGATGACCCG AATATGANCT TCCATTAACA TTOCCNOGAA AANANATTIG	660
	OCANCOGIAN ATATTTICCT GOCAATIGAN ACOGITCINT GAACOCCINC TIGGOGNOON	720

	OCTICCCAAA AACGAANIIC CCCCGINGNI NITITATAGG INCNAAGAAA AANA	774
_	(2) INFORMATION FOR SEQ ID NO:451:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 779 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1326UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:	
	CATCAACAAG CGGTTCGCGC AGCTGCCGGA GAACCTGCGC CTCAACGGGG TGACGCCGAG	60
20	CGGCAAGCCG CGGCTGTTTG TGTGCCACAC GTGCACGCGC GCGTTTTGCGC GGCAGGAGCA	120
	CCTGATCCOC CACAAGCOGT COCACAGGAA CGAGAAGCCG TATTATCTGCG GGATCTGCGA	180
	CCGGCCGCTTC AGCCCGCCGGG ACCTGCTGCT GCGGCACGCG CACAAGCTGC ACGGCGGGAG	240
25	CTGCGGGCAC GCGCTGCTGA AGAAGGGCTC GCCGCCGGGG CAGGGGCTGA GCCGGGGGGT	300
	GCGGCGGCCC AAGAGCGCGG AGGGGCTGCG GGCGGCGGCC AAGCCACGGC GGCGGCTGTC	360
	CTITCTCTCCC CACTCCCCCC ACACCTACCC CTCCCTCCC	420
30	CGAAGAAGGT GCAGTTCTCG ACOCCOCAGC TOCTOCCOGT GGACCTGACG CAGCAGCCGT	480
	CGACGITICAC GOOGCTGGAG GCGAACGGTG GTTGCAGGAC GTGAACAGCC TGTCCGCCCT	540
	GCACGGACGC CGGAGGAGGG GAGCTGCAGC CCGCGTGGGC GCTGTGGTGG CAGGCCACGC	600
35	ACACOCCOTC GCTGTTTGCC CACCCTTCCC NGTTGGCCGT CCTTACGGCA ACCTGCTTGN	660
	COCTITIOCC COGAATICCA CETTOGAACG CCTINCOCCG CENGOSCINON CCCCCCCCC	720
	COCATCCCCC CCCGINNCCC AAAAITTICAA GITAACCCAA NAACAITCCC TITICIGCCT	779
40	(2) INFORMATION FOR SEQ ID NO: 452:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 763 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1327RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:	
	GATCCAAGCG TCTGCAGTAT GCTAAACCAG CGTCTCATGC CAGGAACAAC GTATTATCTC	60
55	GITGAACOCT GICCTCGAGC CTCGAGCCAA ATCTGACCGT TTTTTTTGCTA CAGCATACCC	120

	ANAMEMAL ALCTIONIGE GETANICALE ATGACANTGA TIMOLOGGAG GATGUCTITU	180
5	ATGITICTARA TICATOCCTC GAGGICCCAG TCGGIGCCCC ATGITAGICCT GCCGGCCGAT	240
	TATATTOCOG COTAGCTOTO GTGAAACATC GOCGCTAATT GACGGATAAG CAGCTGTGTA	300
	CCTTATTTTC ACTATTTCTT TTCACATACC AACGACTAAG GTTGATTCCA AGAGGTACTG	360
10	ACTGACCCAG TGGACAGCGT AGTTATCGGA GTAACTGGGC AATGTCGTAC GGGTTCTCGG	420
	GCAGCGCAGG AATGGGCTGC TCAAGGCCGA CGACGCCGGA GCTGACGAAG GAGCTCAACA	<b>4</b> 80
	TOCCCAAGGA OGTOGOGAGC GOCATGAGGA AGTOGOTIGTC GTACGACTITC CTTAATGTGC	540
15	CTGGCGGGGA CGAGCAGGCG ACCCCCATCGG GACGCCCGACG ACAGCGACAG CTGAGGACGG	600
	COCCCACOGA ACTICICAAAAC CAAACCOOCG AANOOGCCCN AGOGCNICHOG ANCAANICHOG	<b>6</b> 60
	GAAAGGGGGA ANITIGCOGA MIACONCIGI TGGCCCONCCC CCGCGGTTCC GAMITIGGGT	720
20	TONCAAAATC CCCTCCTCAC TINCAAACCT NCTGAGINNA AGT	763
	(2) INFORMATION FOR SEQ ID NO:453:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 794 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) Original Source: (A) Organism: Pagl327UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:	
35	CATCOCAGOC GICOCTOCAG COTOCTICITY TICTOTICITY OCTTOCCTAC OCCOCCACITY	60
	GCAGCCGCGG CGCTCCTCAG CGTCTCATAC TTGCTGCCTG CTACTTGCAT GGTTTCTATC	120
	GTCACGGTGC AGCAACTGGG ACAACAGCAC CCAGCAACGG TTGCATTTAT ATAGTGTCTA	180
10	CCTGTACGAT AGGGCACTGA TCGCTCTGCG ATGCGTATCT ATCTCATTGC GCAAGGTTCT	240
	CGAAACGAAA AGCGCCAGTC GCTGTCGAGC GACAATAGCG AACCACAATG ACACAATAGT	300
	GOGOGTOGGC GACCOGATCC CTGCATGAAG ACCGAATGCT CGAGCAGATT CTTGTGCGGG	360
15	CGICAGCGGG TAGCGCGGCT CGICGGIGTGG CGCAGCCCGG ATATCCGATG GCACCGCATG	420
	GOGATGIGCT CGGCGCTCGG GATTAATCTA GCTCTTCGGA GATATGCTTC TGTAGGAGGA	480
	AGAGGGCGTA GGGAGAAGGC CTGGACGCGG GCTTGGGGAG CTCTGCAACG TTGGGGGGGC	540
50	GTGCCGCCGT AGGCGGCGGC ACACCGGGGNA AATNCNONEN GANCCTNGTN CCCTCCNITIC	600
	CNCCCCCAA ACTTGCGGGC NITINCCCINCC CGAATINICAA GGNNGNCCCC NAAATCCTINA	660
	ACCCCCCQNA GGAAAGNNIT GOCCTINITGA NCAAANNACN CGCGTTINAAA NICCCCGGGG	720
5	TITICNOCCC CCCAAAANGG GGATAAACCN COCNACNACC TITICAAATC CCCITICNIT	780

	TINCCCCCAN ACNT	794
5	(2) INFORMATION FOR SEQ ID NO:454:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 757 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1328RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:	
	CATCTCTTCT GCAAGTTTCT TTATCGGAAG CCCAGGCTCT GGATTTCCTT TCTCAACACC	60
20	AATOGIATIG TCTTCGATAT CAGAGAAGGA GCGCTTCGAA TTTTGCGCAC CACCATATGG	120
	ACTOTOTICA TRATTITOGI TATTITOTOC ATCACTITOG CTTGCCAAAG AAGAATCCAT	180
25	COCACCCATT ACATCGAATT CTTCATTATC AGCTTCTCCA CCTGTTGTAG TATTTCGTTC	240
	ACCAPTATTA TOOTGITIGOT TATTGATTGC ATCACGGCCCC ACACGGCTCA TITIGIATCAT	300
	GCTAGATGIA TATGGGACAT AATCCACCTT TTCCAACAGA GGACGGAATC GCTCAACCAA	360
30	GTATTGATTT AAAACCAGGA AGTTCTTTGT ACTGACCTCG GCATATTCCT GATCTTGCCC	420
	GAAACGIGCC GAAATTACCT TAAATAAGIC GAGCACGCAT GAGTIGGCCA TGITATCAAA	480
	GTAAAGATTT TCTTGTAGCA GCTGACAAAT TGGATCAAAA AGATCTTAGA TATGAGATAG	540
35	TIGIGATAAA ATICATCATT TACAGCCACG ATACCCTIGA TACCCGAACT GCAGCCAGCC	600
	TIAACIGIAT AATATOGATG GITCCATTAG TITCCAATAG TCAATAGATG CCATTITICCA	660
	ATATNAACCC CCCTTGACAG CATAATATCA GTTCCNTGTT NINATAATCC CCCCATTTIA	<b>7</b> 20
	CCAAACCNGC NCNGTIGATI NCCCNNCCIC CACCCCI	757
40	(2) INFORMATION FOR SEQ ID NO: 455:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 794 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1328UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:	
55	GATOGGAGGT ACATAAGTGC TCTACCGACC AACCCCGCTC TCCATGCATC AACCAATGGA	60

	GTTGAAACAG TTGACTGGCG AGCAGGCCGC CGCACTAGAT GCGGAACTCA TGGGCCCAGA	120
	COTTOOCTAC TOOCTOCATO AATTICATOGA OCTAGCAGGT CTTOCCGTGG COCAAGTOGT	180
5	CGTGCGCCAT TGGGGCGCGG CACAGGCGAA GAAAAAGGTG CTTGTGCTAT GTGGGCCTGG	240
	CAATAACGGC GGCGATGGCT TGGTTGCTGC ACGGCACTTG CGGCTCTTGG GCTATGACCC	300
	TGTGGTCTAC TTGCCGCGGC TGTGGGCCAA ACAGCCCTTC TACGCACAGC TTGCCAAGCA	360
10	CCIACACTIC GICOGIGICC CAGIGCTCIC OCAGGGGGAT GACIGGGGIG COCATCTICA	420
	GCCACGICAC ACOCTICIOCO TIGIOCATOC OCTETITIOCO TITICITITIC GICCOCCOCT	480
	GCGCGAGCCC TTCGCTAGCA TTGTCGCAGA GCTCAAACGC CATGAGGATG ACATCCCAAT	540
15	TOTOSCTOTO GACATICOCA GROSTIOGGA COTTIGACOC AGGACOCTCA COCCTICAGA	600
	CTTATECACE TETECTGAIN TCTCNTGAAC CCCCCCAAA ACCTECTCCC NCNCACATTIC	660
	AAACTEGTIT TITACCNOCC ATTANITICG CNEWNGTTIC ATCCCNAANC CCCNGCCCCN	720
20	CCTCCNIGIT TITANICCNI CCCCGIATCC TONICCCATC CANANICCGI TITTGANITG	780
	CCATTOCNIN ATCT	794
	(2) INFORMATION FOR SEQ ID NO: 456:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 176 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1329RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:	
	GATCCCGTAC GOOGTGCTGC ACTTCGGGTT CTTCGCGCTG GGCTTCTGGT TGCCGTTCGT	60
40	GOCOGIGIAC GIOCAGITCA AGAAGOCCOG CITGIGAGIT AAGTAGAATA TAGTCIAATG	120
	CTATOCAGOG CCCCCGCCCCCCCCCCCCCCCCCCCCCCCCCCC	176
	(2) INFORMATION FOR SEQ ID NO:457:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 176 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1329UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:	

	CATCCCCGTC ACGTGCCCGC GCCGCCGCGC GGCGCGCGC CCGCGGCCCT GCATAGCATT	60
5	AGACTATATT CTACTIAACT CACAAGCCGG CCTTCTTGAA CTGCACGTAC ACCGCCACGA	120
	ACCICAACCA CAACICCCACC CCCAACAACC CCAACITICAG CACCCCCTAC CCCAACITC	176
	(2) INFORMATION FOR SEQ ID NO:458:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 767 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1330RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:	
	GATCTTGGAT TTGACATTGT CAATGGTGTC AGAGGACTCG ACCTCAAGCG TAATAGTTTT	60
25	CCCTIGTCAAA GTCTTCACAA AAATCTGCAT ACCTCCCCTC AAGCGCAACA CCAAGTGCAA	120
	CGIAGACTCC TTCTGGATAT TATAGTCGGA CAACGTGCGG CCATCCTCTA GTTGCTTACC	180
	CGCAAAGATC AAGCGCTGCT GGTCTGGGGG AATGCCCCTCC TTGTCCTGCA TCTTCGATTT	240
30	GACGITIGICA ATGGTGTCAG AGGACTOGAC CTCAAGOGTA ATAGTTTTCC CTGTCAAAGT	300
	CTTCACAAAA ATCTGCATAC CTCCCCTCAA GCGCAACACC AAGTGCAACG TAGACTCCTT	360
	CIOGATATTA TAGTOGGACA ACGTGCGGCC ATCCTCTAGT TGCTTACCTG CAAAAATCAA	420
35	GOOCTOCTOG TCTGGGGGAA TGCCCTCCTT GTCCTGGATC TTGGACTTGA CGTTGTCGAT	480
	GGIGICAGAG GACTOGACTI OGAGIGIGAT TGTCTTTCCC GTCAAGGTCT TGACGAAAAT	540
	CTOCATACCA CCTCTCAAAC OCAACACCAA GTGTAAAGTA GACTCCTTCT GGATATTATA	600
40	GTCGGACACG TTGCGGCCAT CCTCNNNTTG CTTACCCTGC AAAAATCAAA CGCTGCTNGT	660
	CCTGGGGGAA TGCCCTCCNT GTCCCTGATT CTTCNANTTT GACATTGTCN ATGGGTNCCN	720
	AAGANICONO TOAATINTIG ANTITOTICO COGNOAGGIN TIGAANN	767
45	(2) INFORMATION FOR SEQ ID NO: 459:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 794 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1330UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:	
	GATCAGATIGT TITIGTIGCTAG TACGTCGCGA TAGTACTAAA ATTACCATAT GCCCATCAGC	60
5	ATTATACTAA CTAGTGTTGT TTTGCAGTAA GCGGTAAACC ACCCATTACG CCTGTTGTAT	120
	CACCAGAATC CAAATOCGIT TITIGAAAAGA GGITAATTIGA GCAGTATATC GATGAGCATG	180
	GOGTIAGACCC AATCTCCAAG ACAACCTTGA CTAAGGATGC GCTAATTGTC ATTGCCCAGA	240
10	CACCCCAGCA GTACGCGCTC GCAAACGCAG TTAACTCGGC TACGCTCAAC GCCAATTACA	300
	SCATOCOCAA COTTOTGTCA ACACTACAAA ACGAATGGGA TOCOGTGATG CTOGAGACAT	360
	TIGAGCTOCG GAGTCAGCTG GATATGTOCA AAAAGGAGCT ATCGTCAGCG CTGTACAAGT	420
15	OCCACOCOOC TATICCOCCTIC OCCOCCACOCO CCAAACACAGA CAATGATGAA CTCAGACACA	<b>4</b> 80
	CGITICACGGA GCCTICACGGA GGCAGTCGGC GCGCAGGCTG CCGATGCCCC GCCCCTTCCA	540
	GCCCAATTICA TTACCCCCAT GCCACAAACG CACAACAATA TGTGCAGCAA ACCAAACAAA	600
20	GAAGGAAATG AAAGCCAGGT AGTGACGGCA TTTTGCTCCTG GAACAGCCGG TCCAAACGGG	660
	NICCCACCIC AACCCCITTT TICCITACCC CITINNITGC TICCCCAAAA ANAATTANCT	720
	NUCTITITIAA COCAAAGGCA GOOCCNINIT GCTGAACAAA AAGGGTTTTT GCTNCTNNAA	780
25	AATTINGCONC TNAC	794
	(2) INFORMATION FOR SEQ ID NO:460:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 776 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1331RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:  CCATCATTCT CACCUATUAG AGATTCCTGA TCCCCACCCC CTTTTTCTTC AACGAATTCC	60
	ATCGGAGGG CCTCTAGAGT TGAAACGAGT TTATTATACT CAGCCATTGC TACAAGCATA	120
	TAATCAATAG CCGCAGCGCA ACTCTGAAGA TGATCTAAAG AAGGAGCATC TGCCTTTTCT	180
45	COTAGAACAT TCAGAGCOGT TOCCTCTATA ACTTCATOCT TATAAGTOGA ACCACTCGAA	240
	ATAACATGTG ATAAAGGTGG AGAGTTGGCC AATGTGTTCA AAGCTTCTAA TTCTGAAACG	300
	CARATTAGTG CATACCCAGC AGCTGCAGCT TTATTCTTCA AATGATCGAG AGAAGGTGAT	360
50	TOGOCIACIO TICTCAAATC CAGAAGAACG TTOGAATCAA GGATTICCAA GITTCTTTCA	420
		480
	GATOCATGIT TCTTGAGGAA GCCTTCATCT GGGCTCTCCG TATATCTGCT TCAACTCATC	
55	CATAGIAATC AGCAGAAATG ACAATCCATA TATGGITCIT GGCTTTGGIT TGIAGITAGI	540

	CCATCOCTOG ATTITICCCAT GOTAGAAAGA AGAATATOGT CCTCTTTCTT TICAAACAAC	600
	AAATATCATA TOCCCTTGGC TTTCTCCTGC CAAAATTCCA AAATTAGANA TTTCTNATCC	660
5	CCTTTAATAN TICCACATGT TCCCAATICC TCCCAINANA TNACTGICIA ACTGITTGTT	720
	CONVACCEAA AAANATTOCT TOCTNICOCT TTTCCCCANA TOCTCCTTIN CCAGTC	776
	(2) INFORMATION FOR SEQ ID NO:461:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 808 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1331UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:	
	CATCGTGCGC CTGCTCCACG AGCGGCTGCC CAAGGCCACG CGCTCGCACG TCGCCTGCAT	60
25	CAAGAGCTIAC GICTACGGCG ACGGGCTGGA CGAAACCCCC TGGTGCGCCT CCCATGCACG	120
	CCCCCCGGAC TGCCCCGGGC AGTCGCAGGA ACGCCAGGGC ACGTGCGGGC CGGGGCGACGA	180
	CCACCTOCOC ATCTTCACGC TCTCOCAGCT GCTGCAGCAC CAGTCCOCGT CCCAACATGT	240
30	CATCCCCGAT AGCATGGATG CGGGCGACGC GGTCAGCCTG GGCTCCCCGC AGCCCCAGGC	300
	ASSOCIOTOS CASCACASCI TOTOCOCASA TITOCACSCAC SOSTOSCOCO TITOSCOSCOS	360
	CCCCTTAACC CCCTTGACCC GCCCCCCCC CTCCCCACTC CCCCTCCCCCC TCTACACCCC	420
35	OCCOSCUTOC COSCUTIGAÇU ACAUTICOCGA CASCAASSGA TGAACCCCTA CSTCCTCCAS	480
	COCCCCACCC ACCCCCACAC CCCCCCCCCCC CTCVITICAAG CTINVCAANOC CACCCTINCCA	540
	AAANITTAGG GGINGNOOCC CNOOOCCOCT CAACCOONITG GCGTCCCONAA AANCONNITG	600
40	COOCCINNOC CONNCTITIAA GOCCOCONICG AACNONCINI NITTOGOGNA GOGTITOCAN	660
	ACNCAAACNG TNINNOCCCC CCTTTTTTCT TCNAANAAAG GCCINITTGT GICNNITCCG	720
	CCNOGNOGN AATITINITY YGYGGGGCIG NNCCCINAGA AAACNCCCNC NGGGNCNNNG	780
45	GGGAAAAAA AANITITITT CONINGGT	808
	(2) INFORMATION FOR SEQ ID NO: 462:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 762 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1332RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:	
	GATCHITTAT GITCCTITAG AGCAAGGICA ATTITICACAC CACTICTATC ATCHIATATC	60
5	CAGAATAATT TGAACAAGAA GGTACOGTCT AGTGAACGAC GTGATTTCAT GCCGGCGTCC	120
	AACCITICATG ACTCATTACT GAAAATGAAG CACCACTATA TOGAAAATAG GITGCTCGAA	180
	CTACAAAAC TICATCAGIT ATICIGTAAA GATAACGIGA ATTITICCAA AAAAATGATA	240
10	AATGTCCAAG AAAGAAGAAT CGTAAATCTT CTAAATGACC TAGATGATGA TOCTAACTTT	300
		360
	ACTITICAGA CIGICCATAC TAATTITGIG AATAATGAAC TATICATGGA ACTACATGAT	
15	CACAAGICAG IGATATOGCG CGITTOGACA TIAGATACIG COGAGGATIG CAATCGCATG	420
	AAGAAAAGGT TACGACCATA TACACTCAGC TCCTCGACTA TTTCAGGCTC AAGTTGTCCA	480
	ATATTGATGT AGATCCAACC GCCACTATGA ATTINAGITC CGAAACTCCN TIGANCAGTG	540
20	TTACCTCCTT ATTGTGTTTG TTACNCCAAT TGATCCCTCC ANTITCCGAT TCTGGAAAAT	600
	CENCGAAAAC CNNOGAAANT CCNGAAAAAC CTAAAANAAG GAANACOGTT AACNOGGTIN	660
	GGAATGICIA TIGGGGGGG GCCNNANCIT TIAAAGNINC TITCNNGGGG AANANNCCIN	720
25	NCTCCCNINA AANITITTIC CCCNGGCNAA AAANIINICI GG	762
	(2) INFORMATION FOR SEQ ID NO:463:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 798 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1332UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:	
40	CATCTITITIC ACACGCAGIG TACTATCGAT GAAGCATATG ATTATTATAC AAAACTICIG	60
	TCCCATACTA TTCCATTAAA CCCCCTTAAT AGAAACGAAT TTTTCGAAAG TTCCCACACA	120
45	TTAGAGATGT ATGGAGTCGC TTCTATTGAA AATGGCAAGC ATGGCAAAAAA GGCCAAACAA	180
45	TTGGTAAAAC TGATCAAGAG TACAGTTGAT GAAAAAGGAGT TCCATGATGA AATATGINAG	240
	ATOGACTICC TTAAGAAATT GATAATATAA AAGOCTACGA GCTTCAATAT TATAATACGC	300
50	ATTOCATAAT TTATTACATT AAATTGATAT AGGTATATTT TTCTTCGAAG AATTAATTCT	360
50	AATCATTTCC ATGIGAAGAT ATGGCCCTCT GTGTTACCTG CGGATATTTC GACTCTTAGT	420
	ATATCTACAT ATTTTGGCGA GCCATTATTT AAACTGGCCA GCTTGACTCT GGACCCAAGA	480
5 <b>5</b>	GCCGTAATGG CAGCACCTCT TCCTGAGCOC AATTTCTTCC AGCAATTGAG GCACCATGTG	540

	CCGTCCTTTA ATTCCAGCAC ATATAACAGA CCGTCCCGTC	600
5	TICCCTTTCT TICCCATCAT GITTCCGATA CTOGACATTC CCTGAAATOC AANITTAACA	660
•	ACCOTTATAC CASTGAAATC NTGCGTTTTG AAANATGCCN TGCCAATTTC AACCCGTGAG	720
	GIOCGIAACC IGAACTITIT TIGAAATTIC AACCCCCCCA ATNANINTIC NITTTIGNAA	780
10	CCCCATGCCT TGTTCNCT	798
	(2) INFORMATION FOR SEQ ID NO:464:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 138 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1333RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:	
	GATCACCOOG TGAATATOCT OCTTOOCATA GTTGATATAC ATTGTGAGAA AGTOCACCOG	60
	AAGGATGTCC GACTCGGACA CATGGGCGGG CTTGTCCTCT AGGTAGAGGC TGGTCAGGTG	120
30	CITIOSCIPAT TCTOGATC	138
	(2) INFORMATION FOR SEQ ID NO:465:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 137 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1333UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:	
45	GATOGAGAAT AGOCAAGCAC CTGACCAGCC TCTACCTAGA GGACAAGCCC GOCCATGTGT	60
	CCCAGTCCCA CATCCTTCCG GTCCACTTTC TCACAATGTA TATCAACTAT GCCAAGCAGC	120
50	ATATTCACCC GGTGATC	137
	(2) INFORMATION FOR SEQ ID NO:466:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 766 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1334RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:	
10	CATCATAATC CACTCOCTGT CGAGATACTC GACAGGAATG GACGTCAGCG ATTTCGTCGA	60
	AGAGGGCGG AAAACCTTGT COGTTGGCTC CGGCGTTGCG GTGAGCGTCC CGGGCGGCGT	120
	GCCACCGCTC GACTGCAGCC GCGCACGCTT CCGCATTATC TGGTTCATGG AGAATAGCGA	180
15	CGATACTOGA COCTICATGA TOCACTITAA GOCCACAACC TCGGCCGTAT CATGCTGGCC	240
	CCGCCGGCAC CCGGCCACCC GTCGGCCCGG CACGACAGTC CCGAAACGGC CTCGTCCTTAA	300
	CCCACCCTCC ACCATATACT CCTTCACCTG CACCCTTTCC CCCCCCCTA TCACCCGTGT	360
20	CGTCTTTTGC AGCAGAACCA TCTCCACCAG CTTGTTATAC TCCTCAAATA AGGCTGCGTA	420
	TETTACTOCG TCCCCCCCC AACCCCTCCT CCCCAACACC GTGTCCGTCA AACCACAGCT	480
	CCTACCOCTE GAGATOCTOC GCACCAAGAG AGAGTGTCTC CCTTCATTGA ATTOCACCAT	540
25	AGTAGOGTAC GAACTCATOC NOCCTATOCC CTACACCATG NANCTOGITT CTATTGITINN	600
	TONOGOCCOC NATIONOTIGHT COARCINITIN TRANCTIGGGC CACMITITITY INTEGRIFICOC	660
	CCCCGAACCT CCTTCCCTTA ACCAATCCTG GCCCNCTTTC NCAACAGGAA ACCTTNTGAA	720
30	CACTITICCCC NAAANGINGC GAANAAAAN TITITITINAT INCCCT	766
	(2) INFORMATION FOR SEQ ID NO:467:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 796 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1334UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:	
45	CATOCTOCOC COCTOCOCCO ACCOCCAÇÃO COCCOCOCTIC COCATTICTOS AAACCOCCTIC	60
	COCCOSCOGC CCOCCOSTICC CCCGCCTIAGT CCGGGCTGTA CAAGTCGCCC CCAACAAAAAC	120
	OCTITITOGAC ATCACTOTOA ACOOSCISCO COSSOCISCO CAGTACTACO COTOGATOCO	180
50	COCATCLOCI CYLAICICOC OCOOCOOCOC CICCYCOOOC COCOCCIOC YCCIAILOCY	240
	AGACGCCGIC GCGTGCCAAGC GCGCCAAGCCC GCTCGGGGCT GAGCTCTGGG CGGGGTCCGGC	300
	CCIGITCRIC GCGCCCCICC CCCIGCACCC CCCIGATCRIC CGCGCCTTCC TCCTGCGCCCC	360
5 <i>5</i>	CCACCOCCASC CACCACCACCAC COCCCACCACCACCACCACCACCACCACCACCACCACCAC	420

	COOGTOSCAG AACCACAAGG TCGTCTGCGC GTGCTCCGGC GACACGCTGT GGCAGGACCG	480
5	COSCIECCOCG COCTCCOCCGA ACATCOCATG AACTGTATAC TACATACCTG CTACGTTGTG	540
_	CTCGCCCCCC CCCCCAACCCC CTNCCTCCAN CCCCCCCCCC	600
	CCGCCGGGGG GCCCGGGGGGG GCCCGAAAAC CCCCTTCCGC AACGNCCAAN AANNCCANNC	660
10	CONTACNACN CCCANTTANC CAACACNITC NICAACGGGT TINNINGCCCC CCCCGGNCNC	720
	TICTOCOGNG TITTITITIT CCOGANNATT NCTGNICCON CCGINICCON CCTTATTITG	780
	NIMAGGGGGG GGGGGG	796
15	(2) INFORMATION FOR SEQ ID NO:468:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 791 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1335RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:	
	CAGGCAACGG AGGTGGCGGT GGTATCAAAG GTCTGGTAGT CGCTATGTCC TTTCCGAGCT	60
30	TITGGGGITT TGTGGTCTTG CTTTTGTTGG ACGCTAAGGT TGGGCGGGG GAAATCACAT	120
	SCASTOSSCS CCATTCCASS TCCSCCAAST TAATGCCANA CACCSCCCC CTCACCATAG	180
	TOCTIGIOGGI CCTCCTATIGI GATTOCCACC CAAACGTATG GTCCCCCCTT GOGITGICAT	240
35	TITCIGACGI TGITATTCCC TCCGGGCCAC TAAAACTGCG CCTACTCTGA TTCTCTGTCA	300
	GTAACGCAGA GTAAGACACA COCTTOCTTC GTGTGAGCGA TAGTGTGCGA CATAAATTAC	360
	TATGCGGGGA NCCNINCCAA NIITAACCIN TGNNAANAAA ANACCCAAAC TNITTCAAAA	<b>4</b> 20
40	CCCAAANITC NATTINGGEN NENGAAAAIN CCENTIGGEN AACCCCCCGI NNNGGGGIIT	480
	AAATGGGGTT TCCAAAAAAA ACCCNCCANT TTTCCCCCCC CCCCCNAAAT TNITAAAAAN	540
	NCCTITTAAA AANVINIVITT NIGTOGNONC CCCCCCCCCCC CCCCNAAAAAA AATCCCCCCCN	600
45	AAAAAANCNG GINITITICCC CNINGGGGGG AAACCCCCCC NAAAANNCNN ACNINCNANN	660
	NVGGGCNCCC CNNCCCCCCN ANCNCNVIGG INCCCCCCTT INANAAAANG GNCCCCCAAN	720
	CNITITIIN NUMNUMAA AACNOCCITI TICNNOCCCC CCCCMAAAA AATTITIINN	780
50	NIMMITTIN G	791
	(2) INFORMATION FOR SEQ ID NO:469:	
5 <i>5</i>	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 807 base pairs  (B) TYPE: nucleic acid	

5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1335UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:	
	GATCAGATAA GAATTGAAGC TCAGCGGCTG ATGAGCGCAC TGCTTCCGAT ACGGTGGTCC	60
	TGTACCAGOC TGATAAAATG TGACACTATC ACCATAATGG GGTTGTAGCT GGATACGATG	120
15	TCCCCCATGCG GATGGACTIGT TCTGAACAAG ACGTGCAACG TGCCGAGGCCC ATAGTGGGAA	180
	ATCTAATTAA CGTATTTACA TATCAGTOOC GATGTGTCTA GGTGCCGGCC ACCTCGATTT	240
	CCTGTCACTG GACAGCGCCG TCATATAAAC ATTATTGTTT AGGGTTTAAA GTTGCTTTGT	300
20	GCGGTGGAAA ACAACGTCAC ACACTAACTA AATCTAACTC GAGCCAGCAA GCAACTATGT	360
	TAAATAAGCC GAACAGTTTA CGATTCCAAG GGCACGGTGG AACCCCCCAA GGCCCCGCTC	420
	CNANTONITIC CCTTACAAAA AGGGAGGGGG GCCCTACCAC TACCGAAACC ATACNGGTTN	480
25	NAAACAACCC NAANCCCGIT TTTCCCCCCC CCAAAATTAA ANANTGGGCG CCCCCTGNNC	540
	NONATTIGIT NAIMINANGE GCANAGCACC CCCCCCCGGG GANAGCAICC CCCCANAICNA	600
	AAACCANNAC CCCCACCCON ANAAAAANGG GGGGGGGGGGGG GGAACNCCCC GATTTCTAAA	660
30	AAATTTAAAA ATTININIGAA ACCGNAAAAC GGNGTGINICN TINCCCININIG AAAAANGTTT	720
	TIGINGNINA CANOCCCCAA CINITININAG INNOCCCINIC CCCCAAACINI AAAANITIINC	780
	THENANGEGG AACCANTCCC CCCCCNT	807
35	(2) INFORMATION FOR SEQ ID NO:470:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 782 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1336RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:	
50	GATCATGITT AACCCAGATA CGAAAACTGA GAAGCTAGAG TOGATAGAAA AGCTGCGAAA	60
	AGTAATAGAG CTGAACAGGT TTCACCAACC ATGGGTTAAA AAGITCTTGA ATAGCAGTGA	120
	GAATATTCTC TGAAGAAAAG CATGACCACA GGATTACATA GAGTAACTTT TGTGCAAAGT	180
55	TTATCTGTAT GTACAATTIC ACGITATAAA TITTAAAAGI ACTCGGGCAA AATCGGCACT	240

(C) STRANDEDNESS: single (D) TOPOLOGY: linear

	TOGTAGOGAT AACOCACACT OGAGTGAAGT CCATCCAGTA CATAAACATT ATGTCAACTA	300
	CTTACCATTA TIGOCATTOC CAGATGAAGT ACCCATGTIC TOGTGATTOC CTGACCCATT	360
5	GITTACCACTT GCAGCGCCCA GGITTTGGGGG AATCATGCCA GGAAAGGGAA AGGGCGGGAA	420
	ACCCCGAACA TOOGTGOCAT ACCCATOGGA AACGCCAGOC GOCTGCGGCA GAGAACCGTT	480
	GITTITGITC COCCAAATIG AAGITCITIG GITINCCNNN CCCCCCOCCA AAAANCITAA	540
10	CCCCGTCCCC CNGCCCCCNN TCCCCCCAANC TTTCCCCNNTG NNGTTCCAGC CCCCAAACCC	600
	CCCCATATIVIT TINICTICCCCC CCCCTTTINTIN CCCCCTNCCCA CACCCCCCCC CCCNTTGTCN	660
	NINITACCCC CACCONCCCC CCCCCCCCAA ANCONGINIT AAAAAAINON AANAANNINI	720
15	GOCCCCOGNG CTCCCCCCGCG CTCCCCNTATA CCCCCCGCNN GTAAAATNNC NAAGNGGNCC	780
	CN CN	782
	(2) INFORMATION FOR SEQ ID NO:471:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 793 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1336UP	
	(A) CREATENT. PROISSOUP	
30	(A) Chamasa. Phatasor	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:	
30		60
30 35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:	60 120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471: ATCOCCATTT TAGOGRATGAT CCCCATCACC ACAGCTCCCA GCCCCTTGTA GAAAGCCACC	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGGGATGAT CCCGATCACC ACAGCTCCGA GGCCCTTGTA GAAAGCCAGC  AAGCCCTCCC CGCTGTAGAT GTTGGCCCCCC GTGCGCCAAAA ACCCAGGGGG CTTGGTGCCC	120
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGOGRATICAT COCCATICACE ACAGCTOCCA GOCCETTGTA GAAAGCCAGC  AAGCCCTOCC COCTIGTAGAT GTTGGCCCCC GTGCGCCAAAA ACCCAGGGGG CTTGGTGCCC  TCGTTGGCCC GCCTGTAGAT CTGCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAGCAG	120 180
35	(xi.) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGOGRATGAT COCGATGACC ACAGCTCOGA GOCCCTTGTA GAAAGCCAGC  AAGCCCTCCC COCTGTAGAT GTTGGCCCCCC GTGCGCAAAA ACCCAGGGGG CTTGGTGCCC  TCGTTCGCCCC GCCTGTAGAT CTGCCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAGCAG  AGCGCCTCAA ACAGGCCCGC GGTCCCCCCCC GCAACTAGGT TCACGGCCGG GTTGGTAGAT	120 180 240
35	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGOGRATGAT COCCATCACC ACAGCTOCCA GEOCCTTGTA GAAAGCCAGC  AAGCCCTCCC COCTGTAGAT GTTCCCCCCC GTGCCCAAAA ACCCAGGCGG CTTCGTGCCC  TCGTTCCCCC GCCTGTAGAT CTCCATGCCC ACCTTGATCG TGTCCAATGG GTGCCAGCAG  AGCCCCCCAA ACAGCCCCCC GCTCCCGCCC GCAACTAGGT TCACGCCCCG GTTCGTAGAT  TTCTTAGACG ACATGTCGTT ATCAGGGTAT GCCTGCTGCC ACACTCCCCT GCACGGATCC	120 180 240 300
35	(xi.) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGOGATGAT COCCATCACC ACAGCTOCCA GOCCCTIGITA GAAAGCCAGC  AAGCCCTCCC COCTGIAGAT GITGGCCCCC GIGCGCAAAAA ACCCAGGGGG CITTCGIGCCC  TCGITCGCCC GCCIGIAGAT CITCCATGCCC ACCTIGATCG IGICCAATGG GIGGCAGCAG  AGCGCCTCAA ACAGGCCCCC GGTCCCGCCC GCAACTAGGT TCACGGCCCG GTTGGTAGAT  TICTTAGACG ACATGIGGIT ATCAGGGTAT GGCTGCTGCC ACACTGCCCT GCACGGATCC  GCTACGCTTC TGCGTCCCCCC ACCTATATAT ACAACGGGCA CCGACGGCCG GCCGCCCCCA	120 180 240 300 360
<i>35</i>	(xi.) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGOGATCAT COCCATCACC ACAGCTOCCA GOCCCTTGTA GAAAGCCAGC  AAGCCCTOCC COCTGTAGAT GTTGGCCCCC GTGCGCAAAAA ACCCAGGGGG CTTCGTGCCC  TCGTTCGCCC GCCTGTAGAT CTGCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAACAG  AGCGCCTCAA ACAGGCCCGC GGTCCCGCCC GCAACTAGGT TCAGGGCCGG GTTGGTAGAT  TTCTTAGACG ACATGTGGTT ATCAGGGTAT GGCTGCTGGC ACACTGCGCT GCAGGGATCC  GCTACGCTTC TGCGTCGCGC ACCTATATATAT ACAACGGGCA CCGACGGCGG GCCGCCCGCA  CCTTGTCTCC GACGCAGCGC CAATAGGAGC TCGCCGCATAC CCCCGGGCCGA ACGCGGTGAG	120 180 240 300 360 420
<i>35</i>	(xi.) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGSGATGAT COCGATGACC ACAGCTOCGA GEOCCTTGTA GAAAGCCAGC  AAGCCCTOCC COCTGTAGAT GTTGGCCCCC GTGCGCAAAA ACCCAGGGG CTTCGTGCCC  TCGTTCGCCC GCCTGTAGAT CTGCATGCGC ACCTTGATCG TGTCCAATGG GTGGCAACAG  AGCGCCTCAA ACAGGCCCCC GGTCCCGCCC GCAACTAGGT TCAGGGCCGG GTTGGTAGAT  TTCTTAGACG ACATGTGGTT ATCAGGGTAT GCCTGCTGGC ACACTGCCCT GCAGGGATCC  GCTACGCTTC TGCGTCGCGC ACCTATATAT ACAACGGGCA CCGACGGCGG GCCGCCCGCA  CCTTGTCTCC GACGCAGCGC CAATAGGAGC TCGCCGCATAC CCCCGGGCGA ACGCGGTGAG  TCAACCCGGC CCGAAGCGCG GGCCAATGGA ACGCGTCACGT GAAAAGCAAA GACTTAAAGT	120 180 240 300 360 420 480 540
<i>35</i>	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGGGATGAT COCGATGACC ACAGCTOCGA GEOCCTTGTA GAAAGCCAGC  AAGCCCTCCC COCTGTAGAT GTTGGCCCCC GTGCGCAAAA ACCCAGGGG CTTGGTGCCC  TCGTTCGCCC GCCTGTAGAT CTGCATGCGC ACCTTGATGG TGTCCAATGG GTGGCAGCAG  AGCGCCTCAA ACAGGCCCGC GGTCCCCCCC GCAACTAGGT TCAGGGCGG GTTGGTAGAT  TTCTTTAGACG ACATGTGGTT ATCAGGGTAT GGCTGCTGGC ACACTGCGCT GCACGGATCC  GCTACGCTTC TGCGTCGCGC ACCTATATAT ACAACGGGCA CCGACGGGG GCCGCCCGCA  CCTTGTCTCC GACGCAGCGC CAATAGGAGC TCGCGCATAC CCCCGGGCGA ACGCGGTGAG  TCAACCCGGC CCGAAGCGGG GGCCAATGGA ACCGTCACGT GAAAAGCAAA GACTTAAAGTT  ACTATGTAGC TACACACTTA GGCCTCGGCC ATCTCGCGCA GTCTGCGGAT CGTGGGAGCGC	120 180 240 300 360 420 480 540
<i>35 40</i>	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TRAGGERICAT CCCCATCACC ACACCTOCCA GCCCCTTGTA GARAGCCAGC  AAGCCCTCCC CCCTGTAGAT GTTGCCCCCC GTGCCCAAAA ACCCAGGGG CTTCGTGCCC  TCCTTCCCCC GCCTGTAGAT CTCCATGCCC ACCTTGATCG TGTCCAATGG GTGCCAGCAG  AGCCCCTCAA ACAGCCCCGC GGTCCCGCCC GCAACTAGGT TCACGCCCGG GTTGGTAGAT  TTCTTAGAGG ACATGTGGTT ATCAGGGTAT GCCTGCTGCC ACACTGCCCT GCACGGATCC  GCTACCCTTC TGCGTCGCCC ACCTATATAT ACAACCCCCA CCCACGCCG GCCGCCCCCA  CCTTGTCTCC GACCCAGCCC CAATAGGAGC TCGCCCCATAC CCCCCGCCCGA ACCCCGTGAG  TCAACCCGCC CCGAAGCCCG GGCCAATGGA ACCGTCACGT GAAAACCAAA GACTTAAAGT  ACTATGTAGC TACACACTTA GCCCTCGCCC ATCTCCCCCAC GGCCACAGTC NTCCTTTGCCA	120 180 240 300 360 420 480 540
<i>35 40</i>	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:471:  ATCOCCATTT TAGGGATGAT COCGATCACC ACAGCTOCGA GEOCCTTGTA GAAAGCCAGC  AAGCCCTOCC COCTGTAGAT GITGOCCCCC GIGOGCAAAA ACCCAGGGG CITICGTGCCC  TOGTTCGCCC GCCTGTAGAT CITCCATGCCC ACCTTGATCG TIGTCCAATGG GIGGCAGCAG  AGCCCTCAA ACAGCCCCCC GGTCCCCCCC GCAACTAGGT TCACGCCCGG GTTGGTAGAT  TTCTTAGACG ACATGTGGTT ATCAGCGTAT GGCTGCTGCC ACACTGCCCT GCACGGATCC  GCTACCCTTIC TGCGTCCCCC ACCTATATATAT ACAACGGGCA CCGACGGCCG GCCGCCCGCA  CCTTGTCTCC GACGCAGCCC CAATAGCAGC TCGCGCCATAC CCCCGGGCCGA ACCCGGTGAG  TCAACCCGGC CCGAAGCGCG GGCCAATGGA ACCGTCACGT GAAAAGCAAA GACTTAAAGT  ACTATGTAGC TACACACTTA GGCCTCGGCC ATCTCGCGCA GTCTGCGGAT CGTGCACGCC  ACGTCCCCGC GCCAGCCCGTG GAGACGTGTT ACGCACCACC GGCCACAGTC NICCTTTGCA  CNAACTTGCA NITCCCAAAN NCCCGNAGCG CCGCCCTTCN CCGCCTTCTT TGCCGCAAAAA	120 180 240 300 360 420 480 540 600

	(2) INFORMATION FOR SEQ ID NO: 472:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 767 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic) (vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1337RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:	
	GATCITAAIT TAAAATITTA AI'IAACTATI TATAATITAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
20	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITG TOOCATCITA	180
	ATTITIATTA TITAATIGAT TATTATCIAT TITAACATAAA ACATTITIAAA ATGITATAAA	240
	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGIA TTTAATTTAA TTTTAATATT	300
25	AAATATACCA TITTITATTAA TAAATAGATT ATTAAGITTA TIAATATTAA GIGATATATA	360
	ATTTAATTTA TATAAATTAT TEAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATTITTA TIAGICIAGI AATATTICTA TITAATAGIC TCCCTTTAAT	480
30	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT	540
	AATAATTTAT TATCTAAAGG TATATAAATT AATTAAATCC TTTTTTATTA TTATTTAAAT	600
	TATTATTAAT AGTAAATTAT ATTATTTATT TYATTCACCA TAATTTTTTT GATNATAATA	660
35	TATCCTTINN TAAATOOOGA ATTIATNAAT AATTANCTIC NANGAATIIT AATGAANAAC	720
	CCCCNITANN ATAAAATTAG TTAANNVIGN NCICAAAANN CCNATCA	767
	(2) INFORMATION FOR SEQ ID NO:473:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 799 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1337UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:	
	GATCAATTAA TAAATGGTTT AACTAATAAA GTTAATAATA AATCTATTAA TTATATAAAA	60
	CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
55	ATTICACTITIA TATTAAATTIC ACCACCTICTT ATTICATTIC	180

	TCTTAAAATA TTCTTAATTA TTAAATTATA TAATAAAAGT TAGTOGATAT AGTTTAATTG	240
	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
5	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
	OGIGIGIACC TTACCICICT AATTAAAGIT ATAAAATTAT CITAACTAAT AAAAATAAIT	420
	AATTAAATAA ATAAATAATT AATTAAATTT AAAATGTTTA AAAAAAGAAA TAAATAATAT	480
10	GITATATITA AATAGATCAA AATTICAACA ATTICCATTI CATTIAGIAC TACATCACCA	540
	TGACCAATGT TACATCATTT AGTITAATAG GGTTTACTAA TAACCTTTAN CCTTTTACCA	600
	AANNANDET ANTANINGA AAAATTATNC CCTTAATAAT AACCTTNATN AANNATTNT	660
15	ATATACCAAA ANNTINIGAN ATTINAAAAA ATATNOOCCG AANCINCNIA TITTICINGTAN	720
	CCCCCNCNTA CNCCNGAAAA AANGNITACC CGTGTTCCCC CNTATINNTCN NTNCCCNAAA	780
20	ATAAAAAATG NGCCCCCAC	799
20	(2) INFORMATION FOR SEQ ID NO:474:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 771 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1338RP	
30	• •	
30	• •	
35	(A) ORGANISM: PAG1338RP	60
	(A) ORGANISM: PAG1338RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:	60 120
35	(A) ORGANISM: PAG1338RP  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTOCAG ACCOGTTATAG AGACOGTCGT CGATGOCACT	
	(XI) ORGANISM: PAG1338RP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTOCAG ACCOGTTATAG AGACOGTCGT CGATGOCACT  ACAAGOCCOG CAAATOCTTT GCTTATGAAT AGCACOGTTG AGGIGATAAC CGTTAAGGAA	120
35	(XI) ORGANISM: PAG1338RP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTOCAG ACCGTTATAG AGACOGTCGT CGATGGCACT  ACAAGGCCGG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA  ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTOCA ATGCAAGCAG	120 180
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTOCAG ACCGTTATAG AGACGGTCGT CGATGGCACT  ACAAGOCCOG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA  ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG  AACGCTTTCT GTCTTTTTGT CCAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT	120 180 240
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTCCAG ACCGTTATAG AGACGGTCGT CGATGGCACT  ACAAGGCCGG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA  ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG  AACGCTTTCT GTCTTTTTGT CCAAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT  GAGTTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTTT	120 180 240 300
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCCGTCAC TCANGTCCAG ACCGTTATAG AGACGGTCGT CGATGGCACT  ACAAGOCCGG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA  ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG  AACGCTTTCT GTCTTTTTGT CCAAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT  GAGTTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT  GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATACGCAT TCTCTAGAAA	120 180 240 300 360
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGTCAC TCANGTOCAG ACCGTTATAG AGACOGTCGT CGATGOCACT ACAAGOCCOG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGTGATAAC CGTTAAGGAA ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG AACGCTTTCT GTCTTTTTGT CCAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT GAGTTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATACGCAT TCTCTAGAAA GTTCCTTGGC TTTCATTTTA AATCCTCGTG CACCTCGTCC GTAACAGTGT CTATAGTATC	120 180 240 300 360 420
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCOGICAC TCANGICCAG ACCGITATAG AGACOGTCGT CGAIGCCACT ACAAGOCCOG CAAATGCTIT GCTTATGAAT AGCACGGTTG AGGIGATAAC CGITAAGGAA ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG AACCCTTTCT GTCTTTTIGT CCAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT GAGITTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT CCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATACGCAT TCTCTAGAAA GTTCCTTGGC TTTCATTTTA AATCCTCGTG CACCTCGTCC GTAACAGTGT CTATAGTATC ATTCCGTATC ATTTCTGAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT	120 180 240 300 360 420 480
35 40 45	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:474:  GATCAACCOC AACCCGTCAC TCANGTCCAG ACCGITATAG AGACGGTCGT CGATGGCACT ACAAGGCCGG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGIGATAAC CGTTAAGGAA ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG AACCCTTTCT GTCTTTTTGT CCAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT GAGTTTTATT TACACAGTAG GGTOCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATACGCAT TCTCTAGAAA GTTCCTTGGC TTTCATTTTA AATCCTCGTG CACCTCGTCC GTAACAGTGT CTATAGTATC ATTCCGTATC ATTTCTGAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT CATTATTCTG AGCAGTAATG GCTTCACCTC TATCCTGTTC CAACATACTT TTTTTAGCTG	120 180 240 300 360 420 480 540
35 40 45	(XL) SEQUENCE DESCRIPTION: SEQ ID NO: 474:  GATCAACCCC AACCCGTCAC TCANGTCCAG ACCGTTATAG AGACCGTCGT CGATGGCACT ACAAGGCCGG CAAATGCTTT GCTTATGAAT AGCACGGTTG AGGIGATAAC CGTTAAGGAA ATAGTGAAGG AGACAGTTTT CGTGACTGAG AAGGTGACTA ACTAACTCCA ATGCAAGCAG AACGCTTTCT GTCTTTTTGT CCAAACCTAC CTGAACACCT AAACTTAGTT ATTACAACAT GAGTTTTATT TACACAGTAG GGTGCCACAG CCACAGGAAA TATCCAAAGA AATTAGCTTT GCCTTGATAA AAGATATTCA TCCCTATTCA GCGACCCCTC TAATACGCAT TCTCTAGAAA GTTCCTTGCC TTTCATTTTA AATCCTCGTG CACCTCGTCC GTAACAGTGT CTATAGTATC ATTCCGTATC ATTTCTGAAT GAAGTAGATT CCATATCAAC ACTTGCTTTG GTGGAAAGCT CATTATTCTG AGCAGTAATG GCTTCACCTC TATCCTGTTC CAACATACTT TTTTTAGCTG CCCCGGATTAA CCTCCCTGAA TTCCCTTACG ATGCAGTGGA GACCCATGCC GATTTATCAA	120 180 240 300 360 420 480 540 600

	(2) INFORMATION FOR SEQ ID NO:475:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 796 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1338UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:	
	GATCAGGITT TCCCGTACGT CAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG	60
	COGACOCTIG AGITOCNAGA TACAGGACAA AGCIGITAGG GCOCCAACIG GIOCANCAGG	120
20	ACCACCCCAG GAGCGATTCT CCCCCAAGCG ACGGTGAATT CGAGCCAGCT GGTAGCAGGA	180
	GIGCCGGATC GICTATITIAG TIGCGACGGG CGICGGAACA GGATGCACGT AAACGITIGCG	240
	GTAACACGCG ACGCTGACGC GACGGCTGCT ACGCCGATAG CACGGGAGCG CAAACGACGG	300
25	CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCGCGGTA GCAAGCTGCA GCGGCGGAAG	360
	CAGACACTTG ACCCCCCTCC COCTCCCCCC ACTCCCACAC ACACCCTCCA CCACCTCCCC	420
	GCGCAGCTGG AGCGCCGCTG CGAGCAGCGG TCGGCAGCGGA AGCCGCCGTA CTCGTATGCG	480
30	CHOCHGATCG CCGTTICCCAT CCTACAGTCG CACCACCCCA CCTGACCCTG TTCCCCNAAAA	540
	TACCGNIGNA TTICCNCONI CICCCCTTAN TAACCGGIGI TTITAACCCG GGGITGGAAA	600
	ANANCTICCG GACNACNINI INCITIAAACA ANOGINITGI TITTAAGGGGN GGNNNCCCCC	660
35	TCAAAGGANG GOOCTITTIGG AAAATTAAGG GOOCCNITNA NGGGGGCCTC NCTTNNCCAA	720
	AAAGGGGGAA TNATTTINNG GGCCCANATT TNNCAAAAAT TNINCANTAG GGGGNCTNNG	780
	MAANITINI TONCIT	796
40	(2) INFORMATION FOR SEQ ID NO:476:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 764 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1339RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:	
55	GATICATICOCC TITTAGOCCCA TGTICAACCTT GCCCGCACCG ATCAACTCCG TCACGTCGGA	60

	COOSTICOTO COCTAGO COCASTOTO CALACCTICO TOCTORAST ACCOTAGA	120
	CTOCOCTAGA AAAATCOCAA TGTOGTATOG COCAGOCTOC CAATTCAATA GGAATGAAAC	180
5	THIOCHAGAC AUCTHOOSIG CASTCHOOSC ASCHACACCC CATTGCATCC ASSCHCATCA	240
	OCCOCTITAT ATACCOCTOG OCCAAAGATG ATTGAATACG GTTCGCAGAC GOCTACTGGA	300
	ATACCCCTICG CGCCACAGC CCCCCACTGG ATGCCATGCG CCAATGCGGA AGCCTCCTAT	360
10	GTGACATGTA CTAACAGAGC AGCTTCCTTA TGCACTTATC GAGCCAAAAAC CAACATCTGC	420
	GGAATCACAC TTGACGGAAT CCGGCCCCAT GCGCAGCTGC TGGAAACACA AATCCAGCAA	480
	CTAATAGGGC TCAGTGGTAT AACGGCCCCAT CGCTCTCTCA ACGCCAAGTC CCTCTCTGGG	540
15	GAAAACATGT GATCACGTGC TACATATTCA ACCCCCGTCT TACCTCATAG CTGCGCATGT	600
	CCAGCCCTGA ACTOTTCCGA CCTTCCGTCT TCCNGAAANC CTGATTGCCT TCCTTTAATT	660
	CCCCCTCTCC NCCAACCATG INICOCCCAT TTACTTCCGT TGCTTTTTTA TTTCGTGCAT	720
20	TGITITINIA AAAGNNOCIG TIAANIAAAT NOONICATIN TOGA	764
	(2) INFORMATION FOR SEQ ID NO:477:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 778 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) Original Source: (A) Organism: Pag1339UP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:	
	CATCAGOGCA THIGIOCRITA GIGOCTITICA TIOGRAPART COCRICATIA CCATOCTICAC	60
	TATACCTCTA CTCACCAACG CCTTTGCAAA CAAAGACTGG GGCGTTAACC TAATGTCGTC	120
40	TOCOCCAATG TATAACTOGA TATTTOOGTT GATTGATOCA GACCACOCAA CITGTOCTCC	180
	TAAGCAACAG TCATCACTGG COGTAGCAAT AGCTACCCTA ATATACAACT ACTCAGTGTT	240
	GGTAGTAAAA GAGAACAACC ATGACATCCT AGCAATTGTT GCAGAGGTTC TAAACAACAA	300
45	ATACOGCTCC TCTTCCTTTA TCCTGCGGAA CGAGGAGGCC GCATACAGAC TCCTTGTTGC	360
	TTACOGAAAC TTAAGTACTG TOGAAGOCAC CTTCOCCACAG TTTOCTCCTT CTATCTCATG	420
	GATAAGGAAG CTGAAGAGCC AGTATOGCCA CATATOGAAA TTCCAGGATA TTTTAAATGA	480
50	TATTTAAAGA AAGGTGTACG TATATATCCT ATTCTTTCGA TCGCTGTCCC GAGGCCTTCC	540
	COGAAAAATG CTGAAAACTT COCTCTTTGA CACACAGCCT TTGCCCTTCA ACAGGATAGT	600
	TIGAAGOGAC ATGITCTGIT GACAANNCTT GAACCAGOGT ACTOGICNAA AATTINAANA	660
55	TOTTTTCTCC NCCGAAANON AVITCINCOG AANTTAACOG GAAAAAAAANC CCCCTCNNNC	720

	CTITIVITTAN TAACCCCCC CAGGNI'INIG ACCTIGATIT TIACAAAACC TITITIVIT	778
	(2) INFORMATION FOR SEQ ID NO:478:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 766 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1340RP	
15	· ·	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:	
	GATCOCCTGA TATCCACAGG CACTITTGIA TATTACCAGT ATTCTTGACG ACATAATGCA	60
20	GICAACTCCT ATATAGAAAC COGATACAGT GGTAAAAACG CAAATGTAGG CAATTATATA	120
	TTACICTTCT CGACACCACT AACTICTCGA TAGCOGCATA TCTTGTAAAT TTGCATACAC	180
	CTITICCCAA CTITICAGIOG TCTCGITGOC GIACTITIACA TOCATCTIGG CCCATTCCTG	240
25	CANCACATOT GIGATACAAA ATIGAGICIC CIGGAAAATT ACAAATICCT CTAAAAATGCA	300
20	CTTTCTAATT ACCCACCACC TGTTTAGTTG CTCACCAATT GTCCGTTTGT CCCGTTGAAT	360
	TGICTGTCTG AGTTTATCAT ATTICTGCACC TTTAACGTCC GGATTACTCT CCATAGATTG	420
30	AAGTITIGTOC ATATTTATTT CCACTCTCCT CTGCAAATGT GCTATGTTAT TCCCCGCCAT	480
30	AATTTTATAC CTATCAAACA CCCCTTCAGT GCTATAATAA TATCTATGAA GGTCTTAAAC	540
	TICACCGATA GGIGITICCIC CACTICCIGA COCTOCTITIC TIAGAGGIAT COGOCACOCT	600
35	ATTGAGATGT TTTTGATAIN NTGGAAATAT GANATTTAAA TATCNTGAAT AGTGCCTCTT	660
35	CCTATTOGGT ANAANTGI'IN CNGAATTATC AANCAATTCC TCCATCACNC NGCCAAGCAC	720
	CONCOGRACT TONAMACCT GONOMINGCC COGRAGGETT MINNAMA	766
40	(2) INFORMATION FOR SEQ ID NO:479:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 790 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1340UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:	
	GATCIOCTET ACCTGAATOG ACTTTETCTC CTGAAGTAGA AATGTAATOG CCCCTTCOOG	60
55	AATACATAAC AAACATAGCG GAGACAAAAAA CAAAAGCGTT ATACACGCAT CTGCCGTTAC	120

	ATCACCGTCA CCTCCTTCCA GACCAATAAG CCTTCAAGTT AAATATAGGC TAGCTATAAC	180
	ATATTATGTC OCTAAGAAGG OCCAAATCGT TOCCATCOCT TAAGAATATC OCTGAGGTOG	240
5	CCAAGCCCAT CACCAAGGCC CCCCCCCTCC CCCTGCTTGC GTTTGAGGGC CCTGGGCTGT	300
	CCACATGTOG CTOGTIATOCC ACCACOGTOC OCACAGTOCA CAATACCCCC AGTIAAGOCOC	360
	AGACGACOCT OCTOTOGACA OCGAAGAAGG AGAGTOCGTT TICCOCAATG AACCTGAAGG	420
10	CCTTOCOGAA CGAGTOCCOC TCCCGAGOCT CAGOGTCTCC GOGCGGAAGT CGGATTTGAT	480
	CGACCCCATT GTCGACTTCG ACCTGAAGGG ACCCCTGGGC ACGCCCCGGGA CACCGCCCCCC	540
	GITCCACAGO CCGGGCACGA GCAGCGCCAG CGTATGCCGC CCGTGGACAA GGTCACCATG	600
15	CCCGACATCG COCTTIGACAG AACGAACCCC GTGCCACACC CTGAGAAAAA CTACATACTC	660
	COGANICOVI CNITIGINOON CCAAGOOGGI TICCCTCCCC GITACONAIT CONAAAAGAT	720
	TTTTGCCVCG GAACCCANGA AGAAACCACC CGAACTCCCA GAAGGGGGVT TTNNNANCCG	780
20	AACCGAANCT	790
	(2) INFORMATION FOR SEQ ID NO:480:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 765 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1341RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:	
	GATCACATCC GATGCGAAAC TCGTATATTG TTTTCCCACA ATGATGAAGG TGAGTGTGGG	60
	GCAGCAATTG TCCGGTTGAC GACTCCTATA GGCCCGGGCA TGCCCACGTG ACCAGAAATT	120
40	TOCAATOTGA TICATGATGC AAATOGAAAC CCCATCCAAG TITCACAGTC GCAAAAGAAC	180
	ACTIOGATICE TIGACAAGGIT CITICIGITAG GEAGCICTAT AGACACTEGG GITIGETGITIG	240
	CTGCGGATGC AACGAAAGTG TCCGCCCATG CTTTACTCCA GGCCCTTTTT ACCTCTAACG	300
45	AAAGTGAAGT AACTOCTOGA TGTATTACCT TICAGCAAGT CAGAAACCTG ACCAGGTTCG	360
	ACTACTITIT TATICAACTC CCTOCTCTCT CACTATTICA ACCACTTACT CCCACCAATC	420
	AGAAACTTAA AGAATAATAG AATOOOGAAG ACTCAAAATT TACOOCTACC ATAAGACTCA	480
50	CAGACTTACT CGACTOGAAC GITTITOGTOC GCACTITIGTO CTGOGAGTCA TATACAGAGO	540
	CCTIGITATCGC GITAAAACACC GGATGCGCTA CAGCAAGGTA CTCGCCTACA AGACAACACC	600
	CTACGTACGC CGTTTCACAG TATGCAAATA ATNGAAGGCA TTTCCTCCNG ACTTTTTAGC	660
55	NAAAGGNITT AINCGAACIG ANCOCTGTCC ATACTITATT CCCCCNANCC CNGTTTCNA	720

	AAAANCAGNG AACCATACNA TGCGTTTAAT AATGAACNIT CACNI	765
	(2) INFORMATION FOR SEQ ID NO:481:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 810 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(ví) ORIGINAL SOURCE: (A) ORGANISM: PAG1341UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:	
	GATCAGAGTA GATTTAGTAA AGAGGTAACC ACCACTGTTC CAAGAAGTCC AGGCCTTTGG	60
20	CITGACCAGE ATTOGIAAGT GETGIGGETG GAAATITTOCA CITTAAACGGT CTGAGCTCAT	120
	CTOSTICOCC AAAGACCTAT GAAGTITCAA AACACCAACT TIGCTOCCCA TICTATATIG	180
	AAATGTATGA CAGATGOCAG GTOCCTTACC GEACACTGTT TEATTGGTAA CTGGGTCTAC	240
25	ACCITICACG TICACCITIG CCACATGGAT CAACATAGAA ATTAAAAGAG AGCCAACCIT	300
	ASSCRIGATA TIGIGOSSOC ASAGAACTIT AGACTOCICA ATTIGIGIAT TICTAAACGI	360
	GETTITIGCC CTTIGGACCA GCTICTIGAA TIGGITIACTA TIGGCCCTAA CTTCCTTAAA	420
30	AATOGATTIC TCACTCTICA ATAGTOCTIC CGATCTGTAT TCCATCTCGA CAGCCTTACC	480
	TATAGOCAGA ACCOCTOCTG GITGITCTCA TACCTTCACT GACGOCTCCA GITAGAATTC	540
	CAAGCCTITA CONATTOCCC AAATTGITTA TGAANACACA TTICNOCTNG ANINACCCCA	600
35	AATTGAAATT ANGGGGNCTT TICCANNOON TGAAANAAAA TGINGAACGG NGTTICAGTT	660
	AAGCCCATINT ATCACINGON ANCATTONIN AAAAANGCTT CCCCCCTCCC TITTTAAAAC	720
40	GOGATOTINO CAAAAAACON COCCOINAAT GAACCATTIT NOGAAANCOG GAACCCONNG	780
40	CCCTCNCCGN CTANATTCCN GCAANNCATN	810
	(2) INFORMATION FOR SEQ ID NO:482:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 759 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1342RP	
55	(SS) CENTENTE DESCRIPTION, SEN ID NO-482.	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

	GATOCTGATT TIGATITOSC CATTGCTGAT GITAATGCAC TCAGTGCTGA TGTCCTATAT	60
5	ATCCAGCATG AATTATCCTG GIGGATATGC GCTATCTGCA TICAACAAAT ATGTGCTGGA	120
3	CAATAATATC TOGAATOOGA COGTOCACCT AGATGTCTTC ACTIGIATGA COGGTOCAAC	180
	OCTOTTTOGA CAOCTOCCOG ACTOCTACOG GATCATATAT GACAAGACTG AAOGTGATGA	240
10	ATTATTOGAC GCATGGICAT CGITCGATTA TGICATTACA ACIGATCCCA ACAGCICACT	300
10	GOCTOCTGTT ACAGOCTACA AATGGGAGGG CATOCAAACT ACTGAGGCCT TIGACOGCTT	360.
	CGACCITAAA ACTATACCOG AAATAATCAA CTCAGAAGIT OCTAAGOGAT TCCCIATCTT	420
15	AAAAGATOCA ATACTICTICTG CAGACCTOCA ACCTIGTGAAG OCTOCGTTCA CAGATGTGAT	480
.5	CAGGTGCAGG GATTCAGTGT ATACATATAA AAGAGTTGAG AATTAATAGA ACCAGGGCTC	540
	COCTTACOGA CAGTITICCAT ATAAATATIT ATITATTAAA CTTAAAAGIT CTOCGAGTTG	600
20	AGGAGGAATT TGACTOCTGG AGATTCCGAC ATACTGAAAA CATAAAGTGC ACATTTACAG	660
20	GATTOGGCAG TTACTIGATT COCCOVICCIN NINCCITAAAT GCCIGATONA ACTINAAACA	720
	TOCTATIGAA COCCOTTIGG TONICCAANC AAANINIAA	759
25	(2) INFORMATION FOR SEQ ID NO:483:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 802 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1342UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:	
	GATCOCOCCAG GCCCCCCAGC ACCAGTCCCCG CCCCTTCAAG GAGCCCCCAG ACTTCCCCCCC	60
40	CATCATOCTG ACCAAGATGG ACGGGCACGC CAAGGGCGGC GGTGCCATCT CCGCGGTGGC	120
	COCCACGAAA ACACCOGTIGA TCTTCATCOG CACAGGOGAG CACGTACACG ACTTOGAGAA	180
	GTTCTCCCCCG AAGTCGTTCG TGTCGAAGCT GCTCGCCATC GCCCACATCG AGTCGCTGCT	240
45	GCAGCAGTIC CAGACCGICT CCAACAAGGA GGACACCAAG GCCACCATGG AGAACATCCA	300
	GCAGGGCCCC TTCACGCTGC TGGACTTTCA GAAGCAGATG CAGACCATCA TGAAGATGGG	360
	CCCGCTGTCC AACCTCGCCA GCATGATCCC CGGCATGAGC GGCATGATGA GCGGCATCTC	420
50		480
	CGAGGACCAG ACCAGCCGCA AGATGAAGAA GATGGTCTAC GTGCTCGACT CCATGTCCCG	•••
	CEAGGACCAG ACCAGCCOCA AGATGAAGAA GATGGTCTAC GTGCTCGACT CCATGTCCCG CGAGGACCAC GAGTCGGACG CCGCCGCATG CTGCGCGTCG	540

	CCCGCCNGCC CCNGGNATGT CCCCGCCTCT CNCCTCCAAA NGAININACC NGCCCNANCN	720
	TONVITANCT CAACCONCCC NICANNOCCN CATAATIGGCT NINCOGNIGG GGNCCNEGGC	780
5	CCCCATGCCC CCATTAGGCN AT	802
	(2) INFORMATION FOR SEQ ID NO:484:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 844 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1343RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:	
	GATCAACCAA TGTGTTAAGG AAATTTTTTAA CGTTTTCCCG GGATTTGGCC ATCTTTCCCT	60
	CTAATTOGTA GGAAACATAG TCTGTAGCAC CCATGATATT AGCAAGTTTC COCCGAAGCT	120
25	GAAGCAAACT CTTAAGCCTC TTCACTTGTT TTTCGGAACA ACTAAACATT GCGGTCCATA	180
	CCTGCCTCCG AATAGCCTCT GAAGGACAAG CATTCAATAG TGTATACGGA GCATACCCAC	240
	TAGTIGGIAT CITATAGITA TIACCCATGG TGICCITOGI GAOCIGACCA AGAACAAGAT	300
30	GOCTAGIOCC ACTOGATICC AAATCTITIGC ACGGAATCTT TATGIAGCTG GAAGATAATG	360
	ATTICTICTICT CITICATGAAG TCTTCCCCCAA TAATCCTCAT CITTTCCCCAT AACTGTATAA	420
	ACTOCTITICT GACTICOGOC GACGCATATG COCCIGCTIT TICAAAATCC ICIAGCAATA	480
35	TATOGOCTAC COGTATOTOC TOGOTOCTCA GITTACTOCT TATATICTOG TOCGATAGCA	540
	CTIGITTIAA TCTTTTOCAA AGCACAACAT CTGTATTCAA GATATCATAA TCTCAAACAT	600
	CTGTTCATCA CATTCCCTGA GCTGCGGCAA CAAATTGTTC ATCCGGATGT TGCAACCCGT	660
40	TARACTOCNO ACARINCART COCCOGGORT ARRATOCTOR TITICATOTRI CNARIGATINI	720
	NONCOCARCO TOTTOTGACA ACCOTONOAG TOCTTACARO COTACOCGIT ATGATTITNO	780
	NAATIOCIAC CCICONOCAT TIAGIIGIIC NNNATACCIT INGNOCCOGG GGNGGACITA	840
45	TCAN	844
	(2) INFORMATION FOR SEQ ID NO:485:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 676 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:	
5	GATCGATTAA AGGAAGCATC TOCTTCCCGT CATATCATAT AACATTGTAC CCGGGGCTGA	60
5	GOGGGACCAG TAGOGAATIT GATAGCAGTG TICTOCACGT COCCGGCTCCA CTGTGAGCTC	120
	CTTAAAGTAT ACCOCCTTCA TACACCAGIG CCCACAATGA TGCGTACTTG ACTTGTAATC	180
10	GAGAGCATTG GGCTTATACT GTGATTACGA TGAATGTAGC CAAGAGAGAA AAGGTTCATT	240
,0	CACGATATAC AGTACTCACA TICATGGCAT GCCATCCCCA AATTICCAATA CAGCCATTAG	300
	CACCAATGTA COOCTACTAA TCCCCCCACC TTAATTCCCC TCACTTCACA CTCAATCTCC	360
15	AGCTTAAAAG TCAGATTGAT TAAGTAAGAA AATGACGATC AACAGGGTGC TCAAAATAGT	420
	TGATTACCAG ATTCGGGCGT GTGGTCTAGT GGTATGATTC TCGCTTTGGG TAAGCCGAAGT	480
	TOCOGGITICAC TOCOGCITIAA CTACTAAACA TOTGAGAGOC CCTGGGITICA ATTICCCAGCT	540
20	CGCCCCAAAT TITITGCTCT CGCCTCCCGC GGGAAAGGTG AATATCATTT TACAAGTAGT	600
	TAACTCCTCC CACGITACGI CCTTCTGCAG ACAAGITGCA GCGGITTACA ATGCTCAGGC	660
	TAITTTIGCGG CITCAA	676
25	(2) INFORMATION FOR SEQ ID NO:486:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 827 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1344RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486:	
40	GATCCTTGCG TACTAAGAGT TAGACTTTAA TTAATAATAT TATTTGTAGA AGATAGAAAC	60
	CATACTGACT CACGTCGTAT TTAACCCAAC TCACGTAACC TTTTAATTGA CGAACAGTCA	120
	AACCCTACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA	180
45	TAACTIACAA TAGCIACICI AICGITATAT TACCCIGITC AAITTIGITA TCATAATAAC	240
	ATTIAATTAT TATTICAATA ATTCICATTA TIGITCAGAC TATTICATTA TGIATTATTI	300
	ATTAATTAAT ACATATTGGG CITTCGIGGA TATAATTATT GITAATCCTA CICATATATC	360
50	TAGICGITGA ACGITCITAT AACITTATAA AAAGGATIGI TATAAGCITC GCIGCAGATT	420
	GICCITIATI ATTATAAAAT AATATTAGGA GITCTITOCA ATTAACCCAA TITTACTCAAT	480
	ATATTYAAT ATAATTAAA SOOTAATTA ASASTTYAAA TIAATASTAA TAAATTATAA	540
55	GIAACTTITA TIOGITTAIC AAATACCATT ACAATAIGIT ATATTIGTIC ATTAIGCCAA	600

	ACTTACGITA TIGINCTACI TGIAGIATTA CNATTATACC ACAGITACCC CATCATATTI	660
	ATTTAATANA TACCCCAANT AGNITTITTT ANCATAAAAA GGANCTAATT TCCCTTTTTT	720
5	CNCCAANICC NNCICTCICA ATATTNITAA AAATTTTAAA CNNAANIAAG AAACCCCNN	780
	TNAACCNCAN CTITTITICAN GOCTTICNAN CCINITNAAT ANCCCCN	827
	(2) INFORMATION FOR SEQ ID NO:487:	
10	<ul> <li>(i) SEQUENCE CHARACTERISTICS:</li> <li>(A) LENGTH: 872 base pairs</li> <li>(B) TYPE: nucleic acid</li> <li>(C) STRANDEINESS: single</li> <li>(D) TOPOLOGY: linear</li> </ul>	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1344UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:487:	
	GATCCITATA AAATGOOCAA TAGACGIGIT ATAATATAAT ATACAAAATT ATAAATAAAT	60
25	TTATTTATA AATAATTAA TAATAATTAT AAATTAATAA	120
	AATAAGTATG GATTITTAAC TGAAATTTGT TAAAATGAAA TAAGAATTGC TAGTAATCTA	180
	TTANTAGAA AGTANTOGTG ANTACTICTAA CTGTTTCOCA CTANTCACTIC ATCACOCGTT	240
30	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
	TEARADTIONA SOUTANTANA TEARTITITAT TEARTTEAN ACTACATANA ATACTTATT	360
	ACAGTTACTG TAGGGGAACC TGCAGTGGGC TTATAAATAT CTTTAATATT CCATTTTTAT	420
35	ACAAATAAAT ATATTTTTTA ATATATTTTA TAATAACTAT AATTAAATAG TTAAAATTTA	480
	AATTATAATT TAATAATTTA ATAACTTATT AATTAGAGAG TTAGGGTACA TCCCCCCTAA	<b>54</b> 0
	TOCTATOCAT TATOGITOGI ACCACTOTAA TIAATAAACT ATAATAAATA AATACTAATA	600
40	TITTATATCA ATTAATTAT AATTATTITI TATTAATATT TIAATAITAT TTAATCAAAT	660
	ATATAAATAA AGTATTATAA TITAATAATT AAATAAGAAA TGAAGANAAC GACTCTCANA	720
45	ATTAAATTOC ATTNATAGIT TACCATTAAA CAACATTCCC TTATTCATAT TATTINATCN	780
45	ANIAATTAAT ATCITATTAT INATIAGAAG GANAGONINC CNCCCCIAAT OCTNNOCATC	840
	TIGIOGIACC NUNATTAAA AAGITTACAT NA	872
50	(2) INFORMATION FOR SEQ ID NO:488:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 835 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: PAG1345RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:488:	
	GATCCCAACG TCTGATTATG TGTGTGAATG CTGTTCTCCT GCTCCTCCTG AGTCTCCTTA	60
10	OCCUTIONICA TIGIACACTITI OCCUTATUTT CCTOCTOCAA TATAGCCCAT GATTICGTAC	120
	TTCTCCAGCA CTGACACCCT ACCGGCGTCT TTCCGCTGCC GATATGGCCC TATGGAGAAC	180
	ACATTGITAT TOOCCATTAG CATCOCCGAT TTOGACGIOC TGGCGCTGCC TTTGGTATCG	240
15	AGAAGCTGCT GTTGCTGTTG CTGCGACCAC AGOCTCCGGG TGGATGCCTG GTTGGATACG	300
	TIGAAATACT TATTCTGTTG TGTTTGATGC TGATTATTCA TACTATCGGA GGACTGTAAA	360
	CGTATCCCCA TAAAATAGAG AGCTCGAGCT ACCACCTGAC GACTTGTGTT ATTTGTAGTG	420
20	TIAAATOGAT ATCOOCIATG TICTAAGCTC GTTTTTAAGT GTAAAACATT GCAAATCCAT	480
	ATGCACACAG CTCATCCOGT TCTACCGACA ACCCTCTTGC GACCGGAGCG GTGGAGCTGG	540
	GETGGATAGT TCCCCGASCCC CTATGTAGTA TATACASCGT GCCACGGCTG CGCCTGCCCG	600
25	GCTGCAGGGC CTCAGCAGGA MTGCCCCTTC CNCCACTGCT TTATCCTCCT GAAAGCCGTA	660
	CAACCINCOGG NIVAAATAOOG GOC'ACOC'AAA GCINOCCCGAN GCCCCCCGAT AANAACINIGA	720
	CCAGCCIVIAG NGAGGCCCCG AAANAACANT GCCCTTTTTC AGCGGCCCGT CGCACAAACC	780
30	CCAAGGNGCN TCCCCCNITGG GNNITTIAAT NGCCNNOGGG ANGCCCCCNIT NCTCT	835
	(2) INFORMATION FOR SEQ ID NO:489:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 863 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1345UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:489:	
	GATCCOGCOT CAGCOCAAGC CAGTCTACTG GGGGACGGAG ACCCGCACAG CATTGGCGGA	60
	GOGAGAGCTE GAATATCOCG ATGACCACAT TICGAAGOCA GCTTACGTTT ACTITICCOCT	120
50	AACBGAGGGC GCGAGCGCCA CGCTACGCGA GCGCCTGGGC ACGTCCCTCC CAGAACAGCC	180
	CATCGIGIGI CICAICIOGA CGAGIACACC GIOGACICIG CIGICAAACA GAGCCAICIG	240
	TITICCACGAT GACCACGCGT ACCTGCTTCT GCAATGGAAG GGTATGCTGG TGGTAGCCGA	300

360

CACAACTGAA CTACCTGACT TTAAATGGAG TGGTGACACG CCGGTGGTGG TCACCTCATT

55

	CCCCCCTTCT GACCTCCCCC GOCTCTATTA TACCAATCCA CTTCTTGOGG ACCCCCTTAG	<b>4</b> 20
	TAGGECOCTIC CTOCATOGAG ACCATOTICAC COCCGACACA GOTACTOGTIC TOGTACATAC	480
5	TGCGCCAGGG CACGGCCAGG AAGACTACCT AGTAGGTCAG GCGCACGGCA TTGAAGTCTA	540
	CTCGCCAGTC GACCATGAGG GGAGGTATAT TCTGGATGAT ATTCCTCCAC ACCTCGGTGA	600
	TATOCTAAGA GAAGAGAGG GTAAGCCCCT GAAGGTTACA GACCACAAAG ANTOCNOONT	660
10	CTTCATCAGT TTGCTANAAA AACCCAAGAT GCTCCTGCAT TCCCTGAATA CCACNCTCNT	720
	NICCCINCAA TOGAGICNAA NAACNIGIIT TCNAGANCIA CCCNNCCGIN GITGCNAACT	780
	CATGGACTGA ACTICCCCCN GGAAACCIGA ACACTTTATT TITICCCINCC AGGGGAAAAA	840
15	NCGNICAAGG TTCTCNAAAN CGA	863
	(2) INFORMATION FOR SEQ ID NO:490:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 836 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1347RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:490:	
	CATCATCATG CCAGCGCCCA TGCCGCCCGCC GGCACACCTT CACACCCACC CGTAACTGAC	60
	AATACTOGAG CACCTTOGTG COCTOGCCCCG CTGCCCGCTG CCTGCCCCAT TATGCAACCA	120
35	CCCACACGIT TIATICCACT TAAAAATIAC TIAAGCIGAC GITACGCCIG TIGAAAAATT	180
	TICOCTICAC GGAATITITIC TOOGTGAGAT ATAAAAGOOG CTAAGTTGCA CAGTGAAAAG	240
	GIGAAGITIT TIGIGITTAG ACTICTITTA TGACCICATA GAAGGAATTI GOGAAATCIG	300
40	ACTITICIAGO AGOCTICTICI CAGITIGGAAG TGITTACATA CTACTOCTAA ACGTGCCCTA	360
	AGITAAGATT TICTTITCIT TAGITTTAAA CTCAGIACCT TATTCCATAA AGCGACACTA	420
	CGATGICTIC TAGATICTOC CICGICTOGA ACCIAACCAG ATCCTICAGC TCTGTCCCCC	480
45	OGATOCAACA GATOCOGTTC GCATCGTCGA AGTCGATGAC TGTOCOGGAT GCGTTGAACA	540
	GTOCCATOOC CGAAGAGATG GACCCGTGAT GACGATGTGT TCATCATCOG AGAGAAGTTG	600
	OCOCCAGTAC AACOGTOCCG TTACAAGTCA CCCAAGOCTT GTTTGACCGT TCCGGNAACG	660
50	COGTINGING ANACCCATCA COGAAANGIT TITOCCGTCT TOCGTOGGIN CNCCTGAAGG	720
	CNTGACCCTA TGTCATTCAN TNGTTCACTC TCCAGCAGCA NGACANTTCT GAATCCGCGC	780
	CAAATACANN TIOGIGIGIG CNACONICAN IGITIOCAGC NAAGNOOGNC NOONNO	836
55	(2) INFORMATION FOR SEQ ID NO:491:	

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 869 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1347UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:491:	
	GATOCTACAG AACTCAACTC TTATATOCAG GACTCAGTCA COOCGTCTGC AATOCGCAGC	60
15	AGCCACCCT GCTCCAGCCT GCGTGCCCAT TGGATGGGTG GCCACGACCC GAGTGGCCAT	120
	GIATTCCTGA TAACGITAAT GIGTATGITT ATOCTOOOCG ACCTOCAGGT ATT100000C	180
	CGCGCAATCG GGAAGCTITIC TOCTGATTGT CAACAGCTGC AGGGCGCTCC TGGTAAAATT	240
20	GTGGCACGCA TTTTGCAAGC AAGTCCGATT AGAGAGCTAA TTAACTCTGA AGCCCCCCAA	300
	CATATITIAA GACGOCITIT CGTICAACIG CCACTAGAGA GICTIGOGAT ICIGGIGAGC	360
	GOOGNIGHT THEOCHTICG GITCATHENG CHOGAAAACC CGATHCTATT CCTTGTCGGT	420
25	CITATICIGA CATGGACCIG GICACICCIG GIAACTATAC TCTCTTTCCA TTCGTTTGCG	480
	GAGCATTIGA COGGITIGCT CTICOCATAC CTICIAGITT TOOCGITATA CTOGIACATA	540
20	TAATGATCTA AGTAAAATCT GCAATATTAC ACACGAACGT TAAACTCGCC AGCTGGATAT	600
30	ACCCAAAGAT TOCAGATOCT GTOCTITCCG CCTAATATOC GGAAAGATGA GCAGGCCAAA	660
	CCCAATGCAG AGTAGGTTCG TCATATAGTA ACCATCOCCC AGAATGACAA CTTCCGCCCG	720
35	CTTTOGAAGC ACTCCCCTCC GGAAGGAACA TOCNATGGGC GAATTTTGGC CACCTTANAA	780
33	TINAANAAAC TATCATCOCC ATAATACATC CGANACAATT ACCCCCANAA TATCAAGTAT	840
	CNGAAATITT CNITANITCN CCAATACON	869
40	(2) INFORMATION FOR SEQ ID NO:492:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 772 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1348RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:492:	
	GATCCTTCCG CAGGITCACC TACOGAAACC TIGITACGAC TITITAGITCC TCTAAATGAC	60
55	CAAGITIGAC CAGAITITICC OCTOTGAGGT OCAGITIGOCC CCTCCTCTAA OCAGAITCCTG	120

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	AGGCCICACT AAGCCATICA AICOGTACTA GCGACGGGCG GIGIGTACAA AGGGCAGGGA	180
	CGTAATCAAC GCAAGCTGAT GACTTGCGCT TACTAGGAAT TCCTCGTTGA AGAGCAATAA	240
5	TTGCAATGCT CTATCCCCAG CACGACGGAG TTTCACAAGA TTACCCAGAC CTCTCGGCCA	300
	AGGITATACT COCTOSCTCC GICAGIGIAG COCCAGAACG TCTAAGGGCA	360
	TCACAGACCT GITATTOCCT CAAACTTCCA TCGCCTTGAA ACCGATAGTC CCTCTAAGAA	420
10	GTGCGCAACC AGCAAATGCT AGCAGCACTA TITAGTAGGT TAAGGTCTCG TTCGTTATCG	480
	CAATTAAGCA GACAAATCAC TOOACCAACT AAGAACGGCC ATGCACCACC ACCCACAAAA	540
16	TCAAGAAAGA GCTCTCAATC TGTCAATCCT TATTGTGTTC TGGACCTGTG AGTTTCCCCC	600
15	GIGTIGAGIC CAATTAAGCC GCAGCTCCAC TCCTGTGGTG CCCTTCCGTC ATTCCTTTAT	660
	TTTCAGCCTT GCGAACATAC TCCCCCCGAA CCCCAAAAAT TGATTCTCCT AGGTGCCGAT	720
20	TGTTNCATAA AAACACACCC ATCCCTATTC GCATATTTAT GTTAAATACA AG	772
20	(2) INFORMATION FOR SEQ ID NO:493:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 823 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1349RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:493:	
35	GATOGITATA TATCAGICTO TTOCTATAGA TTACTATAGA GOCCACCACT AATGIACAAG	60
	TTATAACTAC TOGTAACACG TTATATAACA GGTAGGAAAC GGGGCCGCCG GGGATTTTTG	120
	CCTATGGCTT GGCCAGGTAG CAACTGCTAT AAAGGCGGAC GTTTCTCCCCG GAGCTTTTTC	180
40		
	ATCTTGCGCA GTTTCACTTG CTAGTTAGTT TAGGGCTAGG TOGACAAACA TATTCCACAT	240
	ATCTTGCGCA GITTCACTTG CTAGITAGIT TAGGGCTAGG TCGACAAACA TATTCCACAT CGTTTTAATG GCTGGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT	
45		
45	CGITTTAATG OCTOGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT	300 360
45	COTTITAATO OCTOGTOTAC CTGATAACOT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGCTTCCTT GCCGACAAGT GGAGGCACGA	240 300 360 420 480
	COTTITAATO OCTOGTOTAC CTGATAACOT CAAGGGCTG GTTGAGCTGG ACCCCTGGTT AGCTCCITAC GGGGACATCC TCTCTGCGAG ACGCTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGCG CAGTCTAGTT GAGTTTGCGC GCGACGCATA	300 360 420 480
	CGTTTTAATG OCTOGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGCG CAGTCTAGTT GAGTTTGCGC GCGACGCATA CAAGAGCTAC GGGCTGCACG CGGACGCGCA GAGCAAAAGC ATAACGTACA GGGAGTGGGC	300 360 420
<b>45</b> 50	CONTITIANTE OCTOSTISTAC CIGATAACET CAAGOOCTIG GITGAGCTIG ACCCCTGGIT AGCTCCTTAC GOGGACATCC TCTCTGCGAG ACOGTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGCGGCG CAGTCTAGTT GAGTTTGCGC GCGACGCATA CAAGAGCTAC GGGCTGCACG CGGACGCGCA GAGCAAAAACC ATAACGTACA GGGAGTGGGC GCCCAATGCA ACCCGGGCGT TTCTAGTCGG CGACTTCAAC GGGTGGATGA GACCTCGCAC	300 360 420 480 540
	CGITITAATG OCTOGTGTAC CTGATAACGT CAAGGGCGTG GTTGAGCTGG ACCCCTGGTT AGCTCCTTAC GGGGACATCC TCTCTGCGAG ACGGTTCCTT GCCGACAAGT GGAGGCACGA TATCGAACAT GCGGTGCCCG GCGGGCGGCG CAGTCTAGTT GAGTTTGCGC GCGACGCATA CAAGAGCTAC GGGCTGCACG CGGACGCGCA GAGCAAAAACC ATAACGTACA GGGAGTGGGC GCCCAATGCA ACCCGGGCGT TTCTAGTCGG CGACTTCAAC GGGTGGATGA GACCTCGCAC GAGCTCCAGA ACAAGGACGA CTTCGGGTGT TCACGGTGTG TTCGGACCTG GGCGGACGGC	300 360 420 480 540

	ATNOCTIVAAA NIVACAGNONG TIGGTOTCAC COGACCOGTT TGT	823
5	(2) INFORMATION FOR SEQ ID NO:494:	
10	(1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 879 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(V1) ORIGINAL SOURCE: (A) ORGANISM: PAG1349UP	
	(XL) SEQUENCE DESCRIPTION: SEQ ID NO:494:	
20	GATCGCGAAA ACTAACGCAC CAAACCCGAC GGAAGCCAGA GCTCTCTTGT AAAGTGGCAA	60
20	GATAGIGIAT GICTOGCCCG ATGCCTCAGA CGATTTCTTG CGACCATAGT GCCAGCGATT	120
	GACATATOGA GITATCATTG CAAAAGCAGT GOCAATAGCA AGACCGGTTT TGITCCAACC	180
25	OCCUPICION TOTTICATTA TIGOCCACAA GOCATTETIC CAGTAGAAGG CCATCTICAA	240
	CACAACOCTC GCAACAAGGC CIAGAGACCA AGIAATGGCA AACIGCGCGA CACGGCGTT	300
	GICCITCACA AIGCTCITCA AGGICACTGC AAAGITCATC GIGCIGAGAC COGIGGCAAC	360
30	COCAACOGIC ATCAACCICC ACTOCOGITT CICAACTAIG TACOCICCGA TACOGAITAC	420
	ATTAGCAAGT AAAGGGCCGT ACTGTTGAAT CAACGTTGGG AAAAATGGAA CATAAAGCAG	480
	AACTGGGCTC AATACCGCCG CTATCACCCG CCTCATAGCC GGAGATACCC ATGTACCAGA	540
35	GCGGGAAAAA CCATATCATA CACAATAGGG CAGTCAAGTT CGTCCAGAAC ATAAACGAGT	600
	CAAAGGTACT GACAACAATG TAAAACAGAC TTGCCTGATT GGTGATGGGC TCGTCCGGCA	660
	GGTAAACGAG TICTOGTIGCT CCTGCGTGAT AATCACCTCC TCCCAGCATT TCCTCCATTG	720
40	COCCOCCOCC GAGTCCCTTG CCCCCCCAAA NAOCNNOGTG CTTGTCTTTG ANTGCACAAC	780
	CCCCNCGAAG GCCIGIGCCC IGGGIIGCCN AACITINCCI NAGICCICCC AGITIGCNIT	840
	ACTIACOCTO CNAAAAATTO CAAATATOON GGACNOOON	879
45	(2) INFORMATION FOR SEQ ID NO:495:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 829 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1350RP	
55	And the second section of the section of the second section of the section of the second section of the section of th	

	(A) Should bishtrift. Shy ib to 455.	
	GATCICTIOC AATTCCIOCT COGICICICT GIGATCICTA TIGATCACCT TTICGAGITT	60
5	OCTOCOCTICA CAAAGCCTCG CAAAGTTGTT CATAAGTTTC TTATACCGTG CCAGTTTCGC	120
	ASCCASCACA TOSTOSCTISA TOSTISTISSAS COCAATTISSA TOCCCATOOS COOCCATISTT	180
	ATCCTTGACC GCGATATTOC GTGTTGATGA ACTCTGAACG GCCTGGTGGC CTGGACGTAA	240
10	GGCGAAAAAG TAAAATTATA TAGAACAGGC ATGAGATTGG CTGGAAGTTC AGGCAGCCAG	300
	OCCTOGTOCG AAGCACCTTA CAGACCCATA GGAACCCACA TGCGCACGAA CTAGAGATGA	360
	GACCCACCCA AGGTGAACTIC GCCCACGGCA CAGGGGCAGT CTTAGCAACG TGGTIAAACAT	420
15	TAAAAATAAT ACATACCITTA CAAGCAGCCG GCATAGCAAC TGCCTGGAGT CATGITTITAG	480
	AGAAAAATAG AAAAATTATT ATAATATTCC TTGTGTATGA AATAAAACTG CTTTGCAACA	540
	CCCCCCACAG ATTCAGACCT CCCTGAAGCC GTAAAAAGCAC GAAAAAACCGA ACGAATAGAA	600
20	TTAAGATAGA AAAGCAGCAC TCGGCCAAAGG CGAAGCGGGG CGCCCAAGCC GCCCGCGCTT	660
	TOCCTONONO TOAGOTGCAA ATGCTCCTCA GTGGATCCTG CTCCCCCTGT CCCCGTCTCA	720
	CCTCCTCCAC TCCTCCTCNT ATCCTTTTCA TCAAACNAGG CTCACCCCCCC TGTTCACTCC	780
25	ATCTTONONC GONCOCTOG ATAAATTGCT CAGONCTACC TCTTGGNNG	829
	(2) INFORMATION FOR SEQ ID NO:496:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 875 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1350UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:496:	
	GATCCCCATT AAGCCCGACG ACGAAATCAA TACCAAGAAG CTCGACGAGG AGAAGGAGG	60
	GCGCCTCAAC GCCATCATCA ACGGGGGAGC TAGTCATATA AGGGTGCATA TAGCGCAATT	120
45	AAAGGITTAG CGTCATCGAT AGITACATAA AGITAGAATG CATGCTCCGC CACGCGCGCG	180
	TITCEACTOGG CGAGCCAGCG CGAAAGCGCG TCCTGCGCCG CGGGTACGAA GAACCGCCGC	240
	AAGAAGTOGA GITCCTCCCC CCACCOGTCG TAGAGGTCCT GGCTGAGTAC GITGTACTTG	300
50	ATCOSCICOC CCITOGAGAT GOCATICATG AGCCACTGTG TCTCGTGCAA CGAATGCGTC	360
	GOCGCOCTICC TIGTICCCACTT CATCATOGAC AATTICCCGGA ACGCCTICGAA CCCCGTIGATIA	420
	AGCICAAGCA AGCAGAGCCC COCAGCITAC ACTICCGTGC TGTGCGTCGG CTGGCCGCCG	480
55	CCCATCAAGC CCGGCGCGCA GTACTCAAGC GTCGTCGTGA GCGGCTCCGG CGCCGCGTGG	540

	CALACTRICE COGACTICAA GICCOCCAAG AATBCTCCTG CCCGCCACG AGCACGTTCG	600
5	COGTICTTCAT GTCCCOGTIOC ACCACGCAGC TCTCCCCGAAG GAACTGCAGC GCCCCAACAA	660
	OSTCACOTOC GTACOSCCAC CACTOSCCCT TGTCNCGGGC GCGCGCCGGT GCNCCGCTTC	720
	CANGTOGOGT TCAACCOCTC TACACAACOC COOGACCINCC TCOCCACCOC GAANCOOCOG	780
	GTATCCCNAC GTTINCCOCC GCNCCCCCN GGAANGGACC ACTINCOGTC NCGANCONCC	840
10	CCCGCCNGGT GOCAAGNOGG AATTINITTAC CIVICT	875
	(2) INFORMATION FOR SEQ ID NO:497:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1351RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:497:	
	GATCATAATG ATTIGICTTA ATTCTTTICT TAATTAITCA TTAAATAAIT AATTAATATT	60
22	TTATTAATAA AAAATATTTA GAGTTATGIT CGTTTATGAT AAATTCIAAA ACTTTGCAGC	120
30	ACGAACTGAA GACAACTATG TAACGCCTGT AATTAATTAT AAATTATTAT AATTAAATAT	180
	TCAAAAAATG GTAAGATITA TCGAGGATTA TCGAATTAAA TAACATGTIC CACTGCTTAA	240
ac.	GICTGIAACC GICTATTGIT TIGATTTTIA TIATTGCIAA CGIAGICATC AGOÇOGAATA	300
35	CITTAATITI CAITTAATIT AITCITTAAT TAATAAAAA TAAATAGGIA TICAITGITI	360
	ACTOCTAAAA CTACTCOOGT ATOGAATCOG ATTTOCTACT TTAGOCTTOG TTOCTCAATG	420
40	TCAATTAATA TATAATTTAA ATTITCACIT TATAAGICIT ATTCATATAA TTATIATTIC	480
40	ATCHTACTT GAATAATTCT TAAATTATTT TIATTAATTC TAATTATTAT TITAAATAAT	540
	CATCTACGAA CCCTTTAAGC CATTACGAAT AACGCTAACC CCTTTGTCTT ACCGCAGCTG	600
45	CIGOCACAAT TITOGITOGA NNCANITAAT TATATATCIC TITTAAAAAT ANAATCICCC	660
,,	TCATATTAAT AATTITATAT TCANANTAAT TATCMVIATT TAATAATTAT TCAATTTATT	720
	GITACCCANA NIAANAANAN ATTATTATTI ACATCCCCNA GIACNGANCA CITCACATIG	780
50	CCAAATCCCN CGCGITCCNA NAAATGATAT ATTICNANCAC GGATNICTIC TT	832
	(2) INFORMATION FOR SEQ ID NO:498:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 863 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1351UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:498:	
10	CATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
	ATTATATTAA TICTCCATTG GAGCAATTTG AGATTAGAGA TITATTAGGT TTAACATCAC	120
	CAATAATAGA TITTAGITTT ATTAATAITA CTAATTTIGG TITATATCIT ATAATTCITT	180
15	TATTAGTAAT TITACTAATG AATTTAATAA CTAATAATTA TAATAAATTA GTAGGTTCTA	240
	ATTGATATIT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGTT AAGACACAGA	300
	TTOGTOGTAA AGTATGAGGT TATTATTTTC CATTAGTTTA TACATTTTTT ATTCTTATTT	360
20	TTACTATAAA TITAATTAGT ATAATTCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
	TIGIAGIATC AATAAGIATA AITATTIGAT TAGGICTAAC TATTATTGGI TITIATACTC	480
	ATOGITTAAA ATTCTTTGGT TTATTTTTAC CACTAGGTAC ACCATTAATT TTAGTACCAT	540
25	TATTAGTATC AATTGAATTA TTATCATATT TTOCTAGACT TATTTCATTA GGTTTAAGAT	600
	TATCACCTAA TATUATACCT GGICATITAT TAATGTTATT TAGGIGGITT AATATTTAAT	660
	TIAATAGCTA TAAATATITT AACATTITAT TAGITICTTA COCATGAATG CNAATTTAGI	720
30	ATOGITGITT ANAATTOOCC ACCCTANTAT CCACCTAANT TGAGGITTIT TAAATCCCNC	780
	ATTITAAAA TCCATTTATT TACATNNATT AANAATAANA TATTTAATAA TATCCANNAT	840
	TNAANATIT ATAANIITAA AAN	863
35	(2) INFORMATION FOR SEQ ID NO:499:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1352RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:499:	
	GATCCTGCAT COTTTCGTCG GCCTGCAGGT TGATTTTGTT GCTCTCAATT TTATCCTTTA	60
50	TCAAATTCAC AACCTGGCAA TCCACCTCAT GCTTTATCTT CAACGAATGC CTCATCGTAT	120
	TGTCTAACCT GAGGACCATC TCCACCTTCC GTTTAACAAG CTCGACGGTA TCCTGTGTCA	180
	ACAGGITITAT GOCTOGGICG TCGACCCCCA ATTGGGCATC CCAGGCAGIT ACGICATCIA	240
55	TGTTGTTCTT OCTGTTOOGA GAGAAGOGAT ATGTAACOGA CTGCATGTTA AGAAGGOGT	300

	AGGGGGGTC CTGCTCCCGC ACGTCCGCGT CGAGCAACTC GCTGGTGTTG ATGTTGATGG	360
5	OSTOCTICACA CAAATCOCTIC AACAGOGAAA OCTOCTTIGAA GOGGAAGCOC ACGTIGGTOGA	420
	ACASCGACCG TGCGTCCTTG CCCGASCGGC TGGCGGGGG GAACGGGTTG TGCTGGTGGT	480
	COGACAAGTT COOOCAGCTC AGOGACGGAT GGAGCATCAC GGGCGCCTGC TTCGCAGGGC	540
10	CCAGGTCCCT AGGGTCCGGC TGCGGCAACG CGAGACCTTG TACTCCGCCG CCGGGCGGG	600
10	CTOSCOCASC GOCCONGTCA GTCTTCTACA CONCTTGACT CCCCCCACTC CTCCGTNGAT	660
	GACTIONCCOC OCTOTNICATIC COGTIOCTICOC ACACNICACAT CTICOGAATIGN TITTICCACCAC	720
15	CACCONGNAC AACTITOCAC ACCOGGAAAC TONNINGNUT TINGGACCCT GTCTTTACNC	780
7.5	TOCAATOOCN TOTGOTGCAT TITITGNAAAA CICCOCCCAA COCACCCCTC N	831
	(2) INFORMATION FOR SEQ ID NO:500:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 832 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1353RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:500:	
	GATCTAACTA TTAATGTGTT CCTTGAAATT GTGCTGAAAT ATAACGACCT CTTAAATGAT	60
	GICTATUTIG ATGACGATGT CGICAAGITG AGCCAATGGG TACTTCAAAC GIGTAATGAA	120
35	TAAAAATATA CAAGCGCAAA GCCCAATAAC CITTACCCTA TATATCTIGI AATATATTAA	180
	GITAATICAA CCATITACGI GCCATATICI GCGCIGGCAT GGTATCCGIG ATTITATAAT	240
	ATATATTICT COCAGOGGAA GCAGAAACAC TCAAGATCOG CGATTGCCGA TAAAAGAATT	300
40	GCTCCCTGAT TGATTGTTGT TCGAAGGAGA TGCAGATGGA TTGTCCAGAA AAACCGGTTT	360
	TANGACTOGT TOATCAAACT TGITAAACCA TIGOCCCATOG GCTIGCAGTA TATTGCCCAA	420
	GGTTICGCGG ATATTICTIC IGICIAATGA TAATGGTCCC ACAGGCTGGT CAGCGCCTGA	480
45	TOCACAGOGC GAAGAGGGTC GGTCTIATCAT AGGAGGAAAG CTTTCTTCAT CCCGGGGAGCC	540
	GETCOGOCTG TCGGCTAAAA ATGGAGGTGC GTCTAATGAA GACATTAGCT GGACAGGTCT	600
<b>.</b>	ACCOCCTTCC ATATCAAATT CATCATCCGT ATCCTCCTGT TCTTCTACCC ACCCTGTCCT	660
50	TATGITTAGA TCTCCAGCAT ACCGCAGTAT ACCTCCCAAT ATGATACGGT GAGAACCCCA	720
	CTACCACCCA GTOOCCNAAA AGAACTTGAC CCCCTGTNAC CCTNCATOCA TCCACNACCC	780
55	CACCCCCCA ATCNONCTGT ATOSTATGAC CCTCAGANAN CONOCTONGA TO	832

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 877 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

	(11) MOLECULE TYPE: LINA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1353UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:501:	
15	GATCOGCOCCA CTCTGTOGTT CATGTCCTOC ACAAGTTGAC CACTGTATAC CAGTTTGACA	60
	TCAGAGGGGG AAATCATCAG TGTGTGGCCG TACACAGAGC AAATAAACTC CTTTACTTCC	120
	TECACGETICG TETCGACTET CACTITICATA CTCTTCATCG CCAACACGGA CTCCGAAAACG	180
20	AACTOGATAG TTACACCATC CCCGTCCTGG CCGTGGTTGG TACGGAACAT AATTAAGCAA	240
	TOCCACAATG COCTOCOCCC AAACTCAAAG CCCAATACCT CCTGTAGCCT CAACCCCCCC	300
	TGTTCTGCCG CGTCTTCGGC GCCCAGGTAC ACAGGGGTAC GATCGCCCTG CAACTTGGAA	360
25	TOCAMOCATO TOCTTOCOCA CATOCITCTT CITOCAACAC AGGITCTTOC AGCTOCTOCG	420
	CTCGTACTCG TTCACTATAT CACATGCCAT OSTCCGCAGC GCCAGCACAG ACGTCTTCAG	480
	AGGCACACGI TGCCTTATCA CCGCCACCAC TTTATCCATG GAAAGCGTGT TGACCTGGAA	540
30	CTTGACGTTC ACATACGCAA ACTCACTGTC GCCATCGTAA GCCAGGTCTA CAGTGCCGCC	600
	TOCCACCTOC TOCCCACATO CAGOTOCAGA TOCACCAACO COCCOCCACA GOOTOCAATO	660
	TCCTCGCACA ACATGGTCAG ATTCGAGCGG ACGCTGTTGG TATTCAGACA GTATTGCTCA	720
35	GOOGGCCAAG COCCATGTTC TCCCCTGATG CATGATAACC AATGCCNTAC TGCNATACCT	780
	NGCNACTGAT AANTTOOGGG ANGCCCCCCC NTTCACGAAG AAGATCCANG CTCCCNTTCA	840
	AATAGNAANN CNGANTGAAC TGGCCNATNC CNAATCT	877
40	(2) INFORMATION FOR SEQ ID NO:502:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 871 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1354UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:502:	
55	GATOGAACAC GOOTIGIOCCA GOGAGOTTIAG GOTOGTIGIOC ATOCAATTIGA GATOGAAGCA	60

	AAAACCGACC ATGCTTGTTG AACCGAAAGG CGGATGTAGC ATGGCCCTTT CCCAACGGTT	120
	CACATOCTOG TTOCOCCCTC TTACCCTTGT CGTAAATTCT CGCAAAGTCA GCCTGGTCCG	180
5	TOGTCAGCAG COCCTCAAGG GCATGOCCCA GCTGCGACAG AATGATCTCG CGGTCTGCAG	240
	AAGAGTCTGA OCTCAAGCTG AAAATTGGGG GGGCCTGCGA CCGGCGCTGC AGCAGCATTG	300
	ACCACCITCAT CITICCACCAC TITCGTCACCT GOGGGTCTTT CCGCAGCAGC GTCGCAGACA	360
10	OGTOCCGACC ATTCAGAGGC COGAAGTTOG ATAGCAGATA ATGCAGGTOC GACAGCACAC	<b>4</b> 20
	CAGACATOGC ACTOGTTGAC GATACATACC GTGCTTGCCC TTCCTTGGCG CGCTCCAGCA	480
1.5	GTCGCAGGTC CCGCGAGGGC GGCACGAAGT CTGCGATGGC CTCAAATCGA AGTCCTGCAC	540
15	CTTGATCACC COCTOGATGA ACCOCTOGAA GTTGTACACC CCCGACCCCC GGTCCCCGAG	600
	COOCACCACC GACAGCOGGC TOGAACAGGC AGCGTTCCAG CCCGTGCGCC AGCCGCGGCG	660
20	GCACCTCTGT TGCACTGCTC NINCCACCCC ATTGCTGAAC GCCCCNTGAT TACAAATTGT	720
20	TONOCTOCOG GOCCOGGTTG COCCGGTTGC COCTCOCANGC CGCGGCACCC CCGCANCANANT	780
	GGATGANNET TONCTGATTIN NCCAAACCOG TICANNITGT COGGITTINT CANGGNCANT	840
25	NCCCNNICNI TGINCCNNIT NAATGCCCNC N	871
	(2) INFORMATION FOR SEQ ID NO:503:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 1166 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1355RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:503:	
40	GATCATOGCC AAAAAATTOG GAATAGGAAA CIGITTCCAG TACTCATCAA GGTCAGTAAA	60
	AATGITTOCC AGCAGIGAAG ATTOCATCCT TATCTTOCCA TITOCOGATA OGACATTTGT	120
45	TICGATATAC CIGIOGICAG AGGAAAAGAG TGITOCCAGT TGGGTAAGIT CTCGTAAAAA	180
45	CAAATAAACT TOTOTTOTIGG AAGTOTTACO GTACGOGATT CTATTCAAAA TOOTOTOCAA	240
	GTCCTGGCCA TCACGCAACA TATTATTTAA CGACTCAATG AAGATATTAC CAACTTCGGT	300
50	TGAAATOCAC TGAACTOCGI CCAATCTCTG TTGTATCTGA TCAATATTTA TTAAAGOCTT	360
50	TOCAATCCAG TICTICAAGT TOCTTAACCC GIAGITTGIT CTAGTATGAT CTAATACCCA	420
	TAACAGOGAG CCTTTACTOC TCCTATCTGT ACTGTTCTCA AAAATATCTA AGCTTTCAAT	480
55	AGCOCTAAGA AGGAAGAATC ATGTGCGTCT TCGAGCAGAA TGGTTTAAAG TTTTCCTTGA	540
	AGAAGAGTAA ACNINCATTT TIGAAGTITG TTAGGTAGCC ATGCACCAGC ATGAGCGCTG	600

	TITIGCAGAGG AACGITIGCCC TIAAAGGCTG GGTGCGGCTC ACTGAAGATT TCITICATACA	660
	ACCOGACGAG CTCGATCCTA TITIAGAGTGA TATCGGAATC TGAAGTATGA AACACCTTTT	720
5	CGATTICTGA GCCAAGOCCA TCTCCGACCA CAACTICACT CGGGTTTGTG TATTTTATTC	780
	OCCICIOCAA ACCOTOCCIC ACAAAACOCT COTOTITICAA CITCATOCAAC ATAACTICAC	840
	COCTGTTGAG ATTAACACTA ACCAGGAAGT ATCGCGTGTA TGAAGGTTGT COCTTGCACA	900
10	CAACACCCCA CACACAAGOG CTATCACCCA GGACCCGACG ATCTTTGGTT CGAACGTCTC	960
	ATTGATGCCA TAGGTAGCCC TOGTGAATAT ATTGGGTACT TCCCTCGAGA AAACAGAGCT	1020
	TGAGGICCCA CIGITCITIT TCACTGCGGA TGTCTCTGTC TGCTCCACGA CCCCCACTIT	1080
15	CAGATTGTGG TOCATCAAGC GCTGCAAGTG GACTTCGAGA CGGGTGTCTG GGAATTGGTGC	1140
	ASTACOCAAA CTTCTTGTGC TTGTGA	1166
	(2) INFORMATION FOR SEQ ID NO:504:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 887 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: INA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1355UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:504:	
	GATCATGCTA TCAAGTOCAG AGAACACOGA TAGAGCCTAC TCTGCAGGTT CGGCCTCGCT	60
35	GAGOOCOGOG CAGAAGTICEA AGAAGOCOGOC AAATACOGOC TICCOGOCAGO AGAGOCTIGAA	120
	GOCCTOGCAG CCCATCCTGT CGCCGCAGAG CATCCTCCCA CTGCTAATAT TGCTGAGCGG	180
	GOGGTTTGCG CCAATCOGGA TIGCGCTGAT CATCAGTGCA AACAACGTGC AGAACCTGGT	240
40	GATOGACTAC AGCCAGTGOG GCAAGCACGC CACGTCOGAA TACACGCCCA TCCCCGAGAA	300
	COTESTIGASC TACCACTTICC GGACGTCCAT GTCCGAACAG CCTAAGTGGC GGCTGCATTC	360
	CAAGAATGAG TOCGAOCTAG AATTTGAGAT CCCCAACGAC ATATCGAOCT CGGTGTACAT	420
45	ATACTACAAG CTGACGAACT TCTACCAGAA CCACCGCAAG TACGTGCAGT CCTTCGACCT	480
	CGACCAGCTT AAGGGCAAGG CTGTTGCACC AGACAAGCTG TCCGACACGT GCCACCCGCT	540
	CTCGACTAAG GACGGCAAGG CTGTCTATCC CTGCGGCCTG ATCGCCAACT CAATGTTCAA	600
50	CCACACCTTC ACCOCCACTC TOCCCCCCTCT CCAACCCCCCT COCCCCACTA CAACTCACCC	660
	AACAAGGAAC ATCOCCTGGC ACACNGACCG CAACAGGTNN CAAGAAGAAC AAGCTACAAC	720
	CCCCCAGANA INGIGCCOCC CCCCCCCTTG CCACGAACGI ITCCCCCNAA ICCNIANNAC	780
55	AANCCAACCT GOCTGACTINN CTACTTGGGA GAATTTGCGG IMTIGGANIG NNCCCTGCAG	840

	NOTGOONCOT INTIAAANOTIN ONTINOAAAAA AAAAGCAACIN OCCTOOC	887
	(2) INFORMATION FOR SEQ ID NO:505:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 823 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
10	(ii) MCLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1356RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:505:	
	GATCTACATA TOCATCAAAA CATGTOCCTT CATGCGCATC AGTAGTTATG TTTGCGCTGA	60
20	GAGGGGAGCC ATTICCAGCT TGTCTGCACA ACTCCATATC ATTIGCATCA TCAACCTCAT	120
20	TATCOCTATC ACCATOCITA GIOGAGIAIG GAAAGGAGGG TGACACAGCA AGOCCAGAGG	180
	TATCAGTIGA AGACATATOT GIOCTCATOC GGIOGGCOCC ATCATAGTOC GATGACTICG	240
25	TGGAGGATTT AAAGTCATTC TGCGGAGGAT TCTGTGGCTC TACTGACCTT GCAGATTCGT	300
25	TTTCACTTTC GTACAGAATG GACTCATCTT OGAACTTGAG ATCTATOOGT TTGTGATCAT	360
	ACGCGACTCT TTTTTCAACC TTCTTTGTCG TCATTGGCAC GGAGTTTATC AAGCTAGAGC	420
	CCAAGGAATG CTGCTTATCA AAGTTCTTCT TAGCCATGGG CATTTCGTAT CTATCATCTA	480
30	TOOCTTOGIT OGAACCATAC TICACCIGGI AGCCATACIT IGIATIATIAA TAAGAGITGC	540
	GATAATOCTT CGTACCAGAA CTACCOOCAC TGCTAGACTC CAATATOGCT TGCATGAGGA	600
	CIGCGCACGC GAAGTITACT GCCATCCATA TCAATTITGGG CWIGGCTGCC ACATTCGAAA	660
35	ANANTAAGAA GAAGTACGAC TAATCCTCCA CTNOCTACCC CGTCCNTAGC AGCGAACCGG	720
	CIGCIGICIN NONCATOCAC COCCGIGCIT GCTIAGCICC TACNOCONIG TGGITCCATA	780
	ACCCACCOCG TGTCACCCCA TOCOCTGANC ATTNTGAGAG ANN	823
40	(2) INFORMATION FOR SEQ ID NO:506:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 873 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1356UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:506:	
55	GATCTGAACC ATATTACCAA AACCAAACAA AGAATTCGGG CCCAAGCCAC CCGTCCCGC	60

	GINAMOCCCI MINACCADCI IMCOGGICIG TOGGCGCCAT MGANATITICO ATTITICANCO	120
	GAACCAACAC GTCAATCCCA AACTACACTT ATCATGCCTT AAAAGGGATT ATCTTTTCTA	180
5	ACGAGGAGGC CCCCCTGCGC AGTAGGAAGC GCATCTTAGC GGCGTCCCGGC CGGCACATTTC	240
	GOCCOTTOGA CTOCAATATC CTACTTCTGC AGCGGAAGAT AGCGCACGAA AATCTGCGGC	300
	OGAGCAAGCT CAGAATTATA TGTAGGACCA AACATTGTCA GCAACGCCTG CGCCGAGTTC	360
10	TOTTATOCAG TAGOGOGATT TOCTOCGAAT GCCGTTCCTT TTTATCGTTT CTTTTTTCAG	420
	GGGCATCTGC AGAAGCGATG AGGTCCAAAG CATCTTGTTG CATCGATCAC CGAGCCCACA	480
	GOGCAGGTAG AGTAAAGCCT AGTCACCATG GTGGTAGTTG ATAATAGCCG CGGAGGCCCA	540
15	TTCCCATACT ACCCCCCTAA CCTCCCAAAC AACCTACCCA CCCCCCCC	600
	GACTACGACT ACAAGTACCT GTTCACGCCG CAGATATTCA AGCGCCAGAG AAGCTTCAGC	660
	CATTITICTICG ATCHATGCAA AATCCCCCGGT GGTGCTTGGG TGGCNTTTGG GGNINCACNC	720
20	CCCINGCAAN NCTGGCGGNT TINVITINCINCC NCCAATINNIG AATACCGGNG GNGGGAANTT	780
	TGAAAGNVAA NCONACATNC TTATTIGGGCT TNCONGVIGT NGAAGGGGGC TTCNINNAAG	840
	GNONATANN CCCTTGNGAA TCCTTAANAA AAT	873
25	(2) INFORMATION FOR SEQ ID NO:507:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 840 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1357RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:507:	
40	GATCCCAGCG AGGACATCGA AGAGGGACTIA CTGTIACCOCA TGGACAAGCT TCGCTGCCGA	60
	TTGATGAGGG AAGACCGAGA TGAAATGACA GATGGCCCCA CCCTCCCCAG CCTGATCTGG	120
	AAGGAAATGT TITCTGCCGT COGTATGGTG TCCAGOCTCA TGGTAGTACC TGCATGATTC	180
45	TGTCTTTCCG TGATCGGCTT CATGGTGGGC GTTAGCGACT TATAATAGTC GGTGCCGGTT	240
	GCTGGCGCAA GCAGCTGGCA TGCAGTGTTG TCCGACAAAT AGGAGTACCG GTTGGTGTTC	300
	TTATTCGTGG TGTTGTCAGA AATGTTTGCA AAGGAATAGA AACCATTTTC CATGGTGGTC	360
50	CACCOCACTT COCACTTCTG TOCCOCTACT CACATTTCAT TTCTTCTTCT	420
	GOCCOCCTT COCCAGGAAA ATGCCGCCCC TGTGCCCCCA TGTCCTCTTC CTGCTTGTGT	480
	COGFFICIETC CONTICTOCCC TAGGGGCTTG COCTIGNAGAG TITTCAAAGCT TITTGAACTTC	540
56	AAGGAGGGCG ACGCCGGGCC CACGAAACGA TATCGCTTTA CTCCTCCTCA GCTTCCCCAT	600

	AGGLATUION ATGCCATTIT ATTAATATAT TICCCCCGTC CGAACCCCAA ATGTATGTCT	660
5	CCCGGTTGGC AAGGGATTCC GACTTATATA TTATTTGATG TCCACCACAG GTTTCCNAAA	720
5	TATTATACAT CNATTOCCNA ACCICCOCNI TAINCATCAT COGACCNONC CNCATTIGIA	780
	CNCACTAACN TOCACATNING CONATIVINIT AACCCATCAA CNCACCTTING CTOCCCATCT	840
10	(2) INFORMATION FOR SEQ ID NO:508:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 888 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1357UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:508:	
25	CATCCTCCCC TTCCCCATCCA ATTETETTCC TTCCCTTCAC CCCCATATCAC CTCAAAAACCC	60
	GGTCCGAAGC CACCAGCACC TTGTCGCTAT GTGACTTAGC CGGCTCAGAG AGAGCAGTGA	120
	CACAGATAGT ACCCCCGAAG GACCCTCCCT TCATCAACAA GTCATTCCTA GCCCTTCCAA	180
30	COGTICATACC CAAACTTAGC ATGTTGGGAA GCCAGGCCAA TGGCCTGCAG CCGTCTCCCG	240
	CAGCOGGCCA CATACOGTAC CGTGACTCAA AGTTGACCCG CATOCTTCAG CCAGCATTGA	300
	CAGGAGACAG TATCATTACG ACCATCIGCA CCATCGATTC GAAAGCCGAG TCCTCAACCG	360
35	AAACGACCAA TACCGTCCGC TTCGCGTCTC GCGCCAAGAA TATCGCCCTC AACGTGCGCA	420
	AGAATGAAAT GGACTOOCAC GOOGAGAAAG ACAOCATCAT OCAGAACTTG COCAAGCAGC	480
	TTGACGASCA CCACGAGACC ATTGTGATCC TCCCCCCCAC TCCTGCACCG CCTACCGCCA	540
40	ACCIOCAC CACCCOCTE CACACCCTE COCTOCCOCC CACCCACCTT TCACCCACC	600
	CACGCCACAA CATTGGAAAA AAGGNITGCT AAAGGTNGAA AACAGCATCC TCCAAGAAGA	660
	ANCTICCGAGC CATTOCGAAA AAOCNICTCG AANNAGGAAA TGATGICCTC CGAAGAACOG	720
45	CANTITIONCA NATICITINAA ATCTCCCCCT TOGAAATCCC CCCGTCCCCC CAAAACCAGG	780
	NINCAGGGET TGATTTCCNC NGCCCCATTA CCGNNITACT TTCAAAANTA AATNCACNCC	840
	CCCAGGNOON NGAAAATNON TTCCCCCCCCN TNTGGNGTTC ACCGCCNA	888
50	(2) INFORMATION FOR SEQ ID NO:509:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 833 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1359RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:509:	
10	GATCCATGIT TATTCACCCC GCTCACTOGC GTAAACGATG CTTTACGITG CTCACATCGC	60
	COCCACCATT AACAGCGTAT CACATTITAC GITTCCGTGC AGCAAAAAGT CGGTCGGAAC	120
	ATAATOCTOC AATACCACGA TAGGTCCGCG CAAGCGCCTA ACACGTGCCA TCCTGCTCGC	180
15	CTCCCCACGG GCCGCTGGGG CTGTGCTGGA TGAAACTGGC CTGCAGCGTA TGAGCGGACG	240
	GOCATTOGCC CTGCCATTAC TGCACGCCCC ACCGACAGGT TTCCCCATGTC AGCATGCACG	300
	GCAAACCCCC AGAAATCGAT AAGTAGCAGG ACACGCGTCA GAAAGACCAG TGTGGTATCA	360
20	TOCCOCACGA GGACCTAGOC AACCTCGCTT TTCCGCAACC ATGCCCGGCC GCAGGTTCCA	420
20	ACGCGGGAGC GCCTCACCAA GCCGGGATTG CTAATGTCCC TTCCGGCCCAA AGGCCGTCAC	480
	AGCTAAAAGA GAGOCOCCCA OGAAGOCATA TAGCTGOCAG GAAACGATAC GATTCAGCOC	540
0.5	ACTOSCADOS TAASGAACAS GASCATOACA TOGAACAGTO GOOTIGIGGIN TOCATOCOTIG	600
25	AAGGINGACA CTAACCIGAA AAGCGGCGGT TGGCACTAAN TACAAACNIT ACCACAGTAG	660
	ATGCCNAATA CTGCTGACAA ACGAACTGGG ATINCTNACC GGTGCTGNGG ANANAAATCT	720
	NCCAAGAACN TINAACNCAA TIGOCCACTA CCCCICITGA TCCCTCTINN ATCNCACOGT	780
30	TTGGGANCCG GNENOCAAAG CCCTGATGGN ATCCCCTGACN AANTTGGACT NIVIT	833
	(2) INFORMATION FOR SEQ ID NO:510:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 871 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1359UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:510:	
	GATCOGTGTA GTACACOGTT TCCGGCCCCC CTTCTGGCAC AGCAGCTCCC ATCACCGCCG	60
	TACCCCAGAA CTOCCCOOOC GOGTCOCCAAC ACTAGTGOCT GCTGCTGATG CCCGCCTTCT	120
50	AGTOGITIGOC TATTITATTO CTOCCOGCOCA TGT1GCCOCT GICACGGCGT ATCTCGATGT	180
	OCCUSACIONE CACCOCTATIC TITCCOCAGAC COTTCCTGTG CATCTOGTGG CACCACCOCA	240
	ACCECCOCAC GASCIOCOTIC ATGCOSCIOGA COCCCIOCOC TGTCATTCOG TTTCTGCACT	300
55	ACCOGNOSIA CAATOUSICA TATACANOGE CANCOCOGAT GCCGCCACCT TIGHTGGNCC	360

	The state of the s	420
	CTACGAGIAT CTGAAGCTGC TCCACAGGGC GCTGCACTCA ATAGCCGAAA CGTTTGGCGC	480
5	CCGCTTGTGC GAGCTGGAGG ACCATTATCT GGACGAGGTG CTCGAAGCGG TCGACCGTCT	540
	ACGGGCCCAG GCCTGTGCCG CGGTAGGTGC CTGATCTTCT GCTAAACCCA CGCCGAAACA	600
	AAGATAGCAC CCGCCGCTCC GGGTAGCGGC CGGCCGGTCGT GACCAGTTGC TAGCGTTTAC	660
10	TTOCATACCC GTATCTOCTT TAACCGITTG GAAGGITTAN CATCATTAGT TAACTGTCC	720
	CCTTTCCTCC CCCTCCNTTG CCAACCOCC CCTATTTTAA NITACCNCCC CNTTAACCNC	780
	NCCTGAACAA AAATGAATTC NTTINGANAN TOCCCNATTT TNAGGATATC CCCNGTTTGA	840
15	ATTOGANAAA CIGATTIOCC MITTIININI A	871
	(2) INFORMATION FOR SEQ ID NO:511:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 850 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1360RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:511:	
	GATCCTTCTC CTCCGCATTC ACAGAATATA TOCTCGCGGT CATATCCTTC GCGGTCGAAA	60
	TAATCAACCG TCACTCCCCC CACCATGTCA CCCATGTCAT GTCCCCCCAAA TCCCCCCCGT	120
35	GCACCOGGTA GCGCACAAAA GGCGCAAAACT GCCGCTCAGC ACTGACCCCT GGAGTGCGGC	180
	AAATCTGAAG AAACCTCCCA CATGCCAGAG CAAAGAGCTT ACCGTCTGTC GAAAACTTCA	240
	CGICGITTAC TITIGICCTTA AAGITGAAAT GAIGIATCAC ATTCCICGIC TITATATTCA	300
40	CAAGGATIGC CCGACCGTCC ACGTCAACCG AAAGAAGCAG IGIACCCIGG GCATIGACGT	360
	CGATCCTCCG CTATATTCCT TCTATCCTCA TATTCAAACG TAAACGACTT GTTACCAATC	420
	AGGICAAACA CCGATACCCT GITGCCAACG GGGGAGAATA GCAGGGITGC ATCCTCCGAA	480
45	AACACCACAT TICCCTGTCT GTATACAGTG CCTAGCAGAT TOGAAAACTT GAAATCAGAC	540
	TICATOGIAG TOCAATOCCI TOCCTTOCTT GATCTTICAG TOGIGIAGCT CATCTCATCT	600
	CGAATTAAAT TTTCCGTACC ACCCAAAAAA ACANATCCTC CANCTGCATC TCAAGATTAT	660
50	ATATATATO TCGAAAATTG AANATCCACT CNICTAAATG GTACACNGTC ATATGAATGT	720
	GITINITIGE TECANIATES ENACEATIAS CEASICEAGA ATGGGAATAT ATGCCAGGAT	780
	NICOGOCACT TCACCCTGTT TTGACANATT TCTTGAGNTG CTGACAGCCG AGAAAAAAAGG TCAAGGTTAT	840

	(2) INFORMATION FOR SEQ ID NO:512:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 851 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1360UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:512:	
	GATOGATOCA AACCAGGACA ACTACTTAGA AGAGTOCTTG AAAATTAAAA GTGTATTGAG	60
	TGAATITGAA AATGACGTAC COGATAAGAC AGATATCAGA GGAGITCTCA ATCCCGTTGC	120
20	AATTGTTOGT TCCCGTGAAC ATGTGTTCTC TGAAAAAACC GGTGTATTGG GAGATCTCCC	180
	GOCTOGAAAG GAGCAAGTAT TCGGAACATT CTTTGCACGT ACCCTTTCGT ATATTGGTGC	240
	AAAGTTACAC TATOOCCATC CIGATTTTGT TAATOCTATA TITGTCACTA CCAGAOGTOG	300
25	TGTATCGAAA GCTCAAAAGG GCTTACACTT AAGCGAAGAC CTTTTTGTTG GGATGAGTTC	360
	CATATTACCT COCCCTAGGA TTAACCATTG CCAGTACACT CAATCCCCCA AACCCCCTGA	420
	TITAGGATIT GOGTCCATIT TGAACTICOC TACTAAGATT AGIGCOGGTA TGGGGGAGCA	480
30	AATACTCTCA ACOGAATACT TITTACTTGTG TTCAAATCTC CCACTCGACC GTTTCTAGTT	540
	TCTACTATGC ACATCOGGA TACTACTTGA ATATGTTTCC AATATCCCTT CTAACCCCTT	600
	AATTANGNAA TITANICOOG NATTAATOGC OGTCCTOGTC AANCONACCA AAAATNINNA	660
35	NATICINITA ACCCCCAAAN CIGCAAAAIT TATIGIIGCC ATINAACCCN TAACCAAGGI	720
	NOCCONTONO GNITHANONA TOCONTINUOCO NOCCOGUNOCO TUCCOAGUIT TONAAGAAAA	780
	ATTIBAAAAC CNACNCOOGG TINCOCOGAA AATGAAACIN NIANAAGNOC COCCITICAA	840
40	ATTITITIT C	851
	(2) INFORMATION FOR SEQ ID NO:513:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1362RP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:513:	

	GATCATAAGC TATTGGGTAC CCGTTGTAGC CTAGCCTTAA AATAATGGAC ATTTTGGAAT	60
_	TTAGTTATTG CGTGGAAATA AGGTATATAT ATTGCTTCCA AGTTTAATGT COCTTTTAAC	120
5	TCACTAAAAT ATGGATGIAA ATTGTCTCAA TTGGACTTTC ATGTTCTATC TATACACTAA	180
	CTOCGATOCG ACTCATTGTG CTTCAGTATT CAAAACATGT TTTATATATG TAATATGCGG	240
	ACCTAGAAGG CAACTAAATA TGAGAGOCAA CTTAGTCGCT GTCGCTGTCG CTGTTTGAAT	300
10	COCTOGAATC TTTTTCATAC ATGATCTOGT COCCATTATC TTCTTTTAGA ACOCTAAGTT	360
	CCAAGICCIT ATGAGATICC TIGITCICTT GAGAGACCIC GICATCAAAG ATGATCITGG	420
	TGTTGGAAAC GACAGGCAGG TTTTCTGCTT GCGACCTGTG ATAGCCTTCA CTTAGCAGTG	480
15	ACCCCTCGAG GGACACCATT CTGCCCGCAG TGTAGACATT TTTAACAGTA AATTTGAGTT	540
	TICCGICCAG CIGCITACCG TIGCCGICAC CCAGIGGCCT AGAGACCGGG CCIIGCGCAT	600
	CCCTGTGGAG AATCGTTTGG CTGCTCCCGT TGGTACTCTC TTGGTTATGA ATAAAGTCCA	660
20	ACCATCCOGA ATGITATTIC CTAATGAAGC GTTTGAACTT CGTGATCCAN CAACCATNIT	720
	GITGAGGIGA CNIVITICAAAT CONCCONGGA CNATCCONAT TITINGNGACA NOONCAATIT	780
	CCCNECCCO NITAANCCAG GNIATCIGNI CCANIGANIA CATCIONCIT T	831
25	(2) INFORMATION FOR SEQ ID NO:514:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 854 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1362UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:514:	
40	GATCATACCT CCAGOCTOCC AAGCAGACAT CCTGACATCA TACAGCCAAG AGAGCAGCTA	60
	COCTGTCACC GAGCTGGAAC AGAGGCTAAA CGAGTTTCGC ACTAAATGTA GAAAAAATGC	120
	AAGCCACTITI CAGGCACTAC TITICACTGGT AACTGAGATA GACCATCCCG ACAGCAGCCC	180
45	OCTAAGICAC CGTACAGTAG TCTTGACATA CATOGAATAT COCTAAGGAA GGAGGTGTAA	240
	TAGGACACAA AATCATGAGA AGAGIATTGG CITGTGCACG ATGCCGTGGG CACAAGATCA	300
	AATGCGTGCA CAACAACGAG CCACCCTGCT CTTACTGCCA GCACAAAGGC ATAGCGGAGA	360
50	AATOCGTGTT ATCATTTCCG CCCAAGAAGA GCCGCAAGAA GCCGGAACTA TACTTAGAAG	420
	GOSTTGOCAT GOCCCTGOCC GOGTATCCGG TGCAGCAGTT GGAAACTGCA GATCTGCACG	480
	AGCATAAAGC CAGAGCGGAC GGCTCTGATG AAAGCCAAGC TCCTGTGCAT GCGCAGGACT	540
55	ATACCATCCC GAGCAAGCTG CGCAGATGTA CGAGCTGCCC ACCAGATGTA CTACCGCTGC	600

	CCAGOCGTAC TCCACGGTTA TGTCGAGTAG TGCGAAGGTT CCCAGGCGGG TTGATTCTCC	660
	COCCAATTOC CACCOGGATT CTAAACOGAA ANAATGCAAC NCATGGAACC NGCCNTACTT	720
5	TMITOGACTIC TCCCCAGTOC CONATOCATN GTOCACTTOC ATMGAGANNI TGTCATCCTT	780
	CCCCACTGCG MIGITTANAT GANACCNCCC AAGAATACCC CCTGACCGTC TTTGGTTCTT	840
	TTTOCCCCCC NCCT	854
10	(2) INFORMATION FOR SEQ ID NO:515:	
15	(i) SDQUENCE CHARACTERISTICS:  (A) LENGTH: 853 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1363RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:515:	
25	GATCATTATC AGCATTAATC TICAACTOOG CATTGOCTCT TAAACCAATA ACAAAACCOG	60
	CAGATITOCC TCCAATTOCG TAAGGATCCT TTAACCCCTT GAGGGATACT TCAAAAAACC	120
	CITCACTAGG CCAGCGAATA TTAATCTTGG CATGGAACAT ATTCCTAATT TTATCCCAGA	180
30	AGCCTATTIT CTTGGATGGA TCAACTGGAG GTTTCGAAAA ATTGTCTAAA CAATTCATGG	240
	CCTGTTGTAT ACCACCTTCA TAAGAGCCAC CCCATGTCAC CATCGTGATG TCTTTCGAGT	300
	GTATATCCAT TGTTACCTGA CTGTAAATTT TAATAGGCGT TAAAGACCGG CGCAAGCGCA	360
35	ACGAATAATA TAGGTCTATC TCAGAAGAAG TAACGGAAGG AACAAGCGGC ACAAATATCG	420
	TICGIAGCIC CITGGITGAT TGAATCATAT CCTCCAGTAA TAAAGAGGIC ACCATACAAA	480
	TGTATAGCCG GAAAACAACC TTGTTGGGAA GGCATAGCTT CGGCATATGG ACTAACGGTA	540
40	GINGGGITAA CCITNAAANA GCCCCCTTAA TICACCCANC TIGGCTTCCA AINIAAAAGG	600
	GAAGCCNCCA NITATICIGG GITANITTIG GAACCCCNIT TNCCCNCAAN TITAATNAAT	660
	TONONNITTIT ACCOURTCOCA CATHANGGOT TAAANINNOA TGITTITACOC COCONGCCAA	720
45	GANNICONCC ATTTIGGAAA TGITANANIC CANACCCCT TINCATNI'IN NAGGANCTIC	780
	AACTGICCNI TINCCCCAAA AANITAATCC CCCNAAAAAT TCTTTCCTCC TGGGGNITTT	840
	CCCCCCTTAC CVI	853
50	(2) INFORMATION FOR SEQ ID NO:516:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 858 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genamic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1363UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:516:	
10	GATCGAGGAT ATTICCGTAC OCTOGATGIC OCTOGATGIC AAGTACATGG GTGATCGGTT	60
	COCCTITUTA GIGICOCTTO AAAATATOAA COACAATAAG GICTGICTOC TGAAGTCTOG	120
	TOCOCTOGAG GITCTCOCCT GITTCACAAA AGACAGTCCC TITTGGACTAA CATGTGITTGA	180
15	ACTGAGTGTC AAGTTTCTTC AACTCACAGT GCCTGTGAGT AACCTACTAG CACTATTTAC	240
	CTTGGGCAAA GAAGAAGATG AGGACGTCGA AGGCTTTGCT CGTAATATTT TOGATGGCAT	300
	GACCGAAGAT CCACAACTGA ATGCACAGAA TTGTGTGGAG ATGATGAGAT CAAGAGTTAC	360
20	CACCITICAT ACCTACTITT CCCATCTAAC TAACCITGAT TITTTIGITG ATAACCITAA	420
	CCTGGCAGAT ATACCACCCA GCTTATTGCC TGAGTTGTCA TCTGCCTGTG AGCCTTTGAA	480
	ATACGAAGIT GOGCTITICTA GITTIACTIT TCAAGICACC CGITTTAGCA CCCGAACAGC	540
25	CAGGIATAGI ATCCITTICA AAAGICIGAT AGACOGIAGG GICOGIATCA CATIGICATC	600
	GITGCAGIOC GCICTCAGIT AATGCCCCTA AAATCCCCCT GAAAAGGCTC CTGAATACAT	660
	CCGGITTITG AAGITCCCAN TTATATCCAT ATGGICANAC TATACITTIC CIGAAAATTT	720
30	CACTOGICCA COCTGITICT GANACAAAGT CAATOGICGG CAGITICICC CCTACCNTAA	780
	NATIGAAAIG AAACCCCCAN CIIGAACCCC GIINGCAAIA CIGIANGACT ATTINITCCN	840
	CANAACCCCIV CCACGIAN	858
35	(2) INFORMATION FOR SEQ ID NO:517:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 842 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1364RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:517:	
	CATCACATOC ACGICACGIT COCTGCGCTG GGCACACCTA CGGACAAGGA CTGGCCTGAG	60
5 <i>0</i>	GICTOGICCT TCAGCOCGTA CAACAAGATC CAGGIATACC CGCCTCCGTC GCGCAGCGAG	120
	CIGCGCAGCC GCTTCATCGC TGCAACTGAG AATGCCCTCG ACCTGATGTG CGGTATGCTG	180
	ACGATOGACC COCACAAACG GTOOGACACG ACTOGTTOCC TOCTCAGTCA GTATTTTIGTA	240
55	GAGCTTCCGG AGGCGACACC TCCTACGGAA CTTCCAAAAC TAAATAAGTA ATGACTATGA	300

	TAACCTAGAT GGTATACTCG GACGTTTTGT GTTTGTGCTT TGAGGCGATG ACATTGCCTT	360
_	TTATOGTATC OCAGACGITG CCTGAAAAAG ATTCAACGTC TCOGTAACAG ATTTCCOCAG	420
5	ACTACTIGIT GAAAGAACAA AGACCAGAGC GCTGGGATGC TCACCCCAAT GACGAACCCA	480
	CTCCGCCTTA TTGGCGCTGG CTGCAGGTTC CTTAGCACCA ACAATAGGCC GCCACTGCAC	540
	ANGATICTITIC CCTCCAAGAA GCTGGTGAAC AGGATGCTGT TCCGACCTTG ATAGCCGACT	600
10	GACCITCOGG AAATTACTIG CCTIGIATAC GAGCAGTIGI ACACCCAATT AGACAGTTAT	660
	TACGOGCAAT TIGITATACC CONCONCTIG ANGGONCCCA CNITINTATCC TGAAAAGNIG	720
15	CTNGAAAAAA TCCCCGCNAA NGAAAANNCC ATCGCCATCT ANTTGNCTNG AAACAACTGC	780
15	TTTACTGCTG CCCAATNCAN ACCAAAATON CGGCCGTACC TTGACCCTNT CACCCGCTNC	840
	CT	842
20	(2) INFORMATION FOR SEQ ID NO:518:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 869 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1364UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:518:	
	GATCTAGTOC TTCACAACCT AGAACCTCCA ACCATGAAAG ACCGATCGAT CCTGAGAACA	60
35	CITITICIGI OGAGOCITAT CAATOCICIT TCTATCCOCA GCTTCTTCCA GOCAGATGAA	120
	TACTOSCAGT COCTOCACCC TOCOCCATGIT AACOCGITTIG GATATOGTCG OCTGACTTCG	180
	GAGTGGCAGC ATGCGCTGCG CAGCTATGCA TYCCCGATGC TCTTTGAAAT GTGGTACTAT	240
40	GTGGCGTGGA TACTGGGTGT GGCCACCCGG ATGCCGCTGC AGGGGTTGGC ACATGCCACG	300
	GCGCLGIGIG GCGCGGCGGC GCGGCGGGCC LGGCCGCCGAL CYYGGCCGLC	360
	TOOGAGCIOC COGAGCAGC OCAGGAACIG GIOGAGIACT ACGGGGIATT GIACGGGCCG	420
45	CCAGTOGTCA TOOCOOCOGT ACCAGCGTGC COOCAGTTCT ACAGCGTGCT GCTGGTGCCC	480
	AAGCTGTATC TOCGAGTCGC GGATAAGGGG GACGACCCAG AAGGGGCAACG CGGCGCCGGT	540
	CAGCOGGTIG CCCCIGAATG CIGACCATGA CAAACTICTT CAACTGTTIC TICCCCGAACG	600
50	CAACGITCAT CACTCCINCA AAATAACCCC CACNOCONIC COCICTAACC NATTIGGATT	660
	GGANCCOCCE CCCANCTTIG GITCTONICS CCTTCCACON CAACTTINGC GGIGGCTGON	720
	TITIOCCIOCC CIOCACOSCC NATACTITITI ATCITIOCCT COCIOCCIGI TCTTGTGCCA	780

	GGGITTTICN ATACCANINA NACNCICCT	869
	(2) INFORMATION FOR SEQ ID NO:519:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 839 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORCANISM: PAG1365RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:519:	
	GATCTOCOOC COOCOGAAGA COCAGAGGAA AOCGAATCGA OCOCOGGAGA OCOCTACTCG	60
20	ACOGACAAAA OCAGTTACOC GTOCTOCGTG CAGOOGTOC TCAGAGOGAG GACAGOGTOG	120
	OCADOCAGO CAGATACAGO AATGAGOAGT TOAACOGOAG OCADOGATAG OGOGGGGGG	180
	OCTAAGATOG ATOCAOCCGA COCAGATGAC OCGACOOCGA OCTTOGAGCT GCGGCTTTGCA	240
25	OCCUTOCCA COCACCACC COCTICTICAC ASCOCACACA COCCCACCOC COCCTICOCC	300
	OCCIOCOCCIO COCCOCCOCO COCONOCOCO COCOCOCOCO COCOCOCO	360
	000000000 0000000000 00000000000000000	420
30	GAGCCOGTOC GOCGOCGCC CACCAACCCC TTCCGCGTGA TTTCGGTCGG CGGCTCCAGC	480
	ACCITICAACC GCGCGGCGGG CGCGGACGGG CAGGCGTCGC GCACGTCGTC CGCGGGCCGAC	540
25	AAGGCCGCAC CCGTGTCCGC GAACGAGCAG AGCATGCTCA AGTTGCCGCG CNAGCNCANC	600
35	TACCCTGACC ATGAATTCNT CNACTGTTCA AAGANATTAA TTTCCTGANA ACNTGAANAA	660
	ANCOGRECCET GINCTIGAAG AANCOCCOONN ANTAACNACC CCCINGACAG CHONGATTITC	720
40	CICCNCCITA TINIAAAAA TITCAAAINC GOGIGGINCT TCCCCCCNCIN CCCAACNIIT	780
40	TAAAANGITC CCACGGONIN NIGNNOOCIN NATTIGGCCC CCCGITCCNI INCCCNOGI	839
	(2) INFORMATION FOR SEQ ID NO:520:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 851 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1365UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:520:	

	CATCACGIGA CGITCATOCA GCGIGCAGCA CIGCACGACA GCGAAGCGGT GGIGCGCGCG	60
_	ACGCGGGGGG CGGCCGTGCA GCTGTATGTG GGGCCCGGGG GCGGGCTGCG GGGGCCTG	120
5	OCOGRAGOCOC TOGRACCACTT OCTOGOCOGA COCTTAGCOC CGAGCCCACT GCGGCCCGCC	180
	TOOGRATGIGT ACTITIATOCA CCTOOCCCCC CTCCCCCCCCCCCCAA CTCCATCAAG	240
	COCCUTCICG COTOCCICAT TOTOCCCCCC TOCCCCCTCA TTCCCACCCC CTATAATCCC	300
10	ACGCCGCGCC ACTITGCGCAA TTGCCACGAC GGCGGGTGCG CGCGCTGCAA CGGCGGCGGC	3 <b>6</b> 0
	AGTGCGCTGC ACACCTGTCT CTGCTTACAC GCGGAGGAGA ATGCGTTACT GGAGGCCGGG	420
	COCCACCOCC TOCCCCACCA COCCCCCCCC TACTCCCCACA COTGTCCCCCC TTTCACATGT	480
15	TOGGTGAAGA TOGTTCAGAC GOOGATCACG GAOGTOGTTT ACTOGCAGAC CTACCGGATG	540
	GACAGOGACA GCTTCAAGGT ACTGCGGGGG GGCGGCGTCA GGTCCCGGCA GCTACAGGAC	600
20	GOGTTCCCCC GCACTTTTTA TTATATNINGC NGGCNGCTTT CCCNGCAACN GCTAAACTTG	660
20	CTGTTTTINC ATATAAGGNC CCGGCGGTINC CGACTINCAAA GNAATINCCINC AACCNTTCTT	<b>72</b> 0
	INTITICCGAG GCNGGGGAAT TTICCCCGGGA ININNEGCCC CCCCCGGINN TGCCGITACC	780
25	CANTICCCCT GCCCAATCCT CCCCGGGAAN CCNCCNCCAA CCGTCTCGNN TINCTCCACC	840
20	CONCCIONCC T	851
	(2) INFORMATION FOR SEQ ID NO:521:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 823 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: INA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1366RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:521:	
	GATOCAACOG TCAACCAATG CCTCCGAGAT TGCCGGCATA GCGGATGAGA TTGCCAAAAGC	60
	GEAGAAGCAG GACAGCTOCG COOCGGTGTC TGCCATGGGT GCCGTCCTAG GGCATGCAGC	120
45	CAGTOCTITIC GCTGCTITIGA ACCIGCTITAA CAGTTCTGCC CAGCTCTTGA ACCAGCCGGG	180
	AGCAAAGCCT GCTGCCGGTG CTCTCAAGGG CATGATGGAG GCTGCGTCTA ACACGACTAA	240
	GOCAATTIGAC TITCATCATGG AGOGTIGCAAG TCATCCAAAG GCTGGCGCGG CAGAGCAGGT	300
50	GATGGGTCTA GATATGGTAC TOCAGAATGC CGTGAACTCA AGCGAAACCT TTGCAAATAT	360
	CATAAAAATG CAGATGOCAT CGACCGAGGA GTCOCAGAAG GCCCTCCCAA GTTTGTTGOG	420
	CTICTICTCC TACTCCACTC ACAACATCGA CACCATGAAA TCCCTGATTA ACCTCATAGA	480
55	GTTCOGTGAA AAGAGCCCTG ATGTATTGAA TCCTGTCCTA GAAGTGCTGC AAGCTTCCGT	540

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	GARDSTONE ADMITCHIAE COTOCOMANG MATITIMONE PLACACOCAE ATCOTOGRAM	600
	CITCAINITH OCTOCGAGIT ACAAACTOOC ATTICCCAAT CIGCCATTIG TICCCTTAAC	660
5	GGNCCCCAAA GGITTGCACA CONONNICCT NCAGGNITCA ATNOCTACTC CININNCONA	720
	COVANCAATC CHNITGOCCC TINITTAANN CAAATCNONC CANATNIACC CCCAGGITTT	780
10	TTTTOCAAAN COCTTTTANA CCTTTOCOCC CCTCCCTTTN NAT	823
70	(2) INFORMATION FOR SEQ ID NO:522:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 854 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1366UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:522:	
25	GATCITATCA GGATAAATGA TITTOCTCCCG GAAAGTCGAT AAATTOCTCA TATATGCCCT	60
	CTGGGGGAGA TAATATATCG GACTTTCGCC ATTTTCAGCA TTTCTACGCG GCATGATTAG	120
0.0	CITCGIAGGC TICTTAGGGT TAGIAAACGA TIGCAAAACA GGCCACAACC CCCCAAGGAC	180
30	CCTGAAAACA GAAGACTTGC CGCAGCCATT AGGACCTATA ATCAATAGAT GGTTACCATG	240
	CTTCAACTCG AAGTTAAGTT COGOGATAAG GACCTGATTA OCAGGTGTCA CTAGTGGAAC	300
<i>35</i>	ATGAACGAAT TGAATCTTAG AATCGTCGTA TTCTATAATG ACCTTTTCC CATCAGTCTT	360
33	CGAACTACTT CCAGCGTCTA GCCTGTCATT GAAATTTGTT AACCGTAGGG CCTCTCCCTT	420
	TAGCTOCTOG ATACTACOGC GCAGTTCGAC ATAGCCGCCCA ATAGATCCCG ACCCAGTTAG	480
40	CAGTAAACGT CTGTTGGTGA TAAAATCAGC GGTGACATCC TCAGCCATAT TAGAACGAAA	540
	GAAGACOOOG ATAGAGCATA ATATCAAGOC CAGCAGOCC CCAGAOGTAC TICACCAGAA	600
	AGCTAGTACA ATTOGTACAG TGCTCTTAAA TTTATCTCCC CCGGCTNAGA ATAAGTTACT	660
45	GETTANAAAN AAAAACCCAA TCCCATATTC GETNITTGAC CVIGAATAAA CNNINCCNCN	720
	TTOCTTGACC NCACTIGAAT TIATGACOGA ATTACCNOCA TTTTCCCCTG ACATACCGIT	780
	CAATTOONNG TITIGACCICC CACINATIAI GATINAAAIC AACCCATCCN GICCITICNGC	840
50	TITICCCIOGN GATC	854
	(2) INFORMATION FOR SEQ ID NO:523:	
55	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 824 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1367RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:523:	
10	CONTROLOGO	60
	CAGGCCCACC GCGCCTCCGC CGTGTTGCCC TAGCGGATTG TTCATTCCCT GTGTTGCCTC	120
	CTGACTGTCC ACTOGACCTC TTGTATCCGC ACCTTTCTGC CAAGTGCGCC CCAAACTCTG	180
15	TITICCIGIC TGTCCAGAGI TTCCGICTCT GOCTGCGCTA CTGCCTACCT GCCGITTIGGT	240
	ATGGAGGAGA AGTIGTIGTIG TATCTIGATTT GTTTATCTGC TTTCCTTCTC CTATAAGCTT	300
	TITIGTAATGA AAAAAATTAT GAAAACOOGA AATCTGTOGA ATTTOGAAAT OCTOCTGGOG	360
20	CTOCGTTGTT CAACTTCCAG COCCGCCGTC TCGTTCTACT CCTCTGTTCT TCGTCTAGCT	420
20	THOSETAPIT THICHOCHEG GIPPICOCTIC THITTICHEC AACSCAAGGG COCSCTGCGF	480
	CONTRACTIC COACCIOCON COACAACTON COCCOCCCCC CAACOCACCO COCTACTIVAD	540
05	COOSCAACTC TOCCOCCGAT CCCCTGCGGA GOCTTACGGC AGCGCTTATT TAATTGTTAC	600
25	GTAAGTCACG TOGAGCTAGC ACGTOCTTGG CAGCTCAGCC OCACGTCAGC TAGCGTGTGA	<b>6</b> 60
	CTAATCGCGG CGACCTGGTG GGTTAAANGA CGGGTTACNC CGTTAAGTTG GAAACGCNCC	720
	AATAAATTAC MTACCCMTTA AACACACGGG ANAAAAANAN NCCCGGCNCA NAAGNANCTT	780
30	TTGCCCTTGA AGCCCGGTTGC CCCAAGCCCG GNCCNCCCCA GAAN	824
	(2) INFORMATION FOR SEQ ID NO:524:	
35	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 850 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1367UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:524:	
	GATCITATOG GIOGITCTCT AGGOCTGAAA GOCGGATATG GACAGTCGAA ATGOCCAGCA	60
	CAATTIATIA TAAAACGIGC AGGICAGCGI GGGTIACGCG GITGIATAIT GAGGCCAGGC	120
50	TATISTICACTIS STIFCCCCTTC TACAGGAGCT TCTWACGCGG ATGACTTTICT GCTCCGGTTC	180
	CTACOGOGAT GIGTICAGTT AGOCAAAATT CCTGATATTG AAGGAACTGT TAATATGGTA	240
	CCAGTIGATT AUGTGOCACG GITAGCAACA GCGGCTTCCT TCTCGTCATC AGGCAATACA	300
55	CATATGATGG TIGTAAATGT CAATGCCAAA CCAAGAATAT CATTCAGGGA CTATCTACTA	360

	GCACTGAAGG AATACGGGTA CCAGGTAACA TCAGTTCCTT ATGACGAGTG GAGTAAGGCG	420
	CTICAATCGT CGAGICATCA AGAAAATCCT TIGIATCCGC TATIGIACCT IGICCIAGAT	<b>4</b> 80
5	CACITOCCTA AAAACTOCOC AGTOCTGAAC TOGATACTAC TAATOCGAAA TITIGITTIAG	540
•	AAGAAGATTT TOCOCOGACG AATATTGAGC CAATTATCAT TACTTCOGTG TCATTAGAGT	600
	TGTGGGTCCC CATATCTCAT TTTTGCATAA TTTAGCTCCC NANAANAACC ACCTAAAGTT	660
10	CCCAGCCCT GCCNATATIC NCTCTCCCGA CGAACAAATT CCTTAATANC NCATACCNCT	720
	GCNCCGAACA TACANCAACC CNIAAATACC NCAAATIGIN GACAACATGA NIGITTATIT	780
	TTTTTATATT ACAACCTATT ATTAACCAAA TININATCAC GATCNICINT GACGCCCTCT	840
15	CTGACAAATT	850
	(2) INFORMATION FOR SEQ ID NO:525:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 825 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1368RP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:525:	
	GATCATCTGA AGTAATATAG AATCTOCATG GOCGCAAACC GITGCGGTCC AATGTAGCGC	60
	COGTIGTAGCG GCCATCOGTA AAGGTGAGCA ACOCAGGGCC ATCCCATGGT TCCATCAAAC	120
35	ASSCOSCCCA GICAAACCAA GCCIICAGGI TAGAATCCAT GICCIIGIGG TAGGCIICIG	180
	GAACCATCAA GCACATCGCT TCGGGTAATG ACAGAACACC ATTTATCACT AGTAATTCTA	240
	GCACATTGTC CAGCOCCOCA GAGTCOCCATC COCCTTCTTC GATAATCOGA TAAAGCTTCT	300
40	CCAGTTGGIC TTGGAAAACG GCGGATGCCA TGACACCTTC CTTCGCACGC ATCCAGTTTT	360
	TGITGCCTCT TAGGGTATTA ATTTCACCGT TGTGTGCAAG CCAGCGCAGA GGCTGGGCAC	<b>4</b> 20
	GGICCCAAGA TOOGAATGIA TIOGITOGAG AAACGAGAGT GIACCAGCGC CAGGICAGAC	480
45	TIGAAATGAG CATIOGICAA GIOGIOGIAA TAATTATACA CCIGGCAGGG TCAATTGACC	540
	TTIGIACACA ATTGICCOGI TATTTAGGAG CACACAGITA ACAGITCIGA TACCGATGGC	600
	CGITAAACCC NVCTTTCTTT AAATWITAAA CTGGCATCCN GAAGTCTCTC GINATTANCC	660
50	TGAATCINCN CCCGATACTC CTGCCCCATAT TTCTTTCNCN CAACAACGTT TTTGAAATGG	720
	TITICCCAAAA CCAACGAAACC NAAAGAAATN CINTGGACNC CTCCAACCCN AACCCNNATT	780
	TAACAATCOG TACTNOCCAA TITNITICAAG CINAACCTGT NINCT	825
55	(2) INFORMATION FOR SEQ ID NO:526:	

5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 839 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1368UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:526:	
15	CATCGICACG ACTITIGIGIT TTACTICAAC CGIATTOCAA CGATCTICGT TTCCCCCCCCT	60
	TTOGATGACA TTOCTATOGT COCCGATGAA CTGCCATTGG TGACTGCATC CGGATATCAA	120
	CTOGAGAAGC CTGTTCATGT GAATTTTGAC AAGATTACGG CTGTGAATAT TGTGCGCTCT	180
20	GOCCACTGIT TCATGGCTTC CCTACGCAAA ACAGTGCCAA ATATATCCAT CGGTAAATTG	240
	CTCATTCAGT CTCACTCTCA AACAGGIGAG CCGCAGTTAC ATTGCCAGTT CTTACCAGTG	300
	AACATTGGCG GCTCTTTCGA CCAGGTCCTA TTGATGGATG CACAAATAAT CTCAGGCGCA	360
25	GCAATTATCA TOOCTATTCA AGTOCTAGTT GACCATOGTG TTGAACTATC AAAAATAAAG	420
	GITATIGICT ACTTAGCCAC TGAAATIGGA ATAAGAAGGA TAATAAATGC CTTTAACAAC	480
	AAAGTATCAT ATATGCGGGC GAAATTATAT CAGACGAAAG TATGACAGAT GGCCAATGTA	540
30	CTGGGCGAGG GTGAGATTCA TCGACTCAAG ATACTTTGGC TGTGACTGAT TCAGAGCTTT	600
	TOCTOCCCAN GCAGGAATTA ANAACTITTG GTGCTATTGC ATGITACAAT ATTAGCATTT	660
	ATCATCCATA CCATAGCTGC TTTACNATAG CATNIAATTT TACTATCTTT NAACCCACCC	720
35	ACACTATTIT TOCCOCCNIA CITTACNAAN ANITTAANCA ACIGACCOCC OGNIATAATT	780
	OCCCATOCAA CACCCCCCIC CTCNIAANAA ANACCNACTT GGAACGAGTG GGAACCNCC	839
	(2) INFORMATION FOR SEQ ID NO:527:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 851 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1369RP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:527:	
	GATCOCCTAC TIGICICAGG AACTIGITAT CATGAGAGAT GATATGIGCA ACAGGITTAA	60
55	GCGCAATAGC ATTATTITICC CAACAGTGGA AGAGGAACAG AAACAGGAAT ACATGCTGTT	120

	ACAGCAGGAG CTCCAGGATG ATGAACGTAG TTCGGATCTC TCCATTAGTC AACTGATTAA	180
5	GTCCAGGGAC CAATTGCCTG CCAGTGTCCA GCAGTCCAGG AAGATTAGTCA AAACCATCCT	240
3	CGATCAGCAA CACCTTTCGC CCTTTACCTC GCAGGTGCGC CCTATAACGT GGGACTATGA	300
	CTACACGITG CACCIGICCC CAATACCCIC CACTATGAIC ATTIGGGACC CAACIGCACC	360
10	GAAATATGAT GITACTTACA ACGGCTGCAA GAGTATCAAT CCAGGCTCAT TICICCACAA	420
70	GCGCAGCGTC AACTATACTG AGTACACTCC TTCGTTACGG AAAGCAACAG AGGAAGAAAT	480
	TETEGRETAG GACTITAAAC TIACATATAA TETCAAATAT AAAGETITCA GACGTOGICA	5 <b>4</b> 0
15	TGTTTCGTAT CCATATTTCT TGAACTTTTC CCGTAATATC GTATCCCATA CAGTAGACCG	600
7.5	GGTCAATNOG AACAACCOON CGTGCTTCTT CAAACTOONC COCANNCAAT COCAAAAAAT	660
	TMTGGAAAAC TTCCACCTAG ATTTTCTGGC CATCGCNGAT GCCCNCCNCT CTTTGATTCC	720
20	TNCANCCCCA GANNAATCNC CONCITTCCT GNICATCCAT NOCONTINGC CCAATTCCNA	780
20	NOGITAAANG COCCCCCCNC TITTCAACIT INOCATTIIN NINGITITCCG TCCCCNNCCC	840
	COCTINCACAC C	851
25	(2) INFORMATION FOR SEQ ID NO:528:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENSTH: 858 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1369UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:528:	
	CATCAAGACG AAGCAGAAGA AGACGCGGTA CGCATGTACG TGCCACCTGG TGCCGTCGGA	60
40	GOCGOCCAAG GCGATCOCTC TOCAGCOCCA CACOCCCCTG GOOCTOCTAA TATGCGTGGA	120
	CCCCACGGTG GACACACGGG CGCCGCACAT ACAGAGCATT CTGGCGCAGC AGCAGAGGAA	180
	GTACGGGCC ACGGTGCCAA CCATCCGTGT GGCGGTGATT AATTCGATCG AACATTGCGA	240
45	GITGITTTC GGCAAAACGC TCGACCGGAA CACACGGGAC TACCTGGTAA ACGTGAGCGC	300
	TOCANTOGIG GIGITOCOCG AIGIOGIOGO GACCCTOCCC CCCGACCIGA GOCCANTATA	360
	TICGCAAAAC CIGAGGIACC IGAIAGACIG GIIGGAIACC CCIGAGAGGC CAIGGCCGIT	420
50	OCCOGACTIC TATCCOGTGA AGGTATACAC TOCAATOGAC GTOGAGCOCT COCTOCTGAC	480
	CCACCTGAAA TACTCCCCAG AATAATGACT CCCTTGGACG ATGCGTTTTA CCAACGCCAA	540
	GAAACTTACC ATAGTTCCNT CCACAAACGA ACCGTGGAAA TGCGCCCGATC TCCCTACTAC	600
55	CCAAATAAGC GITTIGAAAA ATGACTACAT TNGAATCCCN CCNACCAAAA TTGAACACTC	660

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	CCCGGAANNA NCATACNAAN CCAAAAGIIIT GCTAAATATC TCTITCCNIN GTACACTGAC	720
	CCCNACINIT GCAGGGAAAG GNCTGITTIT AAACTICCAC TCNGACTINA TITTACCCCT	780
5	CCCNCCATCC ACCNAANCAA CACCINITON AACCATAGAA CNNTITICCT TITAAAAACAC	840
	TNAGAAGCAT TTNAAAAT	<b>8</b> 58
	(2) INFORMATION FOR SEQ ID NO:529:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 834 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1370RP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:529:	
	GATCITGTAC AACTGAGCCT AGGTCTTGTT GTTGAACGGT AACCTCCACA TTCATTATTG	60
25	OCTOCAATAT OCACAACOOC GAAGTIOGTA AACTOCTCAG TOCTCATATG ATTAAAACGAC	120
	GCACAGTCAG CAGAATGGAT GCAGCTGCTG CGCAGTCTAG CGGTAGCCGC CAGCGTTTAA	180
	CATGAATCAC ACACGAGTGT AGAGGAAAGC CTGCGGTTTT ACCACCTCTT TGCAAAGCCA	240
30	CHATOCAACA CGAGATGATA GAGFFICACGA ATGCCTCATA TFTCAATGGA AATGGCCAAT	300
	TGICTICGIT AAAGCGIGGG TITGGATCTA TGACAAGATA GITATTATCG CTTCCCAAGG	360
	GGTACCATCC GTTACTGAAT AGTACTTTAT CTTCTTCATT GTATTGCCGA ACTTCGAGTT	420
35	CGAACGAATA TOCATCATCT GTTTCAGAGT OCTTCCTCTC TGTAGCAGTA TTAATGGTTT	480
	CCTTGTATGA AACTGCTACC TTGCCTACTC TTACAGGCGC CTTAAATTCA TTGAGCAGCC	540
	GTCCCCTCCT ATTTCCAGTG CATTCCCCCC ATCCCATTCA TCACTGTCTG ACCAGTCTCC	600
40	TCATCCCTCA CNAATACCAC NACCGTTCCC CNCTCGTTAG CTGCNNCANG ATCACCCNAT	660
	ANCOTITINE TOCCCAANIT COOCGGECON NCANCGNOCE AAAANGGEGG NGGEANICAE	720
	OGGINITICC CANTIGNANT TONOCTITIG AAAAACAATC COCTITAAGN TIMAAGNONA	780
45	AANGGGITICC CTTCTAANTG TGTCCCCTTG GGCCCNCNNC CCCAATNCCG AGAT	834
	(2) INFORMATION FOR SEQ ID NO:530:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 840 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1370UP	

	(xd) SEQUENCE DESCRIPTION: SEQ ID NO:530:	
	CATCOCAGAG GAGGAGCCCA TTCOGACOCT TOCATOGAAG GAGGACACCT TTGAGAATTT	60
5	TCTGCCGGAG GTGACATCCG ATGAGGCGCG CGAGACGCTG GTTTCCCGAGG AGGATGCCGC	120
	CACCTACCTG GCCAAGCTTT TATGACGCCT GICCGTGCTT TTAAATTGTT ACATACTGTA	180
	CATATTOCCT TRACTOCTAC CACATTITICA TCACCICTIC CCAAAACCCCC CTCCCCCTICA	240
10	OCACOCCAR GICIGIGATC ACCOCCITAA TGTOCTCGTG CGACGTGTAG TCCATGGACG	300
	GECTTAGCAG CIGCICIGAC TOGICOCTOC GOGAGAAGIC CADOGGGICA COCTOCATOG	360
15	GCAAGTOGTO GGGGAAAGC GGGAACATCC TTACAAACTT GTGCGATTCG CTTACCACGT	420
15	AGAATGOCTT GCGTGCGTTC TTGGGCGAGGA CCCCTACCGT GTACGTCCCC ACGAGATTTA	480
	TGATGCCGCC GGACTCGGCC ACGCCCTCGG CGCCAACCAG CACTTGTCGA TITTGTGTAT	540
20	GATGGACCCA CCGCGCTGTC CACGATCATC GTCACCGGAT GCCCTTTGCT TGCAGCAGGT	600
	CATACACCIG CITOCCCIGC CCCGAAGGCC CGIGCTCCGI CACGANACAC CGCAAGCAAT	660
	CACTOTOACO TOTTACTOAC ACGAAANNOG COCGCAAACO AGTTOCCAAA AAGTOTOCTO	720
25	TGITAGATCC NCCCATCTIT GINCITITIN INGACOCTIG CCCGAANCAA AACGICCNIT	780
	CONCRETION TOCTONACCO COCTOCCANA INTITITICO COCCOCNOCO NATITONICI	840
	(2) INFORMATION FOR SEQ ID NO:531:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 835 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1371RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:531:	
	GATCGAGAAC AACTACGACA ACAGCCACGC AGACGGCGG GAAGCGCTCA AGCCGAGCTA	60
45	TATTITIGAG TACCTIGCCT COCTCATGIA CCAGCOCCOC TCAAAGCTGA ACCCOCTCTG	120
	GAACOCCATC ATOGTOGOCG GOGTOGAGGA COOCCAGOCC TTOCTOCGTT ATGTOGACCT	180
	CAAGGGGGTC AAGTACTCCG CCCCAAGCTT GGCTACTGGC TTTGGCGGCCC ATATGGCCAT	240
50	TOCTOTOATG CGTAAAGTCG CAGATGCCGA AAAAGACGTC GCCGGCGTCG ACCTOTOAAT	300
	TOCOCCAOCC ACTATCCTOC AGICCATGAA OGIGITATIC TACCOCCATG COCCTACTIC	360
	CCGTCGCTTC TCGCTTGCCA TCATCGACAA TGATGCCGGT GTCAGCATGG AGCAACTGGA	420

	AGTOGAAAAC ATGACCTOOG GGTTCOCCAA GGATATTICOG GGCTATGOCA COCAGAATGT	480
	CTGAGTACCG GCGCGCAAGC GCCGCACCTG TATACTATCT TGTCGCGGCT GCTCGCCAAC	<b>54</b> 0
5	COCTOCCTAC TCACATACAT ATCAAGATGC ATAATCAATC TGCTCATGAA CGCACCTCTG	600
	TITIGIOGAT ACTOTICIOS COCCITATOCT CAGIACOCTIC GAGIOCAAAA ACAGOCACTI	660
	TGAAACAACA CGAGTCGCAG CTAAGGNGAN ATCCGANTAA NCAACNCACA CTTCAATTGA	720
10	CTTATGAAAT GCCCAAGGTT GATTGAACTG ACGTCCTTGG AACNNTGGGN CGTGGAAACG	780
	COCTICTICAN TIGAACCAAA GICCACAANN AGGIATITINI TINAACOGIT COGCC	835
	(2) INFORMATION FOR SEQ ID NO:532:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 850 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1371UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:532:	
	GATCCATTGT GCGTTTGGAG GTCACGCCAC GGACGTGGAC ATGTACGTGA TGAGCTTGGA	60
30	COCCACCTC TICATTCCTG COCCACCCAA CAACCTTGAG TTCCCCGACGT CTCCCCCCGGA	120
	GAGTIGGGG TACCTIGCGT ATTACAGCGG ATACAAATTIC GAGCGCATGG CGCTCCTGGA	180
	COGTICOGGTG GCCGAAAACTC COCGCGAAGGT TCTGGAGAGC CGCGGCAAAAC AGGTCGTCCGG	240
35	CAACGGTCCG CAATACAGGA CTGTGATGAG AACCGGGCGTC GGGGAGCACA AGCTGGTGCT	300
	COGAGCTGAG ATCGACGGCA TCATTGACTT CCGCGAGCCT ACCGGGGACA ACCTGAAGCA	360
	CTACGTOGAG CTGAAGGTGT GTCAGAAGAA CCGGAACTTC TCAGAGAAAC TTTTCTCTTC	420
40	TIGOCTOCAA TOCTITICTOG TOGOCATAAA CAGOCITATT ATTOGATTOC GOGATGAGAA	480
	ATTOGTOCTG AAGAGCGTCG AGGAGTTCGN TACGTCAGAG ATCCCACACC TGTTAAAGGG	540
	CACGGAATAT TCCAATGTAT GIGTGGACGC AATAGAGTGG TATGGTGCTC TTACGAAGTG	600
45	OCTATOTICAG CTCCOCCOCO CCTGAANACA CTTCAACTOT ACAGCTCTCC NOCTCCCNTG	660
	GIGCTTACST NIGCNCCCCT GCCCNACAAT ACTCCCCNAN NGGGACNATT NICCTGTTTG	720
	TTCCCCCAATT GGCGCGGCCC CNATATAANN CANATTCCNN CNITNITTCC CTTNIGNITT	780
50	TAAAAAACCCN TINTTCCCAC CNATTINCCC AGANNACANA GGNNNICCCC ACCANNCTIN	840
	CCCANCONCA	850
	(2) INFORMATION FOR SEQ ID NO:533:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 835 base pairs	

	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(VI) ORIGINAL SOURCE: (A) ORGANISM: PAG1372RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:533:	
	CATCTTAAAA TAAGATAGAA TOGTAATAAA TATCATTCAG GTACAATAGA TOCTOGTGTT	60
15	ACTAAAGGAT TACCTOGAAT ATAATTATCA GGATGTCCTA AAGTATTAGG TGAAAAGAAT	120
	ACAAATAATG AAAAGAAAAT TATAAATACA AATACTGITA CTAAATCTTT AAAAATAAAA	180
	TAACCATOCA TIOGTAATCT ATCIAAATTA CCIGTAATAC CTAAIGGATT TGAIGAACCA	240
20	TGIACATGIA ATAGCATIAA ATGCATAATT ACTATTGCTG CAATAATAAA TGGIACTAAA	300
	TAATGAAATA GAAAGAATCT TATAATAGTA GGATTACTAA CACTAAATGA TOCTCATAAT	360
	CATAGIACAA TATCATTTCC AATAAATGGA ATAGCACTAA ATAAATTAGT AATAACAGIA	420
25	GCACCTCAAT GTGACATTTG TCCATATACT AAACAATAAC CTAAGAAAGC TGCTGCTATA	480
	GITAAAATAA AGATAATAAC ACCAACTGIT CATACAATAA CICTAGGICA TITIATAAGAA	540
	CCATAATATA AACCTITIACC AATATGAATA TACATACAAA TAAAGAAGAA TGAAGCACCA	600
30	TTAAGATGCA TATATCIAAT TAATCAACCT AGITGIACTC TCTCATAATA TGITCIACTG	660
	ATCANAAAOC TAATCCATAT TANATGAATA AOCATNINCTA AAAAATACCN GINAGAATIG	720
	AATACTAACN TAACCTATAA AACCNAATTC NTOCATATAA TGAGAAGGTG AGGGAATCAT	780
35	ACNACTATAA CNATTTAATA TATTGATTCT ATINCCATTT TNITNINAAT TTTTC	835
	(2) INFORMATION FOR SEQ ID NO:534:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 854 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1372UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:534:	
50	GATCTAGAAT TATTAAGTCA ACTATTAACT AATATCTATA ATAATAATGG TTTATCATTA	60
	AAATCATTAA AGATAATTAT TAATAAATTA CCATTTAATA ATCATATATT ATTATCAAAA	120
	AATTATGTTA ATAAAATAAA TAAATATAAT TTACTAATTA ATAATAATTT AAATAATAAT	180
55	AAAAAACATT TAATTAATTT ATATACTITTA GATAATAAAT TATTAGATTT AAGTATICTT	240

	AATAATATAT TATTAGGTAA ATATTTAGTA GGTAGTAATA TOCAATTAAA GGGTAGACTA	300
	TTAAATAGAA ATATTACTAG ACTAATAAAA ATAAATATTA TGAAAGGTAC ATTTAATAAT	360
5	TATATATATC AATGAAGTAA ATTAAATAAT TTATATAAAT TAAATTATAT ATCACTTAAT	420
	ATTAATAAAC TTAATAATCT ATTTATTAAT AAAAATGGTA TATTTAATAT TAAAATTAAA	480
	TTAAATACTA TTTAATAAAT ATTCTAAAGT AATTTCTTAT TTATTTTATA ACATTTTAAA	540
10	ATGITTTATG TTAAATAGAT AATAATCAAT TAAATAATAA AAATTAAGAT GCCACAAATA	600
	ATTICCATTIT CITTATGAAT CAATTAACIT ATGGTTTCTA TTTATTITAC NATTTATCNC	660
45	ACTACINATG TITTITIACC NVIGAATTIN ANAATATATA CICNONANIA NATATIONCA	720
15	AATTATAATA TTAATTAAAT TTAATTAATC TATTATGATC CINNFINTAA ANATATCAGA	780
	ANAATTTAAT ATATATATNG AAATATNITT ATCCCCCNCG NCACTTGAAN AAAANTATAG	840
20	TTTCNTCCCC ACAT	854
20	(2) INFORMATION FOR SEQ ID NO:535:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 827 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1373RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:535:	
35	CATCTTAATT TAAAATTTTA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATTIG TGGCATCITA	180
40	ATTITIATTA TITAATTGAT TATTIATCTAT TIAACATAAA ACATTITIAAA ATGITATAAA	240
	ATAAATAAGA AATTACTITAT AGAATATITA TIXAATAGTA TITIAATITAA TITITAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GIGATATATA	360
45	ATTIVATIVIA TATAAATTAT TEAATITACT TCAITGATAT ATATAATTAT TAAATGIACC	420
	TITCATAATA TITATITITA TRAGICTAGI AATATICIAT TIAATAGICI ACCCTITAAT	480
	TOGATATTAC TACCTACTAA ATATTTACCT AATAATATAT TATTAAGAAT ACTTAAATCT	540
50	AATAATTTAT TATCTAAAGT ATATAAATTA ATTAATCTTT TTAATTATAA TTTAAATCAT	600
	TATAATAAGT AAATATATTA TTATTTATT AACATAATTT TTGATAATAA TATACCATTA	660
	TTAATGGNIN TTATAANAAT TATCTINAAG GATTINNIGG AAANGCTINN TITTAGAAAT	720
<i>55</i>		

	CTITINITNA ATTTAGTTIN AATTTAACCC NCTCCCCINI TIAANAT	827
5	(2) INFORMATION FOR SEQ ID NO:536:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 831 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1374RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:536:	
	GATCAATGAT AAATCGAAAT AAACTGATAC TATTGTAGCC ATTTTTCTGA ATTAGCACCT	60
20	OGAAACACTT TITAACCTGT TCCCCCACTGC TCTCTCACTG ATTICCACTTG ACCCTCTCCC	120
	OCCUPACIOC CICIOCIGIC GICTIAGCIC CGACGITTIC CACIOCCOC COCTOGGICG	180
25	CCACACOCCT CTTCTTCTGA ACTOCCACTG GCCCCAACAT GTGGTCCACT ACCGTTGGTG	240
25	CGCCGCCAAG TTGCTGGAAT AACGCACCCA TCTTAAACCA GTTGAACTGT GCAAAATCTC	300
	CATACOCTIC GAATIGCCIG AGATAGGAGT TOCOCTOCAT OCTOTOGGA AGAGCAGCAT	360
30	CCGCATGCTG ATTGGTGCTC TCATCTAGAG CGTCGCTGGT AGCATCTCCA TCATTTTCGA	420
	TOCTOTOGIT CTOOGTATTG CTAOCATCGT CTGTTTCCOG ATACATAGAG CCAGGTACAC	480
	TCACGTGATT CAACTCAAGG TAGTCTTCCA GCAGAAACCG CTTGGCCCCG TTGACAAACT	540
35	CCTCAGGGCT CAAAAGCTTC CCCGCATTTG TCAGTTTTAG ATTGCGTATA CTCAAGCTTG	600
	CAAGTOOCTG ACOCTCATCA COOCATOCGA ATCCTOOGCA AAAGAGAATT GACCTCAGTT	660
	CAATCGCCCG CCCTGCTTTA AAAACATATT AACTCTCCCN CCGCNCNCAG GANAGAATINC	720
40	TCCCGTACTT CNANGNAGNC ANCINIGCCC NICATCICAA ATIGCGNACC INGINANI'IG	780
	CANCONTICC CCAGCCCCTC TOCCCCCCTA TICANGNICG NCCCCGTTCC A	831
	(2) INFORMATION FOR SEQ ID NO:537:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 856 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1374UP	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:537:	

	CATCITAAAG GCCGATATAA AAGCIGTACA AAAGAAGATG AAGAAGUTIC CAAGGUTICI	60
5	AAACTITIGAT ACTITCCGCCA TIGCCTTGGA AGATGAAGGC GAAACAAAAG AAAGTACCGA	120
	ATTTAGGGCT ATTATTAAAG AGTTTGAAAC ACAAAATAGT TTCCAGAAGA TTTTTATATOG	180
	GAATTAATAG ATAAGACTAG CATCTTTCGA AAACTTTATA TAAACCAGGC AGATTAGCTA	240
	CCTCTACAAT GROCTTCAGA AGRICTOGTOG ACOCTAGGAG TOGOCTCTTT ATOGTTOGGA	300
10	AAACCACTIG TICCAGAACT GICCCAATAT GCTCIGCCTT GGAAATATAA TAAGCGCGAA	360
	CATCOCCATC GATTGTGTCG TCGTTTATAT CTACGTGCTC AATAATCTCA GGAATATAGA	420
	ACAAGGCAAG TTGTCGAAGG ATTCCTTCTA GOCACTCCTT TTCCGACGAC CAATCTACCT	<b>4</b> 80
15	TAGITICCCAT TCTGTAGAGG AAAAATGGAA GTTTAGAAAG AGGCGGGACA TAATCCTTTA	540
	AAAGTAAGG TACACTCTTA ATGCGAACGT TOGTCAAATC GGICTOGTCT CCACATATTT	600
	CAATOCAGIA ATAGITOTOT AGCALTICTOT CATGIOCACA CIGITGAGIT ATTOCAAATA	660
20	TOGANTOGGA COCATTATOC ATCTTAGATA NOSTTOGTAT ATCOCTAACT TOCOCAATCT	720
	CAACCNCANC CINGATATNA TITICCOGAAN TITIGNNAATN NNNATCCCAT TGANAAAATT	780
	CCTTCCTTAG GACCTATCAC CCAAATANIT AACCOCCIVIT NANGATCCCT GWTTGGTCAC	840
25	AACCNOOGT CTINNN	856
	(2) INFORMATION FOR SEQ ID NO:538:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 828 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1375RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:538:	
	GATCTTAATT TAAAATTITA ATTAACTATT TATAATTITAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
45	AATACAAAAC CAITAAGITAA TIGATICATA AAGAAAAAIG GAATTAITIG 1000CATCTTA	180
	ATTITIATTA TITAATIGAT TATTATCTAT TTAACATAAA ACATTITAAA ATGITATAAA	240
	ATAAATAAGA AATTACTITAT AGAATATITA TITAAATAGIA TITAATITAA TITTAATATI	300
50	AAATATACCA TTITTATTAA TAAATAGATT ATTAAGTITA TTAATATTAA GIGATATATA	360
	ATTIAATTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATIITTA TTAGICIAGI AATATTICIA TITAATAGIC TACCCITTAA	480
55	TIGGATATIA CIACCIACTA AATATITACC TAATAATATA TIATTAAGAA TACTIAAATC	540

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	TAATAATITA TIATCIAAAG TATATAAAIT AATTAAATCI TITITATIAT TATTIAAATT	600
	ATTATTAATT AGTAAATTAT ATTTATTAT TTTATAACAT AATTTTTTCA TAATAATATA	660
5	TCATTATTAA ATGGTAATTT ATTAATAATT ATCTTTATGA TTTATGACAA CCATATATTA	720
	TAGANATIGI TAATAGTIGA CTAATATOON ATOCAACCIN TATINATITA NAGATCATAN	780
	ACCITITATA CAATTATTIT NATATAACAT NIACCINATT ANAATAIN	828
10	(2) INFORMATION FOR SEQ ID NO:539:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 688 base pairs  (B) TYPE: nucleic acid  (C) STRANDELNESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1376RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:539:	
25	GATCTATTTT GCCGACTTCC CTTATCTACA TTATTCTATC AACTAGAGGC TGTTCACCTT	60
	GCAGACCTOC TOCOGTTATC AGTACGACCT GOCATGAAAA CTATTCCTTC CTGTGGATTT	120
	TCAAGGCCG TOGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	180
30	ACCCCATCTC COGATAAACC AATTCCCCCC TCATAACCTC TTAACAACAA AACATAACTC	240
	CTCCCAGGCC TCACGCCGAC GTCTCCACAC TCAGTTACGT TGCCGTGAAG AATCCATATC	300
35	CAGGITCCGG AATATTAACC GGATTCCCTT TCGATGGTGG CCTGGAAAAT CAGGCCTTTG	360
35	AAACOGAGCT TCCCCCATCTC TTAGGATGGA CTAACCCACG TCCAACTGCT GTTGAGGTGG	420
	AACCITICCC CACTICAGIC TICAAAGITC TCATTIGAAT ATTIGCTACT ACCACCAAGA	480
40	TOTGCACTAG AGGCCGTTCG ACCCAGCTTT ACAGCCTAGG CTTCGTCACT GACTCCACGC	540
	CTGCCTACTC GTCAGGGGT CATATTCTGC CCTGAGGGTG GAGTATAGGT AACACGCTTG	600
	AGCGCCATCC ATTITICAGGG CIAGTICATT CGGCCGGTGA GTTGTTACAC ACTCCTTAAC	660
45	GGATTCCGAC TTCCATGGCA COGTCCCG	688
	(2) INFORMATION FOR SEQ ID NO:540:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 757 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(VI) ORIGINAL SOURCE:	

	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:540:	
	GATCCAAGGA ACCTTTCCTT CTGGCTAACC TAGGGTACTT GTACTCTAGG CGAACCANGA	60
5	CTITIACTIT GAAAAAATIA GAGIGITCAA AGCAGGCGCA AGCICGAATA TAITAGCAIG	120
	GAATAATOGA ATAOGACGIT TOGITCTATT TIGITOGITT CIAOGACCAT CGIAATGATT	180
	AATAGOCACG GTCCCCCCCA TCAGTATTCA ATTGTCAGAG GTGAAATTCT TGGATTTATT	240
10	GAACACTAAC TACTOCGAAA GCATTTOCCA AGGACGITTIT CATTAATCAA GAACGAAAGT	300
	TAGOGGATICG AACATGATICA GATACCOTICG TAGTICTTAAC CATAAACTAT GCCGACTAGG	360
	GATCOOGTIGG TGTTTTCTTA TGACCCACTC GGCACCTTAC GAGAAATCAA AGTCTTTGGG	420
15	TTCTG0000G AGTATGGTCG CAAGGCTGAA ACTTAAAGGA ATTGACGGAA GGGCACCACC	480
	AGGAGTOCAG CCTOCOOCTT AATTTGACTC AACACOGOGA AACTCACCAG GTCCAGACAC	540
	ANTANGCATT CACAGATTCA CAGCTCTTTC TTGATTTTGT GGGTGGTGGT GCATGGCCGT	600
20	TOTTAGTTOG TOGAGTGATT GTOTOCTTAA TTOOGATAAC GAACGAGACC TTAACTACTA	660
	ANIATOCTOC TOCATTTOCT GTTGCCCTTC TTAAAGGACT ATCCGTTTCA ACCCANTGAN	720
	TITIGAGCATA CAGTICTICTA TOCCCTAACT TOTOGOG	<b>7</b> 57
25	(2) INFORMATION FOR SEQ ID NO:541:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 821 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: ENA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1378RP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:541:	
40	GATCCITATA AAATOGOCAA TAGACGIGIT ATAATATAAT ATACAAAAIT ATAAATAAAT	60
	ATTACTATA AGATAATA AGTATTATA GIATTATA AATTAATA AATTAATA AATTATTA	120
	AATAAGIATG GATTTTTAAC TGAAATTTGT TAAAATGAAA TAAGAATTGC TAGTAATCTA	180
45	TTAATAACAA AGTAATOGIG AATACTCTAA CTGTTTCCCA CTAATCACTC ATCACCCGTT	240
	GAAACATATA ATTAAATAAA GAATATTAAT TAATTTATTA ATTATTAATT ATTATTAATA	300
	TTATTTAATA AATATAATAA ATATTTTAAT TTAAATTATG AATTAATGCG AAGTTGAAAT	360
50	ACAGITACIG TAGGGGAACC TGCAGIGGGC TTATAAATAT CITTAATATT CCATTITIAT	420
	AAAATAAATA TATTTTTTAA TATATTTTAT AATAACTATA ATTAAATAGT TAAAATTTAA	480
	ATTATAATIT AATAATITAA TAACTIATIA ATTAGAGAGI TAGOGIACAT CCCCCCTAAT	540
55	OCTATOCATT ATOGTTOGTA CACTICTAATT AATAAACTAT AATAAATAAA TACTAATATT	600

	TIALACAIN AATTALAALT ATTITTAANA NATITAATAT TATTAATGAA ATATATAATA	660
	AGTATININA TITNATAATA ATAAAAATGA NAAAACGACC CCTAATAATA ATITOCATIT	720
5	ANANITACCC TTACACCICC CNITAAATIT TTACCCINAT ANCONINITA ATTAAGGANG	780
	GUGNUCCCON TOCTCCCCONN TGTCCCCCCCC ATTINIANTTT A	821
	(2) INFORMATION FOR SEQ ID NO:542:	
10	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 852 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1378UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:542:	
	CATCCTTGCG TACTAAGAGT TAGACTITAA TTAATAATAT TATTTGTAGA AGATAGAAAC	60
25	CATACTGACT CACGICGTAT TTAACCCAAC TCACGIAACC TTTTAATTGA CGAACAGICA	120
	AACCCTACTT AGCTGTTACA ACCAAGAGGA TAGGTTGAGT CGACATCGAG GTGGCAAACA	180
	TAACTTACAA TAGCTACTCT ATCGTTATAT TACCCTGTTC AATTTTGTTA TCATAATAAC	240
30	ATTIAATTAT TATTICAATA ATTCICATTA TIGTICAGAC TATTICATTA TGIATTATTT	300
	ATTAATTAAT ACATATTOOG CTTTCGTOGA TATAATTATT GTTAATCCTA CTCATATATC	360
	TAGTOGITGA ACGITCTTAT AACTITATAA AAAGGATTGI TATAAGCTIC GCTGCAGATT	420
35	GICCTITATT ATTATAAAAT AATATTAGGA GITCTITIGCA ATTAACCCAA TITIACTCAAT	480
	ATATTIAAAT ATTGATAATT AAATTTCACA ATTTAATGGG ACTATTAATT AACCCTAGCG	540
	TAACTITIAT TOGITATOAA ATACOATTAC AATATGTATA TITTGTTOAT TATGOCAAAC	600
40	TTACGITATT GTICTACTIG TAGGIATTAC AATTATAGCA CAGTIATACC ATTATATTA	660
	TITATATATA TCCCATATAA GITTTTATTA ACATATAAAC TGINCATTAT TTATCINITT	720
45	TATATAAAAT ATNATTATAT TAATNATTTA TTAANATTTA NACCONTATA TTAAATATAA	780
45	TONITITIAA TAATAAATTA TTAAGGACIN TOCAACCIIT TIGAAAGACO COCCACINCO	840
	ATTAAATGIC NI	852
50	(2) INFORMATION FOR SEQ ID NO:543:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 845 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: IND. (corporate)	

	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1379RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:543:	
	GATOCAATTC TOTOGGTAGT TTOOTTOCAT ATAGAGACTG ATCAACTAGC CACATTOCCA	60
10	CAACAAAAGA GITICIATCT AACGIGCCAT COOGICITGT ATCIACCATG TCGTAGATTT	120
	CACCCAAACT ATCTTCACCT ACATTCCTTC CACACCACAT ATCTCTAACA ACTAACTTCA	180
	ACATTAGACC ATCCTCTGCC ACCTCTCTTG TCTCATCGTA GTTACCGTTA TTCCACCATG	240
15	GGAGCAAGIC AAGATAAGIG TCTCTATTGC TGACCCACAT TCCCTCGTAA CGCTTTCTTT	300
	COCTITICAGT TAOGTACCCA ACATCAAGGT GOGACTTCCA AGGITTIGTCT TCGTTGAAGG	360
	AATTACGGIA TCGAAGATTT TGACGIATCT TCTCGCCCCTT TTTGCCCGCAT CTTCTTCCTG	420
20	CACTICGACT ACCOGAGITG COGTOCCTIC CGTAATCCTC TICAGAGICT TCCCTGTCAT	480
	COCTTAGTTG ATGGGGCTCT GAGCTGGAAC TGTCATTAAG TATACCCCCC ATAGTGGTTT	540
	TTAGCCGCAC ATGCAATTTA CTCTGCACGA GAGCGITIATC GTTCTGCGTA TATATATGTG	600
25	ACCITICACCO CICATICTIC CICCOCCCIA COCCACITIC COCATICCCC TICAAACCIT	660
	CATCCACTIG GANIOCTOCG TIGANANITT OGTATIAATN CAGGAANATT CCTCCGTAGT	720
	CCAGTICATA GGAATITGIT CATGTCAATT ACAANCTITC NACGGGAATC TITTGCGACT	780
30	CNIGICACGI CGANGNATNI GIONICOGIA CANCTICCOGA INCNCCAAAN INNCONCAIT	840
	CICIN	845
35	(2) INFORMATION FOR SEQ ID NO:544:	
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 855 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1379UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:544:	
	GATCCOGRAG TINACACTOC CTOGGRITICA TARCTIGOCA ACAGOGIATG TOCGTGTGAA	60
50	CATAGICGAT GGAGCACATG AATTGGGGTA TCAATACTGA TTTCATAATG CTTTCTGGAG	120
	CCATTGACCT TGCGTGACAA CCTCAAACAT ATTTGGAGCC AATGGTTGGA CTTTATGTGG	180
	GGAGATOCAG TATTCOGATG TATOCACTGT TOGTAGTTCA ATCITTCOGG GACAAAAACC	240

300

TOGTAAGTCA ATTGTCTCTT TGAAGCGCCA CCCGCTCCAT CATCCAGCAG GTTTCCTAAG

55

	TITTIACCAC COGAAACCT COCCCTICG TGTATACCCT TAAGTCGTCG TGCTTTGTCC	360
	TOGACCAGCA AGAACTICIT TGIAGOCICC ACTOGGIGIA CTITICOGACC TITIACAATAA	<b>4</b> 20
5	TACTOTAAAG TITICOGTCAG GAATATTOTA ACCOTGTOGA GCACGAGATT AGCCCGTGGG	<b>4</b> 80
	TITIAGCGAGA GCGATATTIGG TAGAAATGCG TCCAAAACTA TATCTTTCGA TGCAATTACG	540
	ATTICATAAC ICAATTICTIT TICCCAGTCA COTGATATGA CTATCOGTIC OGTATICTICT	600
10	ACAGAGITOG GAGATAGIGT GOGGATAAGI TAATOGGAAC ACGAGGIGGA CATTGGAGIT	660
	AAGGICCIAT GCCCICAATG TCACTCAAGC AGGIATTTAC GTTCCCNAIG TIACTAGAAT	720
	CITCITOCIC GACNOCOGAN INGANOCOCA AGAAAAAATA TOOCOGOCNG AAAANAATIIT	780
15	CCCTEGNETE ACCTETIONAT NACCONACGA AAACNICCTC CTTCGAANGT NCCTTATATT	840
	CIVITIVAAANA ATANA	855
	(2) INFORMATION FOR SEQ ID NO:545:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 847 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1380RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:545:	
	GATCOCATCG ACCTCOCCAA AGTAAGOCAG OCTCTCGACG GAGATCCAGT CGACAAGGTG	60
35	AGGAAGOGIG GIGITOTIAC COTOGAACAC AATTGGCTCC TTCTCGCCCG GCAAGIGGAC	120
	CCCCAAGGIC COCTICTIAG TIGGGIACTG CACAAATACA AAGTCGITCC CGAGCAGGIT	180
	GCCAGTTCG TAAAAGGACT CGTTCAGCCC CTTCAGCCCA CCGTCAACCA CCACTGCCGT	240
40	CTTGGACTCC GCAAGCAGGT CCTCCAGGTC CTGGGGGGGC TCCTTGCCCT CCAGCACCGT	300
	CACGOCCOGC TOOOCCTOGC GCAGCATGTA CGCCACAATT TOCTCOGCCT TOOGTGCCCC	360
	CETETATOSC ATOCCCTCCT CTGACGCCCC ACTGTGGAAC ACCTTCAGCG TCGGGTACCC	420
45	CCCCACCTTC TCCCCCCCCC ATAGATCCAG CTCCTCCTCC CAGTCCACCT CCCCCACCTT	480
	GATGCCCTTC TCGGCCAGCT CCCCAGCGGC CTTCACGTAC TCGGGTGCCA GGTGCTTACA	540
	GTOGOCCACAC CATGOCGCAT AAAACTCCGC CATCACAAGC GGGTTCTCCT CTAAGAACTT	600
50	CCCCAACCTC TCTCCCCTCA ACTICACACT CCACACTCCT CTCCTCCACT COCATCTTCC	660
	OCCURIOCAA CUCUOCCACC AACCOOCGAT GCACAACACA AACCOCTUGT CCAAAANCNI	720
	TOTOGOTIGOS TOTATOCTAS COGTIGETTIN GIGNACTOTIG TGGOCATOAA ANCOGONING	780
55	CNATTITICI TITATACTGA TOCAGAATTC ACCCINTONC AAAACNNITN CONGAAAAGA	840

	NCOCTIN	847
	(2) INFORMATION FOR SEQ ID NO:546:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 860 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1380UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:546:	
	CATCICCOCT GITGICAGIG ACCCCAGIT CCCCCAATTG TACCAGTCCG ACACCAACCT	60
20	COCCACGETA TOGITTOCCA GCOCCACAAC GCOCACGCTG CCCAACCCCCA CCCCGTCCAA	120
	CTOCTCCTGG TACATCTTGA CCACGTCCTT GCCCATCGCA TCCTTGATGT TGAAGCCCTT	180
	CGTCCAGCGG ATCAAAGTGC CGCTCGATAG CGATGTCTGC GCCACGGGAT ACGACAAACGT	240
25	AAACCCGAGC TICAGTIGGC CGCCCICGCT CIGGAGCACT TCAGAGTGGT AGCGCTIGAC	300
	AAACGCCATT GTGCGCTTCG CGATGAAGCC GAACAACTCG TCTCATGTTA CGTCGTCGTC	360
	AAGGAGCTCC TCGGGGATCT TCGACTTCAA CTGCTCCAGC TTGAACGTGT GATCACCGTT	420
30	GAGACGCACC GAGCACACCC GGAAATTCGT GCCGCCAAGG TCCGCCGCCA AGAACGTGCC	480
	CTCCTCAGTG CCATTGGGCC TGCCCATCAC GTACGACGGG ATCATCGGAA GCCCACGGTA	540
	CTCCCGTCCG TCTCTCCGTT CTTCAGACCT GTTCCATACA TTCGATGAAG TACGCGGTCA	600
35	ACTOGOGAG TITIGICCTOC GICACCTOGA AATOCTTACA TATTITOGIOC ACTOCTOCTO	660
	CACTITICCCG CCTTCCCCTT CTCCAAATCT TCVAAAANAT CCTCCTACTG TAAANATTAG	720
	ACTIOGANAC GITGGICGAG TOTTICNNOC TINCCTACTO NOONOCONIG TONIANIATI	780
40	TTGANGGOON TOCAATAAAA AACCCTTING GGGGTCNCAA GNCACCTCCC ACCCTCTTTT	840
	GTTTCCCCNT CCCNNAATGA	860
	(2) INFORMATION FOR SEQ ID NO:547:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 835 base pairs  (B) TYPE: nucleic acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1381RP	
55		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:547:

	CATCATTATA TTATAAAATA TAATAAAGAA TATATTTAAA TAATAATAAT AATATGAAAT	60
5	ATTATATTAA TICICCATIG GAGCAATTIG AGATTAGAGA TITATTAGGI TITAACATCAC	120
3	CAATAATAGA TITTAGIPIT ATTAATATTA CIAATTITGG TITATATCTT ATAATTCTTT	180
	TATTAGIAAT TITACTAATG AATTIAATAA CTAATAATTA TAATAAATTA GIAGGITCTA	240
10	ATTGATATIT AAGTCAAGAA ATAATTTATG ATACTATTAT AAATATAGIT AAGACACAGA	300
70	TIGGIGGIAA AGIAIGAGGI TATUATITIC CATTAGTITA TACATTITIT ATICITATIT	360
	TTACTATAAA TITAATTAGT ATAATTCCTT ATTCATTTGC TATAACTTCA CATGTAGTAT	420
15	TIGEAGIATO AATAAGIATA ATTATTIGAT TAGGICTAAC TATTATIGGI TITTATACIO	480
13	ATGGITTAAA ATTCTTTGGT TTATTTTTAC CACTAGGIAC ACCATTAATT TTAGTCACCA	540
	TTATTAGTAT CAATTGAATT ATTATCATAT TTTGCTAGAC TTATTTCATT AGGTTTAAGA	600
20	TTATCASCTA ATATTATASC TOGICATITA TTAATTGITA TTTTAGGIGG TTTATTACTT	660
20	AATCTAAANC CACAAATATT TAACNITTIN TIAAGITCNN CONATGAATG CTATTINAGT	720
	ATGINIGITA GAATTINIAT CITATACONG CITANINIGA AGININAATA CNOCNIATNA	780
25	AACTATTIAT TOOTTATTAA ATTAACANIT NAACNOOCNA TTANITTINIA TNOTT	835
	(2) INFORMATION FOR SEQ ID NO:548:	
30	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 863 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1381UP	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:548:	
40	GATCATTGIC CAATATTCCC CACTOCTGIA TCATATAGAT ATTGATTATA ATTTCTAAAT	60
	CAACGIGATT GITCTAACIT TAATTAACAA TIATGAATTI TIGOCTAGIT ATTATTITIT	120
	AATTAACTAA TACCTAAATC ATTATAACCI TGACTTAAAA CAAATAATTA TI'ACATTATT	180
45	CTTPATTIAT TATTPAATAT TTAGTTAAAT TTTAAGTTCA TTATTCTTAA TTTTTTACTCA	240
	CGAGTACACC ACTTATTAAT ACTATTAATT AATAATATTA ACGITTGATT CGCATGTGTA	300
	ATGROCTIAG TTAGCOCITA ATCTGAACCA ACATCATGIT CTCATTATTA TTAACTATIT	360
50	TTAATTATTT TAAATAATTA TITAATACCA AAGITATAGG ATTCGAACCT ATGAAATCAT	420
	AAAGATTIAT AATAOCTCAA ATATTACACT TIAAACCACT CAGTCAAACT TICTTAATAT	480
	ATATACCTTA TATATOGITT CATAATTTAC TTATAATATA TAGTATATAA TITAATGATA	540
55	AACTOTTATO ATTITAGGIGO GIAGGGITOA COCCOCTATI GOTAGICAGO AATATGATGI	600

	ACCICCIAAA IGATAAAGAA GIATAATATA TAAATATIAA TATTAAAGIA TITAATGAAT	660
5	ATTATTATTA TTIATTIAAT TATTATTTIT ATTIAGIAAA TAAATAAATA TITCCACTIA	720
3	TIGAAATATA GGITCITINGA TIAGAAATAA GCNATNATAA TGINCCATTG ACTATTAAAT	780
	ANTIGIGCTON CHARACTTOC CTATTINCON INGANAANIC NGAANATCAG AANANAGATT	840
10	CCNANAINIT TAATININCCC CCA	863
	(2) INFORMATION FOR SEQ ID NO:549:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 845 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1382RP	
	(ii) GRANICA IPDISOZIU	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:549:	
25	GATCTCACAC GTGACTAAAA TCACTAACAC CACGTGACTT CGTGCACGTG GCATCGTCCC	60
	ATTOTOTOG TOGOTAGOAT TOTOCCOGOG CATOTOTOTO AGGOCACTOG GCAGOTGACO	120
	ACGCCGTACC ACGGCAGGCT TCACGACAGA CGGCAAGCTC AATCGCTATC TACGGTTTCA	180
30	GGTGGAATIT CTTACCGGCA TCCGATTAAT TGCTTTTTIG GCTTCCTTTT GCCCCTCTTT	240
	TICCAGIGGG TIGCITCCIG AAAACAGGGA GCTAGCITCC CGTAGTACGT AACAGTCGTA	300
	GAGGGITAGG CATCGCTGAG CTCCACACCC GGTGATGCAA TGTGCACAAC CCTCGTCTGC	360
35	GCAAAACGGG CACGAAGATT GAAAGTATCC AGGAGTGCAG CCCAGGGTCA TGCCAGACAG	420
	AATGGGCCAG AAAAAGCGAA AAAATGGACG ACCCITITAT ATATATATGT AGCGAGCCCG	480
	GOCGITICCCA GAACGGGACC CGACACAACT TGTTGTAGAA TTTCTATCTG CAAGGAATCA	540
40	AATACAAAAT GGAATCTAGA TTGGGATGGC TAACTGGTTT GAACTAGGAC ACTGGTTCTG	600
	CATTGAGAAG AACTCCATCA TCCGGACAAT GGTCCTAAGA CCAACCACCC AGANACTING	660
45	TOGANCTTAA AAAGGNOGGT TGAACATOCT GAGAATGAAC TTCTCGCNCG GTCCTACAAT	720
70	INCCACCATC GGIGNICNAA NACCCNNAAT TCGAGATINI NCCNGITAAC NITGGCCITG	780
	CTTTGAANCC AAGINCCTGA ATNAAATGIN CCTNTCGAAA NITANTACCN TCCCCTACCC	840
50	AAANC	845

	(2) INFORMATION FOR SEQ ID NO:550:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 862 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
15		
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1382UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:550;	
25	GATCTATAAC AGGTGCCAAG TTGGCAGATT TGTTTCAGGG GCTCGACCAT GTAGAGTCCA	60
	GIAGAATOCT CIGIAACCCC AGAGCATACT TIGOGCGAAA GICITTATCT GITGAAATCA	120
30	ACTOSOCIAT COCCTTICAT CCIGIOCOGG AGGITGATOC CITICITICAT COCCTTGICC	180
	N/TIMPOTENCE PROSERVA AND AND AND AND AND AND AND AND AND AN	
	AGTATCIGGT TGGTAAGCTC AATGAGCTCC GCATGACCAC GICCCATATT GITTIGAAAA	240
35	TACTACTAC ANTACTAM CONTRACT AND ANTACTAC	
35	TAGCACCAG AACCACCATOG AACCCCCAA ATACTTCCCC ATCCCTCACT	300
	GICACAGITA TAGTAAATCG TOCAGATTAG GICTTOCTAC CAATATTCCT GOOGTTATAT	
	OF CLASSICAL PROPERTY OF CHARACTERS OF CANADACTICAL CANADACTOR GOOGLEGATATION	360
40	CTGCAGAGAT AAAGGCAGCT TITICGCATGC TATGCTGCCC CGCAAAGGAA CTGCGTGGTA	420
	THE THE PARTY OF T	420
	TAGCCGITICA GITTICTTAAA CIGAAGGAGG CATCCATTTIC TCAAATGCCC CGICAGCTCA	480
	The state of the s	400
45	GETTICCATT TOGTACAATC ACACCTITIAA CAACTCCAAA GAATCGTATC ACAGCGTCGG	540
		3.0
	TIACAGAATT GCCACCIGIA GITTATAAAA GCGCCACTCC TAITAAGGAT TITITIGACC	600
50	GOCACAGAG GACTCAGATT CACCATCACC TGATTCACTC ACATGATGTC TGCGTCAGCC	660
	TIGIGOGAGI CATTOCTOGI GGATTACCTA CGATCTIGOG GAAAAATOON AAAAAACATT	720
55		
-	GACNATCINA AACCAGACIT CITINITIGON ATTCCCAAAA AAATTGCGNN GNGCCCNGGT	780

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	TINNATCCCAN CATOCCCITA AAATITIAGAT CCTTGACCCT ACTCCNANIT GNINCCCNAA	840
5	AAAAAACTA TCAATGININ CT	862
	(2) INFORMATION FOR SEQ ID NO:551:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 823 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1384RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:551:	
30	CATCTOCATC GCGTCCACCG TGGACTGGGC GGTCGTGGGC GGTCACGGAA AACTCGGCGG	60
30	ACTOGRICAT GGTGCCGGCA AGGGTCTCGT AGCGGATGGG CACGACCTTC GCAAAGTAGG	120
35	AAAAGAAGIG GCTATGGCCG TTGGGAACCT CCATGGCGGG GCCATTGAGC GGCCCGGGGT	180
	TGCCGGCAAT TTCGGGCCCA AAGGAGAGAC TATGGATCAC GTGGTTGAAG GAGAGATGGG	240
40	OGTGTTCCTT GTACAAGGAA TOGTOGTOGG CGTGGCCCCTT GCCAACGTGC GCAGAGCCCG	300
	COOCCAACTG AATGITICCCG TCAACGCGGT TCAGCTGCGC CGTGCCAGCG ACGCGGCATC	360
45	CCTCGTTGAT CTGCTCCTGC AGGCGCTCCG TGTAGCCCTC GCGCTTGCAC TGCTCAAAGC	420
	CITTIOCCATC CAAAGIGGCC CAGITCATCT CIGOGIACGC COCCCCCACC TCCCCCCACG	480
50	TCTGACAGCA CACGOGCTCG CTGCGCGGCA GGTTCTCGTT CTGGTCCTGG TCGCGTGCGC	540
	CATACACOOC CACAGTAGTC TROGTOGTCT GTAGACOOCA ACGTCTCOCC ACTCOGAATT	600
	CCICCTICCC CACGICCGIC CNIGITIGIC CACCNITITT CCTIGATCCT CCTCCAACNA	660

	ATTCACTOR CICCOLOTTC TCHNIANNIC CATTICATAC TCCCCCGCAT CITGCAAACT	720
5	TATATONAAC COCACTOONC TOTOCTOCOG TOCTTCAANC ACTONOCOTO TOCCTOCOCCA	780
	NITCCCTCCT ANCAAANACN CGTTCACAAC ACCNCNTATN CCT	823
10	(2) INFORMATION FOR SEQ ID NO:552:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 849 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1384UP	
25	(A) CAGAMISM: PAGISBAUP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:552:	
30	GATCACTTIC TITICICICIC CACCATAAAT GOCCICGETA CACACTITIA CCACTCITIC	60
35	TIGOCIGAGA CCOGACAGGI CAATCICAGA GITTITIACTA TICATTAGIG AGTAGATIGA	120
	COCCITACITIA TITATCAAAGG CCACCOOGGA ATTICITIAAAG AAGITGGAAA CAGATGATTI	180
40	CGACATOGIA TAGTICIGIA OCITAATIAG AACOGOCAGG TCTGAGCTCT CCGCGACGGG	240
	AGTACTGTTT TGAATGOGTG GCACAGCCAG TGGCGGTTGG GGCGTGACCA TGCCAAGCTG	300
45	TECCECCOCCT GTCAGCCCCG CTGGTACTGG ACCCCCCACG CTTATCCCCCG GGTCTCCTGG	360
	TGTCCCCAT TTCCAAATAC CGTTGTTCCA CCCTCCTACG TATTTTTCCC CCTCCCCTCC	420
50	GCTCATCTTC TTCTCGGTCA AAGCAGGGTC GAAGTTCAGA ATACCCTTAC TCTTCGTCTC	480
	CTCTGCAATC ATGTGCAACG TTTGCGCCAT CTTCCCCCAGC TTGTGGTCAT AGGGCGCCAG	540
5 <b>5</b>	GTCCCCCGAG TTCCCGGATCA CCTGCCCTTT CATGCCAAAG TTAACGAAAT TCTTGTAACA	600

	GCGITCGAGC CAGCGCTICC CAAGCGGTACT CGCAGCGCAA ATCGTTTTCC TGCTGGTACT	660
5	TGITGTCNAT ATTGAATCNA ACAGGCCCCC CAATAANCCT GTCCCACGGG CCCCGTTCCT	720
	GANNAAACCA GCATCACACC GCNAAAAAAAC GGGCCCCACN CGTCGTCATC NAACTTACCC	780
10	CICCACACTG NATATOCANA OCATINONCCT TITTTINICCC GIGINICIGA AANINCNAAG	840
	CCCCCACCT	849
15	(2) INFORMATION FOR SEQ ID NO:553:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 862 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1385RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:553:	
	GATCCACCTC GTCATCATGG GCAAGCAGGC CACCGACAGC GACAACAACA ACACCGGGCA	60
40	GATOCTOSCG GOCCTTCTCA ACTOCCCOCA GOCCACCAAC GCCGCGCGTG TTGAGCTGGA	120
	COCCACTOCC ACCCCTCCCA CCCTCACCCC CGAGGTCGAG GCCCCCCAGG AGGTCGTCAG	180
45	TOCCOCCUETE CCACTOGIGG TCACCACGGA CCTGCCGCCTC AACACGCCGC GCTACGICAC	240
	GCTGCCCAAC AAGATGAAGG CGAAGAAGAA GCCGATGCCG AAGCTCAACC TCGCCGCGTT	300
50	CCCCGGCGTC CACTCCGCCG CCCGCCTCAA TCTGCTGCGC TTCCAGCAGC CGCCCGCGCG	360
	CGCCCCCCC ACCOTICGTCC CCTCCCCTCCA CCAAACTC CCCAAACTCA CCCAACCCAA	420
55	GGCCGITTAA CACCTATATA AACTAACAGC CCCTATTTCC TCCGCGGACG CAGCGTCCCG	480

	CTCTCCASCA CCCCCSCCCC CTGCTTCCCCC ACCTACCTCT CCTCCTACCA CCCCTCCCAC	540
5	TCCCCGCCCT GCGCCCCGC CTGCTGTACG CTCTTCCAGC ACGCCCGCC ACTCCTCGTC	600
	CCACGCCGCG AGGITGCTCC CCCGGTCGCT GCCGCCCGCG CTATCTTGCA ACACCCCCAG	660
10	CTTOCAGTTT COCCCGCCCC CCCCGCATGT INCCCNCCAA CNCNTTTTTA CACNGGATINT	720
	TNCCCNITIC TINICCNINN NITCCNCCCC GIGGAANICN TITICCCNITIC CTIGANAATIC	780
15	CTANCCAACC CCCCAATTIG ATNONOCCC CCCAAAATNA ACTITICCACT TIGCCGAGAC	840
	CCCGCCCTGT NCCCTTNTTT AA	862
20	(2) INFORMATION FOR SEQ ID NO:554:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 851 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: INTA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1385UP	
35		
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:554:	
40	CATCCTTCAG COCTOGTTCC TCCCCCTTCCA CCCCCCCCCCC CACCCCCACC TCCCCCCCC	60
45	GECCEGGACC TACGECGCGC CCGCGCTCCG CGAGGTCAAC GCGGCGCTCG AGGACTACTC	120
	TOCGTOTICTIC TOCCOCCOC CTGCCGTCCC CTCCGTCCCCC ATCCTGTTCG ACCCCCACCT	180
50	TODOCRACIOC GIGOCCCOCT GOCGCATOCA GCAGGAGCAC GAGCTGCGGG AGCGCTGCGG	240
50	COCCOCCATG ACCGACOCOC AGGTOCACOC ATTTCTOCAG COCTACCTOG TGTOCTACGA	300
55	CONCINCIAT OCCOSTICIOS TOCOCCASOS OCTOSCAAC CTOCACOSOC TGACTGIOGG	360
99		

JEDOCIDE ED OBSSEROAD E.

	GCTGCACGCA CACCGAAAAG TTACGTATGT TAGCCAGAAG AATATGTAAT GCCGAGTCTA	<b>4</b> 20
5	TACTTCCTGG TCCGAGATGT CCTCCCAGGG CATGAGATAG CCCGTCTGGT CCCCCTTGTC	480
	200000000 200000000 2000000000 A200000000	540
10	CGCCCTCCAC CCCACCACCC TCCCCCCCAG CTCCTCACCT CCCCCCAG CAACCCCTCC	600
	GTCTGCGCCT GGCGCGCCT CAACGCCTGC AGTCGCGGGA ACGCTGCCCCA NCACGTTCGT	660
15	COCCOUNTICC ACTOCNOCOG ACTINITAAA CACTOCTOCT TICCTOCAAT CCTTCAACNA	720
	NCGCNGTTGC CCTTTNCNAC TNINATGANC CCCCCAAAACC CCTNTTTGNG COCTGCGGGC	780
20	NCCCCGCCCC NUNCTCTCG CONGGIUNG TGTCCTUNAC CCINCCCCTT TNCNTTAACC	840
	GINIANNI'IN N	851
25	(2) INFORMATION FOR SEQ ID NO:555:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 857 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(-)	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1386RP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:555:	
	GATCOCACGT CATTITACCT ACAGOCTOGG CTTTTGAAGA AGACGCCTGC ATGGTACAAT	60
50	GTCGTAGCCA GGATCCCACC TGTGACCAAG TTCGCCAGAG AACCGAAGCT GCATGACCCA	120
	GTTAGCGGCA AGTACAAGGG CGAGCTGGAT ATAATGACGG ATAGATTAAA CAGAAACACA	180
55	GAGACGTACA AGACACOCOC TOOGAGTTCC GACCOGCAGA COOCCOGCGT OCACAAGCCT	240

	TCTAAGCTGC GGTTTATCGA GGACAAGCTG CGGTCGCTGT TTTTCCAGCA GCATCCCTGG	300
5	GAGCTIGTOGC GGCCCAAGGT GCTGGTGGAG AACATGGGAA ATGAGCAGTA CGACTGGTCG	360
	COCATGITOC ACCTACOCAA OCCOCTTCAC OCTCACTCTC TOCTOCACCG CACOCTCTAT	<b>4</b> 20
10	CTOCTGAAGT COOCCOCA CCOOGAGATG CTGOCCOCAT ACGACCAGOC GCGGTTTGAG	480
	TTCTATCGTC TGAGGATGCA GCAGGAGCTG GAGGAGCAAA TAGGGTACGA GGAGGCCACG	540
15	ATGGTTGGCG CTGTGTTCAA GACAACCGCT GTGGAGCACG GTCTGCAGCA AGAGCAGAAG	600
	GICCICGACA GIOGAAAGAA GACTITIGITIG CCOOCITITIGC CCTICATITITIT OCNAAAAAAA	660
20	ACTICTACAAA GCAGTICCIVIG GGCCNAACCC ACCGAAGAAA AAGAAGAACC AGGACINVITGC	720
	CCAACCCNAA GACNCCACCT GTGNACTCCN TTGCCAACTT TGTTATAAAT TCTTACNNTT	780
25	TTATTCCCTT NGTACAATNC NANNTACTGT TNTGTGCCAT CATGTGCCCC AACAGGTTCC	840
	CCCCNITICGA NAAANCC	857
30	(2) INFORMATION FOR SEQ ID NO:556:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 856 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
10	(b) Torologi: Timear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1386UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:556:	
	CATCCATOCC TOGITATAAC TGAGCAGAAG TGTGCATGOG AACAGAGGGG TTTCCTTGTT	60
55	CCTTGCCAGT TCCCCCATTC CCCAAGTTGC ACTGCAAAAT GIGAATCATT GAIGICTTGT	120

	COLORCATE GOLOCOCION MAGNICETOT TECCOLINGAE COCNITICION CANDESCANAL	180
5	TOTAGGOGGO GCCGTGAGAG TCCAGATGAT GAATCTGAAG TTGAGGCCCA GCACGTGTGC	2 <b>4</b> 0
	TTAAAAGATT GTAATCOOGT GCTOCTTTGT GGTATCCACA TGTGCAATTA CAAATGCCAT	300
10	GCAGGCAAAT GTCCTCCCTG CTTAGAATCA GATTCCAATG ACCTTATCTG TCCCTGTGGT	360
	AAGACAATOG TACCAGCCCC TGTCCGTTGT GGAACAAAGC TCCCTCGCTG CACTCATCCA	420
15	TGTCCAAACT COCTOCTOCA TACTTOCCCC TGCGCACACA GTCCACCTTC GCATAATTGT	480
	CATCCCTTAG ATGAACCTTG CCCCCATGTA CCATCACAGT CAAGAAAACT TGTCCCTGCG	540
20	GIAAAAACGA GATCAGGACA TICTOCTACA ATGATGATTG TCGTGTTCGA GACCGTGTAA	600
	GAAGCCATGT CCTATTGCAA TCACTTCTGC CAATTNCCTG TCATTCCCAT GGCAATGCCA	660
25	GCAAACTTGT TAGCAAGCCT GTGGTCNACC ACCGAAAGCC GCACNTGTTT GTTAGGGAAA	720
	TECNIESCNI NOCENATECCT GAATCCCTET NONAAAAAAA AANCNOOGIC CETTETCCAT	780
30	CNCCACCAAT MIGCNIGATT IGCIGGAAGA GAANGITCOG ACACCNOCCC GTCCTGNAAG	840
	AATGTGCAAT CNNCGN	856
35	(2) INFORMATION FOR SEQ ID NO:557:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 830 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1387RP	
50	(15) OVERATORS EMOTIONINE	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:557:	

	GAICAACCAC ICGIGIGCCI AIACATAGGA ACCAAAAAAGC CTICIGGCCT GGICCTCAAG	60
5	TAGTATTGIA TAAGTTTGGA ATCCTTGTAC GCGGTTGCCT TCCGCGCACC TTTCATATTT	120
	TOOGTAAAAG OCTOCACAAG GITOCTATOT TIATOCTIGA AGITGIOTOC ACAGGACTOC	180
10	CACAAGAACG CCCCAGCAAG CITCITATCT TICACGTAIT CCTTCTTTAT TITCAITGAA	240
	TCCACATTGT CGTAGACGAC AAGAGTTTTA GTATTAGGAT CGTAGCTATA TOCAGAGACC	300
15	CAAACATTOT CAAACTTCTC TOOGCCGTGA GCTAGCGGCA ATTGGTTGTA TAGCCACATA	360
	CCCGGITCCC CTTCTGATCC TCCGCCTACA CCAGAATATT TCTGGCCAAT TAGTTGTTCA	<b>4</b> 20
20	CCATCCCCCC GAACCTTOCT GAACCCACCC CCATACCCTC CCATCCCCAG TOCAATTTTT	480
	CTTGGGCTGA CCTTAAATTG TTCGGTCATC ATGAGTATCG CATCATGTGC ATTCAACTCA	540
25	TCAAAGTTGT CAATACCCAT ATCTTCATAC CGACGCTTAT CTAGGTGCGA TTGTACGGCG	600
	AATTOGTAGO ATTGTACAAG TIGCTATOGT AGOCTGTTCG CTCTGACCAT GCACCGTGGT	660
30	ATCGIATGIC ATCATATCON CATGCTGAAA ACTGITCACT CNCAACCGGA AATGCAATINT	720
35	CIGAAGAACC NOOCTOCCAG CITNATIGAA CCGICCIGIN TCCCCCCCCC CNANATNITT	780
	CCATCTCNVT GTINGCAGCG GINCTITINNA AAACTGGVTC GNICNCACCA	830
40	(2) INFORMATION FOR SEQ ID NO:558:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 857 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1387UP	

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(xi)	SEQUENCE	DESCRIPTION:	SEQ	$\mathbf{I}$	NO:558:
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5	GATCACCACA	ACACAGAAGC	ACGCAACGCT	ACAGGACTIC	CCTGTTCTTT	TOCTTOCACA	60
	CCTCCAGCCC	AGAGGACGAT	TACACCOCCG	TCAGOGITCG	CTAGTCTCCG	GCAGCACAGG	120
10	CTCCTTATCA	CATTTTCCAT	TTTCACGCTC	OCACATOTCA	CAAATAACCA	AATACATCCC	180
	CAAAAGCACG	CTTTTCTCT	OCCOGITCIT	TCTCATCGCG	TCAGACTTCG	TACTCCCTAT	240
15	GAGCGGCAAG	GGCACGCGCG	CAGGGAGCTC	ATCTACAGGC	ATCGGGTCGC	COCCACOCC	300
	TCTGCAGCGG	CTGCGGCAGC	TOGTAGOGCA	TCGAGATCCG	GCAAGAGGCC	CCTCAGCTGC	360
20	ACTTACGAGC	ATCGAAGAGT	TTACTAGGAG	ATGACAGCGC	CTGCACGTCC	CTGAGGCTAG	420
	CCTCCCGAGG	202222222	OCTTOGTATA	GGGTTTACAT	AGCAGAATGG	CACGAATATT	480
25	TOCTCTAGGC	AACTGCAGGG	ACGGAAGGGG	CTTCATGCGA	AATCCTTGCA	cccccccccc	540
	CCGTATATAA	GGTGACGCAG	CTGCGCAGCT	G99900993CA	TOCTAACCAC	GACAGGATGT	600
30	OCACTOCTOC	OCCATTATAT	ACGACAAGCC	CCCCTCCACC	GTCGGTGCAC	AGGCAGGACA	660
	CCTGGCGGAA	ATCCCAANTC	GTTGAACAAG	GCAACTGGTG	CAGCNGGCGC	AATCTACAAG	720
35	AGITGITGAN	GGCGGCCCCIC	ACATTTGCCG	TINCACTGAC	CCTGTCNCGA	TCCANGAAGA	780
	OGNCTOGCAT	NTCCCANAAC	CTCCCCACAG	CIGINGACIT	GAACTOONGC	CTACCTTCAT	840
40	TTGCANNCCA	GAAAAN					857

#### (2) INFORMATION FOR SEQ ID NO:559:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(vi)	ORIGINAL	SOURCE:

(A) ORGANISM: PAG1388RP

	9	;	

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:559:

CCTGGCTGTA CAAGGCACTA ATATGAAGAT AGAGTTATAG CGCGTGAGAA GGAAAGGCTC

CACTGGGTGT TGCATGGGAT TTCAGGGTCG TGATAATAAT GCCAGGCAAT CATATAGATT

ACCACGAGGG AAACATCAAC GCTATTTAAG GTCATCCTTT TTGACATCTG TOGAGGAAGT

OCGAATACCT GTAAGCOCAA CTCTACAAGA TOCCOCCGTC TCCAAGACCA ATOCTAAGCA

CCACAACTCC AATGACCTGA TTACTGGGGA GCAATTCCGT CCTCGAAAGT TGGCACGTCG

ACTGACTOGT TTTCTOCCCA GAGATCAATC NATTGATCON TNATCCCTTA CATCNCCGGA

CTITINGAAAA COCAAATTAA AATTOOGNAN NOCAAAATOC NOOGATTONG CACCCTIGAA

CTACCCACNC GGCCCIATTA TITITATAATT GCNNACAANN CCCGATCCCC CGNNAACCCN

1	С

	GATCCACCCA AATTCGTCTG TGCTGGACCA GCTTTCCCAA CAGTCTCCGA GGTAATCAGG
15	CTACTGOGIT CCTATTTTAT GOCCTTCAAT AACTCTTTAT ACTTAATTTA GACGITAACT
	TOCACATOOG GIATITITICA CATOTGAGAT ACTOSCAAGO ACCOCTACOT TIAGGAGAAC

20

TGTATCCCAT GACTIGIGGA CAGGGGCTTT ATGAAAAAAC GCCTGTCCGT GTAAGGATAT ACAAAACATA CIGAGATOOC TITTIGITIOCT GAATCAGACA TICITAGGIT ACATITITOOG

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(i) SEQUENCE CHARACTERISTICS: (A) LENGIH: 838 base pairs

(2) INFORMATION FOR SEQ ID NO:560:

(B) TYPE: nucleic acid (C) STRANDEDNESS: single

GTAAANCGAA AACCCCCCGG NVTTCGGACC NNCNTTTTNC T

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1388UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:560:	
15	GATOCAGOGG CTTOGTAGCA TOCTGGCCGA GGAGTTCGGC TGTYCTGGTT T1GCGCGCTG	60
15	AGGCTCACTT ATAGGTGCCG ACTTCGATTG CCACTTGTGG CCAAGACTTG CTTCTTTTACA	120
00	TAGCTAAATG CCACTGATCA TATAGACTGC TTATTCCTGC TTAACTGCCT CAACGTTCCA	180
20	TACCATCTCC GCGTACTCCT CTATGCAGCG GTCACTGCTG AAGAAGCCAA CGTTGGCGAC	240
		210
	GCACAGGATC CACTICIGGA GCCAGGCCCG GCGGTCGCCG TGGTAGACCAG	300
25	ACCCTGGCAG GCTATGTAGG AGTCGAAATC GTCGCTCACC AGGTAGTAGT CCCCGTGCTG	360
	The second contains the se	300
	GOCCACOGAG TCCACCAGAG GITOGAATITC ACOCAGGTCC TGAGGGGAAA ATGCGCCCGA	<b>4</b> 20
30	GCACAGCOTC TCCACTACGC GAGCAATGGG GGCTGGCAAC TCTTGGCCGGT GATACCGGTG	480
	district reasonable district delicates removally	100
25	CCGGTAGCOG AGGTCTTCGA CATCTTCTGC GAGATTACCA AAGAGGAAGA TGTTGTCTTC	540
35	COCCATOTOS OSTIGICATOT CGACCITOSO COCATOCACE GIGOCEATAA TCACACACA	600
	SCONICIOS CONGRICI CONCOTIGOS SCONICANOS GIGCONIAN IGNAMACA	600
	TICATAACGA ACTICATGIT NGAATICOON GAACCICATT ACCOSCIGIC AAANGIGCIC	660
40	ACTAATOGGA ACNOGGANAA TATTOGOOGG GAANATGTAT OOGGAATGAA ACCOCTICAGA	720
	ACTIVATORA ACTOTORICA GARRATGIAT COCCARTIGAA ACCOTORICA	720
	AATACNATOC CTCTCTTANA CACNOCCONC TTATTACCTA TATNOCTGCC NITTTACCCG	780
45		
	OCCUTINGCC CIVARANIACC TIGAGRAGIC COCCINININ GGINCCOGIN CONTITIA	838
	(2) INFORMATION FOR SEQ ID NO:561:	
50		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 826 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single	

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1389RP	
10		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:561:	
	CATCTTCTTT TTGAAGCCCA CAGACACAAA CTGTGATGGA GTGCTGGAGA CGCCAGCTTT	60
20	GCACCACTIC CITTICITAG ACCOCCAGI CITTITICCIA GGIGIAIGIC TITICCTIGGI	120
	OCCUTATING CICACAATIG CCTTTAGCIC TICCACCACA ATCTTTGTGG ATAACCTTTG	180
25	GOCATCIAAT GAGOOCTITIT CAATIOCACC TITGATOCAA CATCITOCAT TOCAAACGAT	240
	ATTOGICACC ACCAACATAT TAGTOGAGIT ATCTTICCCC CATGATAAGT AGAATCTOGT	300
30	ATGIATTICA AACOCACCTIC COGAGOGIAC ATCIGGOGIC TICGITATCT GCTCCACTAC	360
	TATGIGAGAG TICACATCOC AATGIAGGAT TITTTCCTOG ATCAAGCATC GCGICTGCTT	420
35	AGGACCAACA GGATTGITTA ATGOCTTGAT ATATTCATAT TCCCTCACAT TATCTGAGAA	480
	TICAGACOGT ATAOCTGAAA TATIIATGAIT AGOCTGITITI TCTAATATCT TITIOCAAGIA	540
40	GGACGTGTCC TCACCAAATA ACAGCTTGTA CACGACACCC AATGGTGCTG CGATGGAATC	600
	GAATCATCAA CAATAACATC TOCTOGTTOC TOCTATAOGT GITCITCGTC OCAGGANGCT	660
45	ACTAGOGOGA TATINGTAAA TATTAAGANA CANFIGITGA CIGITNGAAC TOCCNOGIAC	720
	TIGATINIAT AAAACCTCNN AATGITACCG TICNACNCTT INGAGANTIN ANCCCTCNAA	780
50	TCCNITCCNC GIGANITINC ATCICCCCIC NICIATACIG ATACNI  (2) INFORMATICAL POR CITA TO ATACAS.	826
	(2) INFORMATION FOR SEQ ID NO:562:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 839 base pairs

	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1389UP

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:562:

GATCCGTCCC ACTITICAACA TIGIGAACGA CTTCACACCG GAAGAACACG CTGCCATCCG	60
CCGTGAGAAC GAGTGGGCCG AGGACCGCTA GCCACGGCCC GCCTCTATGT ACCATAAGTA	120
GCCGATATCT ACCOCTOCCG GCGCGGGGCC CGCCCGCGCC ACCGTTGCGT GCCAGGAGCT	180
GETCTOCCGA CTATCCGTGC CAACGTACGA AACGATOCTG GTTTATGTGG TCCGCCCGCC	240
OCTOGITACA ATTAACCOCC CCAGGICATC GGTAGACOGA GCTAGCTACT CGTTGTCCTG	300
TAAGTGAGTT AACOCACAAG GOGAACTATT CGTGTGGTCA GOCAGCAGAG ACOCTGCAGG	360
ACATACTACG AGTTATTTCT CATAACTAAA CATTTTTGAA ACCTTTGTTG COOGGGCCAG	420
GIOGITTOCC AAAAGCCCCC GGAATAAACA GCCACCACAC GTACATCCTC TTCTCACCCA	480
GAGGETIAGCA AGGATIGOCAG AACAGCGGAA GCGGTICOCGG TICGCTICAGAG AGAGCGCGCG	540
GOCACTITIC AAGAAGCATA CGGGGGGAAGG GGCGGGGGAA GGGGCGCGCG ACAGTGCCAA	600
AGACGGTTAC GACCCGAATG GGGAACCGCG GANCGGGCCC GAGCGGTNAT TTCAAGTTGG	660
COCNOGGAAG GCCCGANITT NAAACCOGGIG TNTAGACAAA AACTIGICCA GITCNCACCC	720
GINGITTACC AANNININAA TCTCCNCCCC NGGGINGGIG GCCNGAACCC CCNCTGGCTT	780
ACCESCINCOA CATCTCTCCC CCCCCTCCCA TTAAANACCC CGNCNCCTTT TNTCTCNCC	839

(2) INFORMATION FOR SEQ ID NO:563:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 740 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1390RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:563:	
20	GATCAAGTAA TCAATCAGTT AATAATATTA AGAATATAAT ATGTAGACAT TTAGTCTAGT	60
25	CTATTAATTA TTAATTATTT TGTAATTIGT TGTTAATTTG TIGATATTTT ATTGATTTTG	120
	TIGACATUT GUIGACATGU TGATATGUTA TAAAATATAA TUTAATATTA TUTTATATAA	180
30	TEATTATTAT TATCTAGICA TAGACTCATA TAAATATGAA TATATTCCAT TATTAATTGT	240
	TTAGGATAAA CATAAATTAA TATAATAACT TATTTTTAAG TTCAATAAAT ATGTTCATAT	300
35	TTATATGATT AATTCATAAC GIATTOGATA TAAATATCTC ATACCCTTTT ATGAATTAAT	360
	TAAGCOGIAT TAAATTAITC TGATTOGATT AAGITATTAT TTAATTTATG TTCCTAACAA	420
40	TTAATTGATT CCATAAATAT CGATATTTAT TATTATTTAT TAAAATATTA ATGATAATAT	480
	TGTAATACTT CAATTATTTT ATCAAATGGC AAGTAATCTA TTAATCNITT AATACGATTG	540
45	ATAAGAAAGA AAAGAATATC ATCIATCGTA TAATATATTIT CAAGTATGAC CTCTTCAATA	600
	TAATTAGAAG TITAAACTIG TAGAGAATTA AGAATTIAAT AIGAGICTIA CATTAAACCT	660
50	GATATGAACC TITAATCTAC TIATTIGTT AACCGITGAA GAGAGAATAG TIAATCTNAG	72
	TATNACITAT ATATTCATAC	74
65	(2) INFORMATION FOR SEQ ID NO:564:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1390UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:564:	
20	GATCAAACTA AGAAACCTAA TAAACTAATA GAACCTATTA GATAAATTAT AGAAATTTCA	60
25	CCAAATACAG GITTITTTAGA ATAAGITGAT ACAATATGIG ATATTATACC AAATAGIGGI	120
	ACAATTATAA TATATACTTC AGGATGACCA AAGAATCAAA ATAAATGTTG ATATAAAATA	180
30	GGATCACCAC CACCITGTAC TICAAAGAAT GATGTATTAA AATTICTATC TATTAATAAT	240
	ATAGTAACAC CAGCTGATAA TACTGGTAAT GATATTAATA ATATAACAGC AGTAATTAAA	300
35	ATTGATCATA GAAATAAAGG TATTTTATGT AAAGITATAC CATTAGTTCT TATATTTAAA	360
	GCTGTAACAA TAAAATTAAT AAGTCCTAAT AATGAAGAAA TAGTAGTTAA ATGTAAAGAG	420
40	AAAATAGCTA AATCAACAGA AGCACCAGAA TGTGATTGAA TAGAAGATAA AGGAGGATAA	480
	ACAGTICAAC CAGTACCTAG ACCAGATTCA ACTATAGTAG ATGTTAATAA ACAAATTAAT	540
45	AGTOGTOGTA ATAGTCAAAA TGAAATATTA TTTAATCTAG CAAATGATAT ATCAGAAGCA	600
	CCAATTATTA ATOGTAAATA ATAATTACCA AAACCACCAA TTAATATAGG TATTACTAAA	660
50	AAGAATACTA TTAAAATAAG ATGTCCAGTA ACTAATACAT TAAATAATTG ATTTTGACCT	720
	TGTAAATATT GITGACAGGT GCTGATAATT CTATTCTAAT AATAAATGAT ATA	773
C C	(2) INFORMATION FOR SEO ID NO:565:	

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(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 749 base pairs	
5	(B) TYPE: mucleic acid	
3	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1391RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:565:	
20	GATCTITTIG CICCAGGITA TICCCTICIT GGACACATIT ACGAAGIGIA TITICAAGAC	60
	CTGACTCGCG CATTTAGGTG TIACGITAAA GCCTTTGAGC TAGATGCCGG CGACCTCGTC	120
25	OCTOCTAAAT ACATOCTOCA ATACTATAGT GACCTGTGCA ATTOGCAGOC GOCCOCCAAC	180
	ATCHGTGACC GTGTAATCAA GAATGATATG CATCTCAATT CCGTCAACTG GCCGTACAGA	240
30	GTTCTGGGTG TTTATTATTTT GGAGCTTCAA CAGGAGGCTG AATCGATCGA ATGGTTCCAA	300
	TCTGCTTTAC GCATTGATTC GTCTGATGTT GAGGCATGGA TAGGCCTGGG ACAGGCGTAC	360
35	GCCGCATGTG GCAGAATCGA AGCCTCGATC AAGGTTTTTG AAAGGCCATT AGAGCTGTCT	420
	CCAGAACATA AGIATICCAGG GITATICCTG QCTATATCAT TATICCCAGCT TTCAGAATTC	480
40	CAAAAAACTC TOCACGCCCT CACAAAACTT GTCAATAACT ATOCACAAGA AGCTATCTTC	540
	AAAGAAAGAC TAAGIGCAAC GITGGIGGAG CATGCTTTGC AGITCTTCGA CCAAGGITTAC	600
45	CIGATAAAAG COOCAACTIG COCTOCTGAG GIGATATOGA TCATAGAAGG CATTGTATCT	660
	GAACAGGTAG AATATACAAC CAATATGTGG ATTACTTTAT CAAAGGCTTT GAATATTTTT	720
50	ATTICCACCC GITCICAGIT CGACAACT	749
	(2) INFORMATION FOR SEQ ID NO:566:	

55

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(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 767 base pairs	
5	(B) TYPE: nucleic acid	
3	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1391UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:566:	
20	GATCGCCCCC CAGATTGTCC AGAACGTCCT TGCACTACCG TCTCTTACGA CAAACGACTA	60
25	CATOCAGICG TIGOCTICCG AIGITICIGI CAAICAIGIG COCICCAIGI TIGICAAGCT	120
	GETTGAACTA GOCTTTCTGG TCCCGCTTTC CAACGTGCAC TACATGCCAC TGGCCGATCT	180
30	ATGGGATGTG CTCTACAAGA AGGAATACAA TGCTATTCCA AAGAATTCGA CGTTGTCAGA	240
	TOCCAACAAA COTOCAGAAA CAAACOCCAA GACGAAGGIT CAGITCAATA CGITOCIGAA	300
35	GAATGTCGAA ATGAGCAACG TACTAATGAC TGATATGCAG ACTTCAATGA GACGTGTCCA	360
	AGACAATCTT CCTCTAACAT TTAACTTCGG CCGGTACATG AAGCACCGCC GTTCTCGGCA	420
40	SCTIGIACAG TITISCACGIT CCCGIGIGGG GAGCGIACCA GCCATGATCT ATAAGGIGGC	480
	ACTGAAGATA ACCGAACAAT GTGCCCGTGC GCTTTCAGAT CCGCTATGTG AGACAGGCCT	540
45	AATOCABGAA CTTGAGGAGC AACTGOCTAT TCAGGAAGAT ATGGCGCTAG ACGATGAGAA	600
	GCTACCGGGC GTTACATTCA ATGCGGTGGA CATATCCAGA AACTTACCAA ATAACATGGA	660
50	CCTACGTGGC ACACTGACTT CTATGCCAAG AAGATCACCA GAACGTTGCA CGCACCAAGG TCAATCCCAT AAGCGGVIGA AGGCTGAAGA TGGGATGGCT GTAGCAG	720
5 <i>5</i>	(2) INFORMATION FOR SEQ ID NO:567:	767

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 753 base pairs	
5	(B) TYPE: nucleic acid	
5	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1392RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:567:	
20	CATCCCCACC ACCGTCACCC GCCTGCCCGG CACCACCGG TTCGTGAGGT ACCGGTCGCA	60
	CCTCACCACC ACCTTCCCCC GCATCTCCCC GATCCCTACG GACTCCCCCA CCTCCTGCAG	120
25	CITICAGGAAC TOCTOGICTA CGAAGCOCGA GCTCTCGTGA ACGATCATGT ACCOGTCCTG	180
	OCCOCAAGOS TICCCCOOCCE COCTOCCATC GICATICCAG TOGICIOCCA GOCACGCCCG	240
30	COGTIAGOGO: ACGITIGCTICC CCOCAAGOGA CTOGAAGTTIG TTGAGGTOCA GCOCCGTOGT	300
	GTGCCGGCAG TTGCGGCACA TCAGCGCAAC GTGAGTCGCA CGTGACGTCA GCACCGACGT	360
35	TGACACCACG ATCCCCCTCA GCCCACCAC CCCCCAAAACG CTCTGTGAGT CCACCTGCCG	<b>4</b> 20
	CAGCOCCTC TCAGCCCCC COCTCTOCAG CTCCACCTOC ACCOCCGCA GCCCCCCCCC	480
40	GTCCTCCGCC CGCAGCCGCC CCATCCGGCGC CGCTATTTCC GTCAACGGCT GCTCAAAGAG	540
	GGGCACCGIC TCCACAGGCT CGTCGCGCAC AGTTTGTACA GCGCCTCGTT GTACCAATCA	600
45	CATCCTCCGT GTTCACGCGC ACCCCGTACG CCGCACCACC ACCTTGTTCC GCAACTGCTC	660
	GCGATATAAN NAACCGCGCG TCNAACGAAA CTOCNGCACA AANCNCONGA AGAGCGCACC	720
50	NCCICCEANC GETOGITECE COCCOCCTC CTC	753
	(2) INFORMATION FOR SEQ ID NO:568:	
55		

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 752 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1393RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:568:	
	CATCACOGAT TOCCCCAAGT ANTOCOCAAC AGTCGTCAAN TCTGACATAT CTCTTOCAAA	60
25	TOCTAGOCTIC TOCOCOCCTTG AACTAACCAT TACTTCTAAT ACCTOCCTAG CTOCCTCCAA	120
	ATCCGGATCC AAAAAAGCAA TATTTATACA TAACTATACA CGAAATCTCA GITCATCGCT	180
30	AGCTAGCTCA TOGTATOCOG GACTGGGAGA GGAACTCAAT GCTGTGGAAC CCTTCGAATA	240
	TOSCASCOTIC GOCCATIOTTIC ACCAAGGACT COCCTOGOCC AAACATOCOG ATOCCACNTA	300
35	GETGGETETC TYTIGCCGTTC TOGTGETTAG TCACGACCTC GATGCCCAAA AACTGCCACT	360
	TCAGCAGGCC GTCGGAGGGT CGGTTGTCCT CGAAGGTGAA CTTGACCCAC CCATTGACTT	420
40	900GACTICT AGGGTCTTGT AGTAGGTTGC GTCGGAAGGG CTGTGGCCAG CGTATATGCG	480
	GAGCGTCTCC NANGTGTAGG ACTCATCCAC GAAGAGCGAG AAGTACATGG CAAGCTGGAT	540
45	GATGICAACG COCTTOCTGA AGAAGACGIC TATGGTGTGT GOCTGGCAGC CGTCGCTTTG	600
	CCANAANGIG GCGGGGTAT CATCCNAAGG CGTTTTCCAT GGGGTANCCG GCCTTGAANG	660
50	AAGAAGOCTT CCANTAGGCC AAGNAAGTGA TATONACTTA CCCTGGTTCT CCAATGTTTG	720
	CAAGCCCNCC TGTTATTTNG NCCAGAAAAG AC	752
55	(2) INFORMATION FOR SEQ ID NO:569:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1393UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:569:	
	GATOCAGGAT ATCATGCCCA AAATCCTTGA AGCCGCTGCA AAGCCCCTGG TGCAAATCAA	60
25	GAATCIGCAC ACGGCAGAGA ACTTACTCTT CGIATTTTGC TACCTGACTT CTATTGATGC	120
	GCGGCAGACA GTGGACTTTC TTTCATCAAC GATCATCGAT GAAGGGGGCC GTACCGCCCT	180
30	CCAGOCTATC GTTCCGCGTT GOCTAGAAGC ATTCGAGGTT CTCCGCGGAG AACATAAAAT	240
	CAAAGAGAAC ATTTIATCCC TTTCCAAGCT TTTCTTCCTT GAGGATCCCC GTATAGCGGG	300
35	CATCACGGTC AATGGGGATC TGATTCCCCCA CGATGGCGAC ATCATAATCA CCCGCTCCAT	360
	GOCCAAGAAA ATGCCTGATA AGIACACGCA GATCTCCGCG GCCGAGAAGA TAGTCAAGCT	420
40	CITTGITIGCA CAACTAGCCT TCCAGCAAAA CCAGCCTGAC CCTGGCCGTT ACCCTAAAGA	480
	COOGTICTOOC CCTOCTCACC CACATGACTC CCAGGGAGAC TCAGCTGATG AAGACTGGGA	540
45	GGATGICGAT GACATOCTIG ACTACGAAAA ATTGCCCCGAG TACCCCGATG ATAGTGACAT	600
	TGACGACACG GTGACAGCCT TTTATTCACA AGTAACATCG AAGAGGATGT AACCACTCTG	660
50	CTTACTCAAT TCTTCAAGGA AGCOGTTGCC AGAAATGCCT CTGGCTTCCA GGAGATCTAT	720
	AGCAGGCTCA CTGAACAAGA GAAGAAGAGC TATCTGCATG CATGGTATAG GAT	773
55	(2) INFORMATION FOR SEO ID NO:570:	

	(1) SEQUENCE CHARACTERISTICS:		
	(A) LENGTH: 755 base pairs		
5	(B) TYPE: mucleic acid		
	(C) STRANDELNESS: single		
	(D) TOPOLOGY: linear		
10	(ii) MOLECULE TYPE: DNA (genomic)		
	(vi) ORIGINAL SOURCE:		
15	(A) ORGANISM: PAG1394RP		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:570:		
	CATCTOCACG ATTACCOCCT ATGATTATAT COCAGCAACA TEESCACACG CCCCACACAC	60	
25	ACACATGATA CTGGTCGGTG ATTCGCTGGC AATGTCCAGG CTGGGTCATG TGTCCAGGGT	120	
	GCACCIBGAT CTGCAGCAGT TCCAATACCA CGTCCGGTCG GTGTGTACAG CACCAGGCTC	180	
30	GICCITIATA ATTOCAGATA TOCCATATOG TAGCTITICAG CGAANCATTIG ACCAGOGAGT	240	
	ACAGACOSCG ATCTOSCTTA TGAAGACATC CAGCAGOGTG GGTGCTGTTA ACCTOGAGGT	300	
35	TGGCCGCGAA GAAAACGACT ACTGTCTTGA GCTTGCCGCA GAGCTCTGCA GGCGCGGAT	360	
	CCCAGTAATG GOCCATGTON GOCTGACCCC GCAGCGCATG CATGCATTGG GCGGGTACAA	420	
40	OGTICACOOC GCAAAGGACT TGOOCCAGOC GCTGOCGGCG TACCACCGGG CTAAAGATCT	480	
	GCAGGCTGCA GGCTGTTTTT CCATCGTCAT CGAATGCATT CCAACTAAAC TAGCCGGTAT	540	
45	CATAACCGAG AAACTCAGTA TACCTACTAT TOOCATTOOC 0C000CCCCC AGACAAGCGG	600	
	GCAGGIGCTC GTACAGICGG ATCTGCTGGG CATGITGCCA NGGAAGGCCC CAAAATTTTIG	660	
50	TOCHGAATTC CCCOGACTTC CHCHOGGACG CCATANGTTC CTTGTGCCCC CTATGTTGAA	720	
	AANGIGOCCA NGOCNICTIC CCNAAAGING GOOCA	755	
c c	(2) INFORMATION FOR SECO ID NO.571.		

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 773 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1394UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:571:	
	CATCGAACTC CATGAAGGAG CGTAATGGCC TCGTGCAGCT GCACCGCACT GGGTGCGTAC	60
25	ATAGCGGGAT GTAGGAATGC GGGGATAACG ATTCGGAAAA GCTGACTGGG CTGCGGCCTCT	120
	AGCTTCAGCT CAAGCTGGCG CAGCAGCGTT GCTATAGGCT GTTGTGGCGA CAAGGTCGAC	180
30	ACTICAGITG CAGTAGGAGC AGGTAGCATA CGACTAGITA TATCGAACTG GTGCCGGTAA	240
	TGAGGATGAG GGTCAATTTC TGGCTCCGAG CGCTGGCTAG CACCACAATT ATCACCAAGT	300
35	CCATACCTCC ATGCAATTCT GAGATCTTGG CTACGTGCGA CCGGTTTTGC ACCCCCTCCG	360
	OCTAMBITIT GCACOGIGAC CTICGATICC TOCTOGGAAA TGCGAGATIT CTITIACCTCT	420
40	TIACGIGIOC CCIGGAATAT CCCCGGCAGC TCCTTCGCAT ACTGAGTGIT CAGCGTGATG	480
	ACCACCACAT GOGIATICCC TCCCCGCIGI GCGCCGCGAC TTTCCCGCCG GITATGIGCT	540
45	GCTCCCTGCG CTGCAAAGAG CTTTCCAAGT ACCGATGCAA AGTCTGTACC CCCTTGTTCT	600
	TOCACCAGAA GCATCTGGCC CATTGGCAAG CCCATATGCC CTAGGAGCCG ATCCATATCT	660
50	GCACAACCCG TGCATGTTGT GGCATGCCAA GTAACCGGCG ACGCACGCAA GCCCGGATGC	720
	GACTIGOCTICS CINCOTCACTIC TTIGGATICOCA ACCTICTOCAC GOCTICTINGAA AND	773
55	(2) INFORMATION FOR SEQ ID NO:572:	

	(1) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 746 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1396RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:572:	
	GATCAATCAT TCTAGACCIG GACCAAAGGA TACCTATAGG CTTGCCTCGT CATTGCCCCC	60
25	TITICATTATT ACATACCCAT CGITCCACAG CGIGICACAT TCIGCCATIC GAGAGCAGGA	120
	CACCCAAGIT TICAAACAGA ACAGCCICGI TCICTTGGIA AAAGITGGAC CTTCTAACGG	180
30	TGTCCTCATC GAAGCCGTCG TCGCCACTGA GGACCTTGAG GGCGTTGGAG GTGGCTTTGA	240
	TGTAGTCGTT CAGCATACCA ACCOGGTCGT COGCAACCTT ATTGAAAAAT TOGTACTTGT	300
35	TOOCTOTOGA OCTGANCTOC AGOOGAGAGC AGTTOGGTCT TCTTTTCGAG GGTTGCCAGC	360
	TOCOOCTICGA OCTOOCTOGT GACTOTOTTG AATTICTOTICA OCAOCAGCAT CCCCTOTTOG	420
40	GCAAGGGAGT TTTGGGCGGA CGCCGGTTCG GGATCCTTAA CCGGGACACG TGGCACGGG	480
	ATGTOGAAGA OCAGTTOGOC GTAGGTGGAG GTCTTGTOGA OCTGGATGGT GTAGTTGATG	540
45	CGCACGGGG GGATGGGCTT GATGTGGGGG TTGACACCTG GGGCAGCTCG GTGAGCTTGA	600
	GGTACTTOCG AGOCTICTOCG GCGGGCCGCA GGAACTTAAC GATCATGGCG TCCACCTTGA	660
50	TGACAACTTG TCGTCGTTCT GCGTGCTCTT GCCGTTGCCG CTNGGGTCTG CGACNAAGAA	720
	CTCTTGAACA GGATTTCTTG TNAACC	746
55	(2) INFORMATION FOR SEQ ID NO:573:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 772 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: INA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1396UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:573:	
	GATCGGITAC TTAGAGGGAG TGCAAGACCT GGCCTGACTT ATCTTAGGGT TATTAGCTAT	60
2 <b>5</b>	GACOGGIGIG TICOGATTIC TGIOCAAGGG TITAGATGCC ATCAACTCCC TGAATTCGCA	120
	CUACTITICOS TIGICOGUOS AUGAACAGAA COCCATGACT TUCGUUGAGC GUATUAGAUA	180
30	CTACAATTOG ACCITTGAGG GGATCTGTGT GGTCCTGCTC GGGCTGATGT ATGCCGTGTA	240
	CGTGGGGGG ACCAAACTAA ACGAGGGGG CTCGGACGGT CTGTTGGAAC AGCTGAACAA	300
35	GITCITCTOG CAGCACCTOC AGITTOCOCG CGTOCGITTT TCGTCCCCCC ACAACCGACG	360
	OCTOCCATAC ATCAGCGATC GGAATGGCAC ATGGTGCACC GCATTCGCTA CGGGGGGCAC	420
40	GIGIGIGGAC CATATIGIGG IGAAGGCICA CTACCCGGGG CGCTICAACC CTGIGGGGCT	480
	GCTGGTGCAG AAGCTGCTGG GGATGTTCTT CCCGCAGGTG GTGGACCGCA CGGCGATGAG	540
<b>4</b> 5	TITICTOCACG TCACCGTICAC CCCCAACGGG AAGTGCACGA AGGACGAGAA CAGCGCGTT	600
	CAGOCGACOG AGGACOGOCT GAACCOGTTC COGTTCATCG CGTCGATCGT CCACAAGAAC	660
50	GOGATGAACG ACTOGOGOG CAAGAACTAC TTOCTCTOCT TGACTCACNC GTOCGANGOC	720
	GAAACTCTCC CATGGAANTA CTCTTCATGT CCGANAACAA CCACTGAACA AC	772
55	(2) INFORMATION FOR SEQ ID NO:574:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 753 base pairs	
	(B) TYPE: nucleic acid	
5	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1397RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:574:	
20	GATCCCATTA TICTACAGCA AATATTACAC GGCCGGCGGA CCCTCGACAA TGCAGAATTC	60
	GATOCATACA CAAAACATAT TACTACAAAG CITTCAAAAG GTGTCTCTCC CACAGACOCA	120
25	TITICIAGGO CACTCAAGGT TTACATTCTC AATTGCAGTT TGAAACGTTT ACGCTTGCAG	180
	AAAGCACACG TTATACTTCT TGATAAAATT GCGATATTCA TCAATACAAA TGTGGTCCAT	240
30	GIGICIGICG AATCGATACA TACGATACIG AAAAGITITAG CIGAATATIT TATIGATGCC	300
	AAGGAATATA AGGGACTCAA CAACGIOGTC AATATTTCAT TCAACGCATA TGTGATGTAT	360
35	AAGCATGAAA GCCTTATACG ACTTGCAGCA GATCTCGAAT TATTTCTCTT TATGTCCGTC	<b>4</b> 20
	AAACAGGACT GGTCAATGIT TACCAAGTTC GAGAAGTTTA TITCTGTCGC TTCAGGAGAC	480
40	ATCICAGIAT COCICITIGA ACAGIGITIC AATGITTATG TTATGTTCOC GGATCCCICA	540
45	TTOOCCOGOC TATOGGATGT CTOCTTGAAC AAGTCGTTGA AGTGTTTCAA GAAATTOOGA	600
45	CTAACTAGIT ACACAGACTT TAAGGCATCG TCCGAGCCAA TGCTAGTGTT GGTATACAGT	660
50	GGATTTGTTT CTGATATTTT TACAATACCT TATAATGGCT GGGCTCCGCT ATCGAAAATG	720
	TTATICATGG CATTAAATGG GGTCTATAAA TTG	753
55	(2) INFORMATION FOR SEQ ID NO:575:	

JONNOTH- JED MEET 2082 1 5

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 767 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1397UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:575:	
	GATCIGAAAT ATTOCICACC CCCACCGIGA CCIATGIAGA IGAACGIOCT GGAGIICGIG	60
25	ATCATTCIGA CGAATTCATC CICTTCIGGC TTTGAGCCAG TTACTATCCG TGTTGAACCC	120
	AAGTCGCAAC AAAGTCTGGT AAAATGTTCT TTAAAGCGCA GTTCAGTCCT GGTCAAGTCC	180
30	CCATOCOGET TTAAAACAAT OGAAAGICIG CIGICIAGGI TAAICITIGG AGAGAICICT	240
	CCTCTGAATT TAGTTAGTAG CTCGTGAAGG AAATTTATGG ATGGTACGCG GCTCACAGAA	300
35	GCATCGGAAA ATATACTGAG AGATTCCCAT GGAACCAAAC TGCATTCGGA GCTTATTACC	360
	AGAAACGIGI GICCIAACCI 100000CTCI GGIGCCTTGG CATGATAGIC GIGAATTAGI	420
40	TOCTCAAGIT GAATATGTAT GAGATGAACG TCAATCTCAT CATAGGCATT TTCTTCGCCA	480
	TOGAAAAGCA ATATGICAAA GATGAAGTAT ATCAAGTCCT CCATGAATTC CACCITCTTT	540
45	TOGTGAGGAA GOGCATOOCA ATOCACCTIT AAAAATAACT CTAATATGAA ATOGTOCACC	600
	TGTTAGAACA TAGACOSGIT TCCATACTGT CTTCTTGTTG GAAGATTTGT TGTAAAACCT	660
50	TTGAAATCCT AATTTGAATA NIGCAAAATG GTTTTATCCA ACTGTTTTTG GNIGAAGAAA	720
	CCGCNGAATC CCATATCCAG ATCTCATGCG GGGCNICNAT CTACATC	767
<i>55</i>	(2) INFORMATION FOR SEQ ID NO:576:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 774 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: UNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1398UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:576:	
20	GATCOCTCTT CTTTGAAAGA ATATGTAGGC ACCCTCTCCT ATCTTGCGCC GGAATTGGTT	60
25	COCTOCAAAG ATATGAAGAC GATGACACCT OCAGAAGCAG AAAGAATCCC AGAGTACOGT	120
	GCAGCAGTOG ACATATOGOC TCTTOGTGTC CTCTGCTACT TCATGATGAG TGGCTATATG	180
30	CCGTTCGATT GCCAAGACGA TGCCCAAAACT AGTGACTGCA TCTTGAAGGG TGACTATTAC	240
	GITGACCACG AACCTCGTGC CAACGCCAAT CACAGCTATA ACAGCTGCTG CAACTTCATG	300
35	CAGCOCTOCT TTACGATOGA TGATAATATC COOCCOCCG CACACGAACT CATOGGCCAC	360
	GCATTCATGC GGGAATACIT CCAATCGGCT GCGGCCAAIG ACTTCGCATC TATCCCGCTA	420
40	CTCCAGAGAT CAAGATCCTC GAACTCCCTG CACCACTTAG COCCGCCATC ACOCGCACCG	480
	TITATICTOST CTGGCGTGCC GGTTATTAAC CACCGCCTG TGCCACGTGT TGGCTCGCGT	540
45	GAGCGCAATT TOGATAAGIT GCGGGATACT TTGCGGAAGA CCTTTCCCTC ACTTCGCTTG	600
	AACCTATOCG CITTGITGCT CAAGCGAATA CTCCTAATCC TAATAAGAAG AACTCTACTT	660
50	TIGITCTICA COCACCICCT COCACGOGGA GICTAATGAA TGGGIGITIC ACGICACACC	720
	GGAAAGTAAT CCAACCTCAA TACGCCAGTC CTTTCGCGCA GAAGCTCCGG CCAA	774
	(2) INFORMATION FOR SEQ ID NO:577:	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 756 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: ENA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1399RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:577:	
	GATCATTACT COCAGAAACT GAGATGTTAG COCCACCAAA CTCTTTTCTT TGATGAGATA	60
25	COCCACCATC COCTOCICAGA ACCAGAACAA TOCACCAAAAA COCACGAAGA ATOCCAACGA	120
	GAAAAGCACG CATCGCTGCA TATGCAGTCC CACCCCATAG TAGTTCCTTG COCCATATGC	180
30	CT00000CAG AGTGTATCTA ACCTTGTTGA AATACCCTCN AATATTGCCA AAGTGATATT	240
	GGTGGTCATG GAAGCCAGGG AAACCGCTGC CAACTCATTC TTTCCCAGGT GACCCACAAC	300
35	TAATGCACAT ACAACCGGAA ACATCTGCTC AAGCAGAAAT GTAAATATGA GCGGCACGGA	360
	GTAACACAGA AGCACCAGAC TCTCGGACTT CACGGTGGCT GGTTCGTCGT CGAGATCCTC	420
40	GCACCCTCGG AACGCGCTGG AGGGGCCGCC CTTGCTGCCA ATGCAGTAGT AAGACACCTT	480
	TCGGGGCCGT AGAACACGCA CTTCTGCCTT GTCCGACGGC AGTTGCTGCT TAACCCCATG	5 <b>4</b> 0
45	CATGAAGTGA GTGTAGTGCA CCATGTCTGG CGCGGGGCCC TCCACATCGA CGGCCACGAT	600
	GTCCTCGGCG CTGCCGTTAA CAGTCGAGTA CCGCCGTTCG TGCTCCTCCA ATATCCAGTC	660
50	TACATTCAGT GCAGAGGACG GCCCGCCTCA CTCGCAAGCG TCGACGGCAG CGAGACTGTC	720
	COCCACACOT CTCCTCCGTC AAGCACGCCC TCCTCC	756
55	(2) INFORMATION FOR SEQ ID NO:578:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 775 base pairs	
,	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1399UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:578:	
20	CATCTTGTAC GACGGCCGCG GAAGAATCGG TGCCATCGTT TCCAACAGAC AGTTCCAGTT	60
25	TGACGGCCCA CCACCACAGG CTGGCTCCAT CTACGCCAAG GGTTGGGCCC TAACCGAGGA	120
	GOGCAACTIG GOCCTAGGIG ACAGOGACGI CITICIACCAN IGICIGICCG GCAACTICIA	180
30	CAACCIATAT GACCAGAACA TOGCACCACA ATGCTCTOCA ATTAAGCTCC AGGCAATCAA	240
	ATTOGTOGAC AACTOCTGAA CAGOCCACAAA GGTATATAGT GCATATATTG TATTAGTTAA	300
35	ACTAGGAATT TTIGITGGCA GCTAGACTGC CCTACGTGGA TTTICTCGTTG CGGATCCTGG	360
	OCTOCCOCTG OCOCTGACOC ACAAGAGCAA CTGCACAACT ACTOCCGTAC COCATGCCTC	420
40	CTTGTGCATT TTTGCCGCGG TGGACGTCGC TGACGTCAGC GTGGCACGTG ATCATAATAT	480
	GTCCCGGGCC AGGCCCCTAT TGTGGCGGAC AGGAATGCAT GCGGAGGTGC AAAATGGTGC	540
45	AAAATGGTGC CCGATGCAAC TCTAGGCCCG AGCTGAAACA AGATTACCTG GGCAGCCTAA	600
	ATTIGCAGOG GCTGCCTGGC AGCCCACATG TGTATTGTGC TTTTACAGTT CTTGCTGCGG	660
50	CTGTCCAATA CAGCCGATCG CGACTTTGCT GCGCACGGGC CACTAGGCCT GCGCGACAAA	720
	AACTGCAGGC GCGCCGGCGT GAATGGCGGC GGACGATGTG CTGCCGCGGA ATTICC	775
	(2) INFORMATION FOR SEQ ID NO:579:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGIH: 757 base pairs	
_	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1400RP	
15		
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:579:	
20	GATCCIGICA AATATOOCCA ATACCAAGCA OCCOCCIGIT GTACAGCATG TOGITGAACT	60
25	CAAACCCTCA AGCAGCCGGG TITTIGGACTG TGCACAGGAG ATATTGTCTC CATTTCCACA	120
	GTCCAAGAAC AAGCCCAGGC COOGGGACTG GAATTGTCCC TCTTGTGGTT TTTCTAACTT	180
30	CCAACGGCC ATTGCATGCT TCCGGTGCTC CTTCCCAGCC ACTAGTGCAG TGACGGTCAG	240
	CAAGCTGTIAC AAGCCACAGC AGCAACGCCA TTATCAGAAC CCACACCACG TCCCATCGAA	300
35	ACAACAGGIG CAGCACCCGC AGATTCACGA CCAAGACACA CAGCAGCATT CTCAACATTT	360
	CAACATCCAG CAGATGCCGC AGCAACTCCA AATGCAACAG CAAGCGCACG GTACCGTTCA	420
40	AGGGGCAGT AGCATGCAGC AGTACAAGCA CAGGCCTCAG CACGGCTTAC AGGCGTATCT	480
	TOOCTOCTAC CAACAGCAGC AGOCGAAGTC ACAGCAGCAG TACCAGATGA ATCAGCAACA	540
45	OGTIOCAGATG ATCOCTOOCG ACOCCAGAGA COGTIATAACC OGTIACAACAA AATOGTIOCAG	600
	GOCAACGGC AGAACGGTAA TICTTGTACG GAAATGGCTC CCTGGGCAGT AGCAACGTGC	660
50	CCTTCAGAGC TOGCGACTOG AAGTOCTTGA ACTGTTCTTA CCATAATTTT GCCAAGAATA	720
	TIGITIGICT GOGITGIGGT AATCCAAAGA CGGCCAT	757
55	(2) INFORMATION FOR SEQ ID NO:580:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 775 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1400UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:580:	
	GATCOBCOGG TACTICAGGI CATTCICCIC CACCACCACC ACCAGCIGCC COGGCCCGCG	60
25	CTCATACAGC TGGTACGCCA CGCGAACATG TCGCTCCGCC TGCGGCACAT CCGCCTCGTA	120
	GAACTGATCC GCAGCCACCA GCCGCGTCGC GCACTCCCCG CCGCCGGCTT GCGTCAGCGT	180
30	CCCCACTAGC TECCCGACCG GIGIGAGCIG CACCATCICA GOGGCATCA GCCAGCICAG	240
	CGICCATGGC ACCACCAGTG CGGCCCCAGTA CCCCCTCGCCG AGCTTCCCCGC TGAACTCGAC	300
35	CTCCCCCTCC CCCCCCCCA GAACCCAATIC CCCCTCCATA CCCCCCACCC ACTCCACTTC	360
	GTGTCTGGGA AGACGCTCAG ATTGCCATTG TTTGAACTGT CCACAGTTAG AACTTGCACT	420
40	ATGCTACCTC COCGGCGCCT GCGCGACCCC ATAGTCACAT ACTATCATCC TCACACAACT	480
	CAGIACTICC TECGAGICCC AACTCAAGCT AACGAGIACC AGACTIGGIT TIGGCIGITG	540
45	CTGTATGCAT TCCAATGGTT TGTATAATCG AAAAATTGTT CAGTTGCTCA GCACATCTCA	600
	TACAAGCAGG AACAAGAGCG AGTCGCGAGC CAAAGACCTC TTAGGCATTA GTATCGGTAG	660
50	CTAGGATGTC GOCAGAACAG TTGCGACAAG TACACGCAGT TGCAGGGCGA ATTGGAGGAG	720
	CTOSTOGTGA CAGACAGAAG CTOGAGACOC AGCTOCAGGA GAACAAGATC GTGAA	775
5 <i>5</i>	(2) INFORMATION FOR SEQ ID NO:581:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 723 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1401RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:581:	
20	CATCTTGTTG TTGGCAATAC CCTGTCTTAC GTTGAAAAGA AGTGTCTCTG AGGTGTCCAT	60
25	CAACAAAAAT ATTACCAGTT ACAACACCCA COCGAACTCT ATTGGCCAAA ACATCCAACA	120
	ATGICGICIT ACCTGCACCT GAATAACCCA TCAGAGCAGT CAAAGTCCCA GGCTTTACCC	180
30	AACCATCCAC GITGGITAGG ATCCTCCTGG TITCATTCTT AATCTGTATA TCATAGCAGA	240
	CATCTCCCCA GTCGAAAATG CTATCAGAAC CAATTCTCTG AATAAGTTCG CCCGATTGGT	300
35	CACTICCIAT AGIACIAGAT TOCTITOCIG GIGCATTACC AAATICIAIG TOGCAGITGA	360
	TGGCCTTTT ATTTTGCTTT TTTATTTTCT TCAAAGTTGA CCTTAGGAAT ACAGCCATTT	420
40	CACCITITIG CATCCCACTI TIATIATACI CAATTAAGAT CAGATAAACA CCIAAGAAGA	480
	AAAATGCATA AGCAAGAACG ATCCCCCAAT TCATCCACTT GITTITGGIG TIGIAACCAT	540
45	AAGCAAACTC TATGTAACGG GTCCCATTTA CAAAGCTCTG ACCAGGAACT GCTCCCACCG	600
	ACAAGCAGAC TITATICGAA ATAGGGAATC CCTCATAGAA ACTACCATCG GGTACCATTC	660
50	GAGAACATTC GAATATOCGT CCGTCAAATT CATTCOCAAC CATGOCTTCC ATGATGCGTG	720
	CCA	723
55	(2) INFORMATION FOR SEQ ID NO:582:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	•
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1401UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:582:	
	GATCIOCIGA GATTAAGCCT TCGITGTCIG ATTIGTTTIC TATTIOGAAG TCTGCAGGAG	60
25	CAGOCTITICA AATACAGTIC TTATGITATT TAACGTOOOG GTAACCAGTA TACAACCATA	120
	TGTTTATOCC TATOCTAGIT ATATOCTTIG AAGAGGTOGT CTGCAGCTGG COGTCTATTT	180
30	TATTITATIT TITCATTICA CTAAGACTIT ACATTITITIT TITAAATTAT TITTITIGGG	240
	CTAAGACTGT GAACAGGGAT TTTAGAAAAA AGCGAAAAACG TTCAGGAGGC CTCAGCTACA	300
35	TGATATCCCA GOCCTTGTAT TIGTGAGACT GCACTCCCGG GCTAGGITGT GACCAAGAGT	360
	TGACGIGOGG CGGCGIGCGG ATIGCAGGGC TTCACAGIGI GGTTAATTTA ACAATTIATA	420
40	GAGAATAGAG ATGCCCGAGC TTAATCAACT GTCGGGGCGC CCAAATTCGA TTTTTTTGGAG	480
	TTTGTCGATT TTCACAGCAG ACGAGAAAGC AGGACAGGCG GCCGCGCCA GGCAGTCCCC	540
45	CCTGCAGCCG TGAGCGGACA CAGAGAGAAA ATACAGGAAG ATGAATACTG ATAATCTACA	600
	CATTICATIC ATATCTCATT GATCCOCTGA TTATCAATGA AAGTACCCAA TGATCCATGA	660
50	AGCCAGTAGA TGITAGIATA TTITATTAAA TATATGCACC TTTGITATCC AAICTCTGIT	720
	(2) INFORMATION FOR SEQ ID NO:583:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 719 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1402RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:583:	
20	GATCAGGAGC CCATCAAGGC GCCTAAAAAT CGCATCCCCG CTGTCGGTTT TCCCCGACTAC	60
	OCCOCIGITG CTTGAAATAC AATTACTOCT GTAGTTCCTC CTGTGATGCT OGTTGAAATG	120
25	TTGCGGCGCG AAAGGGTCTG CCTGCTGAAA GGAGCTGAAA GGTGGTGACG TGGTTCCGGG	180
	ACTACTAGGG TCTGCAACCG TCTTTGAGCC CAAAACACGG AGGCCGATTA CATTCCCGTC	240
30	ACCORDECOG ACCORDAGA ACCITCOCCIG ATGOGAGITC ATGCTCTTAC TGCCGGTGTG	300
	GEANTAGIAC TCACCACCAC TOCTCGACGA AAGCOGGAGCA GOOGGTAGCG CTGCCATCTG	360
35	TIGITOCCIC CIGCGACGIG CTICTAACIG TGCCAAACGC AGCIGIGCCT GTIGCICCIG	420
	GIGCGCGTCC ACCITIGCCCA AGACCTCCGG ATCATCATGC AACATCTCCA GCACCTCCAA	480
40	TTTCGCCCCT AAGCCACGIG ACTCCGCTIC CAGGICGICC ATTICTCGAT GCTTGATCAT	540
	GACCIGCAGA TOGAGCIGCI CCAGAATCIC GCGCITCGCI ATCICGTATT TIAICCGCIC	600
45	CGTCTCCTCG CTCTCACGCC CCAGCGGCCC CTCCTCCGCA CGCAGCCCGC TGTATTCGTC	660
	GICGCCCAGG GAAAGCTCGI GCCGCCGACIT CGGIGICGCC ACCIGGIAAT AIGCCCGCC	719
50	(2) INFORMATION FOR SEQ ID NO:584:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 726 base pairs	
55	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1402UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:584:	
	CATCAAGITA TOGITGATCA AAGOGICAAT ACCOUTTION CHAAGCATGI GOCAGGITTIC	60
20	CITICGCGGCG CGTAGGTATG GTTTCCCCGTA CAACGCAATG AAGCAGTAGG CATAGTGGTT	120
	GAAGTACTICT GOCATCCATT CAAAGACACC AACAACOOCA TOCAAGATTA ACCACAAGCA	180
25	CTOCATCCAC CCACTGTCGG ATATCCCCGCA AATAATCCCCA TTGCGAAGCA GCTGAATAAT	240
	CTGCCGCAGT AGTTGAATCA GAGACACAAT CAGCGAGCCA AAGCAAATGG ACCCAAAGGA	300
30	AGTOGICAAC OCTUTUTTA ATGAGOCAAA AGCTGGOCAA CGTGGCATGC CTTGGTCCCA	360
	CTICGAAAAA TAGIACCAGC AGCCGIAGAT GCCCGCGAIG GIOCAAIGAA TCACAITICCT	420
35	GATGACCTCA GAAATGTAGA ATCCACAGAA GAAAACGAGT ACCAAAATAC CAATTAACTT	480
40	TCCACGIGAG CAAGAGCCAC CAGATACATC GCAGCCACCA TICICOCTCT TCGGGTCATA	540
40	CTITATGIAG GICGCAACCA ACACTACAGA GAATATGACA GAGAACGCAG CCGACACAAT	600
45	GETACCTAAT AATGACACAA GCCACGTCTG TGGATGTTTC TTCATAACTG ACATGACCGT	660
	ACCICAAGACA GCGACACTAA ATGGAATCCT TGAGCGCATT AACCAGTAGC ACACCGCCGT	720
50	CAGAAT	726
	(2) INFORMATION FOR SEQ ID NO:585:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 731 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1403RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:585:	
	GATCCGTTCC TTGAGAAGCA CCTAAAGCCT GAACTCCTGG CAGAAGCGAT CAAGGGAACC	60
20	TCTTGGGAGG GIAAAGITAG TATTAACTTG GTAGACGCAT TCGACCACTC GTATTACTTC	120
	GTCAGCACGT TCGTGCCGGA ACACGCAAAAG TACCATGCAG AAAAAGTTGGG TCTAGTTTGA	180
25	GATTICACGI TOCOCCIGIT AATTOGIATA TACITACATA TITAGICATA TCACOCCITC	240
	ANGTACTICTG ATTICTGCATT ATANGTGCAG COGAATGCCA GCCTCCGGCA GTAATGGCAA	300
30	COCAAACIGA ATTIOCCOGI AGITCAACCI TOOCCOGITG CAGCACOCGI ATOCTCCGAG	360
	CAGACTCAAA CGTCGCTATT TGGCGGGTAT CTACAGCCTC GTCGGGATCT CCCTGCCCAA	420
35	GACAGOCCACA GATIATICACTO TOCAGOCCOC AGGAGTAGAG TICACCTITIG TOGGITAGAG	480
	CTAGGTTGTG GTAGTCTCCC GCAGATACAG CAATAAACTT CTGGCCTTGT TCCAAATTCA	540
40	TCTTCATGAA TGAGTCCTCG ACGATATCAC CATTATTCAC CTTCAGGGTG TATGTGCTAT	600
	TCTCGGTACA TAAAACCAGT GTCATGCAAG ATGCCTCAAT CTTCGTTTAA CCGTCCATCA	660
45	AATGGCAAAT CAACGGTTTT TGAAACGCCA TGAGTGTATA TCCACAGTTT GCGCCCATTG	720
	TTAGTAATGT A	731
50	(2) INFORMATION FOR SEQ ID NO:586:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 717 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1403UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:586:	
20	GATCTCAATA TCAACCAACT TGTGACGTCG CTTAAAACAC CATATGCGGA GGACATTATG TCCATCACCG TGTACAAGGA CAATGTTTTT GCCACGCACA AGCAGGGCAT TACGCGGTTC	60 120
	CACCAAGGGA ACGIGAACIT CIGGAATGCT CACCAGGGAC TCGTCTTGAG TAGCGAAATA	180
25	TIGCOCAAGA OCTGIACCAG TAATCGIATA GATCOGATGG TTACTOOCGG AAATGATOGG	240
	TCATTAGOGT TGTOGAATAT TAACGAATGG CTGAACOGTA CAGOGTCCCC GGGTGGATCA	300
30	GCCCCGACCG AAGAACACTC GCTTCCCTCT GGCCAGCGCC GAAATTCTTG CACCGAGTAT	360
	CAACAAATCC AGITAGATAA CGATCACATG ATTGCAACAC TGCGGGAATT CATTAGITAC	420
35	CAGACTIGTTT COCCAACTCCC AGAGCCCCAA AATATCATCG ATTCGCGTAG GTGTCCCAAC	<b>4</b> 80
	TRECTIGEARA ATCRETTCAC TRAGCTOGGT GCTAACCATT GTGGGCTTAT ACCTGTCAGT	
40	ACACGCAGCA ACCCGGTGGT TCTCGCGCAG TTCAAGGGCA ATGCAGCCGC GCCCAAACGC  ATACTATGGT ATGGCCACTA CGATGTGATA TCCGCGGACC ACCGTCGCAG TGGCACAACG	600
45	ACCOTTCACG CTCACTTGOG AAAATOGGTA TCTTAAGGGA AGAGGGGTGT TGATAAC	660 71 <b>7</b>
	(2) INFORMATION FOR SEQ ID NO:587:	717
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 710 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1404RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:587:	
	(AT SECONDE DESCRIPTION: SEQ ID NO:587:	
15	GATCTCCAAC GITACTCATT ATCCTGTAAG CCCTCTTTTG CGTTAAAACA TCCTGTCAGT	60
	TAACAGTCGT GITGAAGATA GAAAATAAAG CAGTGTATGA TGATGCTGGA ACAACOCTGG	120
20	ACATAACCAC CACAAGATCT AGAAGTGTGG CACTCATTTT TGGCTGGCCC TTCACAGGTT	180
	GOCTAGACGO CICCITATOC ATGOCATOIT TTAGIAATOC GCATACGITA TCAAACGIGT	240
25	TAGACAGGIT TICCOCAGAA GIAATTIICA AGIATOCCIC GAIGGITTICC AAAATATAGC	300
	TCCCAGOGIT GOGIGCAGIC TGCGIGIAGA CATTGAAAAG AACGGCCAAC ATATTGGGCG	360
30	ATTICTOGGA GAGGTATICT ATGITTTICT CCGCTTCTGT CGGCGGGAAT TGCTGTCCCA	420
	TAATAATGIC GICCITATAC OCACCATCIC TGTATAGAAG ATTACTTGTG ACCAAGACCT	480
35	TCAATCCATT GCATATGACA GTACGCAGIT CAATTCTGGA ATAAAGTAGG GACGCTAACT	540
	CIOCAGCAAA CICATCOGIG AATACATOGI TIAGATCIIT TOGAAGAAOG CAGAACTGAG	600
40	GGAAGGTAGA CCACAATTGG TCAACAACAG TCTGAAGTAA TGTGCACTGG ATAGACTCCT	660
	TATOCAGITT CTCAATOGIG GACTOGAAAT GACGAATOGT AGGAATAAAT	710
45	(2) INFORMATION FOR SEQ ID NO:588:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5 <b>5</b>	(ii) MOLECULE TYPE: DNA (genomic)	

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(vi) ORIGINAL S	SOURCE:
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(A) ORGANISM: PAG1404UP

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:588:

10	
15	
20	
25	

CAGGCCAAGC GCAGGCTGGC CGGCTGGGAG TCAGGAAAAG TCGGAGGAGG TCGTACAGGA 120

GCCGAAAAAC GCCGAGCCGC TGGCGAAGCT GGGCGACGGG CTGACGGTGA CGGCGCTGAC 180

GGGCAACATG AGCTACTACC GGCAGCTCCA GGGAAGCGTG AGCTGGTTGC TCAGTTCTGT 240

GTCGCAACTA ACGACGTCCA CCCGGGCGCC AGAATGCGAC TTCACTGAGC AGTTCATCAC 300

CTTACTCGTG AACACCTACC ACGACGTGG TCTGCATGCA ACCGTCACAC CGTTCGACAA 360

GACTAACCCG CCATCTGCTT TTCTCAACAA GGTAGCGCGT GCTGCGGTGG AGCGTTCTGA 420

CATCITICAGO AAGATCAGOA CCACTIGAOG CACTACAAGA AGTACOGGCA CTGGOGGTGG

G: 35

30

GCCCCTTCTA CAGGAAATAA AGCCCGAGAC CCAGGACGTT CCACAGGGGT CCGTGCCGCTC

GCAGCAGAGC ATCGCCATCG GACGTCCGCG CGATAAATGG TTGTTGACCT GCACGCGGAA

GGIGGCCTGT TCCATGAACC ACGGCACCCT ACAGGGCAT CTAAGCTCCG CTTTTGCAGA 600
GGAGGGCCAT TTCTTCTACT GGGATCCGGA CTTCCAACGG TTCCAAGGCA TCACGGCAAA 660

ACTICTAACC GACACTGGAG ACATCTGGGG CAAAAATTACC CCATGTCTTT GGATC 715

# (2) INFORMATION FOR SEQ ID NO:589:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 729 base pairs

(B) TYPE: nucleic acid(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

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(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PAG1405RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:589:	
10	GATCTITCAT ACTITICOGGT TOGTOCTATA TAACTAAGAT TOGACAGAAC TOCAAGOGCC	60
	ACAGAGGAAG AGCTOCTOCA TTOCACATTA GOCAGGAACA GCGAATGTCT ACAAATGCAC	120
15	ACTACACACT ACCOCTCTCA OCCGATICCCA ATCTCAGATG COCACAGCAA GOGACCCAGT	180
	TCTTTGCCCA TGCCGCTGTA CTCGCAGCGG GGCGCAGATG GGCTGCTAAC CATTAATGCG	240
20	ASCOCITGIGG GCTCGCCTGT GCGCCCCAG CCGGTGATAC CTCCACTCAT GCACCAGGTG	300
	GCGGTCGACA AGCACGCTCA TATCATGCCA GCCTCGTACG CCCTGCGACA GAGCTCCCCC	360
25	CAGGICACOG CGATTATOGG CGAGTTAGCG ATOCTGAAGA AGTCGATATT CCAGTCOCTG	420
	AACGGCCAGT TGACGACGCA GGAATACAAC AGCATCITACC AACATTTGAG TCAACTGCTG	480
30	COCTOCCTOC CACCOCCOCT CGACCCATCT CCACCOCCACC CCCACCTOCG ACTOCCCTCG	540
	ATATCTCAAA TTATGCCGGG AACAGAGCCC CAGGAAGTCC AACGTACCTT CATCATAGCA	600
35	TOCTOGRAGI CACAGCAGGG CCAGCOGTAC ATCTOGCCGC CGITAAGCTC GACAATGTCT	660
	ACGCACCOCC TITICACCOGG CATGTOOGTA GCCAAACCGA ACTACTCCGT GAGCACCAAG	720
40	AAGAATGIT	729
	(2) INFORMATION FOR SEQ ID NO:590:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 715 base pairs  (B) TYPE: nucleic acid	
50	(C) STRANDETNESS: single (D) TOPCLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

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(vi) ORIGINAL SOURCE:

# (A) ORGANISM: PAG1405UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:590:	
10	GATCCAAATA ACACCACOGT TITICATCOGC COGTIGICIT COCTCGIGAC TGAGGATGAG	60
	CTACGGCTT ACTICCAGCC ATTCGGACAG ATAGTCTACG TGAAAATCCC GGTCGGCAAA	120
15	GCATGCGGCT TTGTCCAGTA CGTGGATCGC AGTTCGGCAG AGAACGCGAT CGCCAAGATG	180
	CAAGGATTIC CAATIGGTAA TICGAGGGIG CGGCTCTCAT GGGGCAGGAG CGCAAAGCAA	240
20	ACAGCCOCTA TOCAGCAGOC GITTOCCATA OCACTACAGC AGCAGCAGCA GCAGCAGCAG	300
	CAGCAGCAGC AAGCCCGCCC GCAGCATTCC CAGCAACATC AGTATCAGCA TCAACAGCAT	360
25	CAACAGCAGC CTCAACATGT CATTTCTGCA CAGCCGTTGC TGCAGCAGCA ATTGCAACTA	420
	CAATITOOCI ATCAGCATCA ACCIGOCATG COGCAGGOCT ACGGITACAC ATTGGACTCG	480
30	TICAGCGGCA COGGITICGAA ACATGITICCA ATGCAGGGIT TICITTICCGG TAATATCGGC	540
	TICCAACCIT CTACGGCAAT TGATAGCTCT CCAGCAACGA CCTTGCTTCC CAACCITTICT	600
35	TOSTIGGACT ACTOROGET TOCACCTICO ACGICAGOST TOACTITICA COCACGAACT	660
	CTTTAGGCAC AGCTTTCACA ACATCGCCTA GATTCTCAAC AATGGCAGCG TGTCC	715
40	(2) INFORMATION FOR SEQ ID NO:591:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 699 base pairs	
45	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	The same of the sa	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1406RP

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:591:	
	GATCTCCTTC CAGTGACGCT GATGCACAAC TGCGGACCTC AGCCCGCGTG CCTCACGTGA	60
10	CCACAGTOGA CATTITICTCA GITTAGCOCTC GITTAGCTTA GCTATACGAG GCATGGCACC	120
	ACTIAGGOCC TOCTOCOGAA CCAGATACGA TGAAGCCGCC CAAAITICGAT AGAAITGCTOC	180
15	CTCGCTGAGC CGCCGTCATA GGGAAACGAC CAAAGGTTCC GTCTGCCGCA TCGTATGTAT	240
	GIGICIGIGI ACGAGGACCG AAAAGITGAC TITTIAACGAA GIAGATTITI TIAITIAGATA	300
20	TITTAAGCACG TATGCGTTAA CGAGCAGCTT GCAAGGCGIA TACCAAGGCT CIGIGCGCTT	360
	ATCATTAGCA GGGCGACATG TCAGAATCCT TGCTACAGAC AGTGGTGGGG TACGTGGAGT	420
25	TOGTOCTOCA CCACTICATG COGFTGTOGT CCACCOCACCA CCTGTCCATA GTAATAGTCG	480
	CACCATTCAT ATACTCOCTG GIGTOCCAGA CGITTATATTC ATTCAGGAAG GATAGAGTAC	540
30	COCTAGTOCC GITCATOGTA CCCTOGGTGG GITCCOCCCT COCGTATOGG ACCCTCCCT	600
	ACCACITITIT TOOCAACTOC ACCACAACTA TOOCCATGIG TITICCGTTCA TOCTOCTOCG	660
35	COCHICHENTE ACCICITATIC TOCOCCACCAA COCCCACCA	699
	(2) INFORMATION FOR SEQ ID NO:592:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 709 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
50	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1406UP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:592:	
5	GATCITCATT AGAACOCOCG GATTAGTCAA AAAGTOCCOG AATGITCCAT CCACTAGOCC	60
	ATCTOCCTTC ACCCACOGAT TOCAAATOCA GACAAGGITT ATTAGAATTA TACCGATTOC	120
10	CCAAACGTCG CCTGCAGCAG TAGGAGCTCG GAGCTCACGA CCGAGCGATC CGCGCTCGGG	180
	TOCCATOTAG TAAGACCAGC CTACOCAGAC ATTOGOOGCG AGCTCCGGCA CGGGTGTOGC	240
15	CAGCCCGAAA TOGCATACAT GIACGITGIA CCATTIGICC AGAAGAATGI TCTCCGGCTT	300
	TAGGICGCAA TGATAGACGC CGAGTOGGIG GCAGTAGAAA ATAACCTCGC ACAGCTGCAG	360
20	GAAGACCITC TTAATCAGTA GOCCATCCTT AGCAAAGACT TGCTCGTTGA CAATGOCTGA	420
	GAAAAGGTOG CACGTGATGT AATOCATAAC AATAAATGTT GOCAGGCTTG ACTOCATCAC	480
25	CTGATGTATG GTAACCACAT GTTGGTGGGT GTGCACAGTC AGGTGCATCA GCAGCTCCTT	540
	ATAATGTGGC GCGTGGGCCA GCTGCTCTTG GCATAATGTC CGCATCGATT CCAGGTCCAC	600
30	AGATGGTAGA TACAGCCGGT TCTGGAAAGA TTGAAGAAGT GGTACAGCTG GGTGCGCAAA	660
	ATTICTOGACC COCCTGACGC CTCCTCTGCC CTCCCCCTGT CCTCCTTCA	709
35	(2) INFORMATION FOR SEQ ID NO:593:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 707 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORCANISM: PAG1407RP

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:593:  $\ensuremath{\mathit{55}}$ 

	GITCARCAG ATMACTATOT TAMAGAACAA CCCGAAAATG CGCAAAGCAC ACCACGGGTC	60
5	CTTCGGTGAT AGACTGATAG AGATACAGAA AGTAACTTCT GTGTCAAGCG AACCGGAGCT	120
	COGGITTITA CACCITOGCA ACAGCIGCCC CCATGCCATA GCACTCITTG AGITCCICTA	180
10	GITCCTTTCC ACTANACACC GCTCCGATGT TTCACAGAAC AGGTTTAATA TCGGCAACCA	240
	AAGAGGAGGI TACACICAGA GAATCACAGI GTOGAAACAC CGGCTATICA ATGAGGCATT	300
15	CCCCCAAGIC CETTICITIG GITTICGATTG CCATTGCCTA GIAATCCACC AAATCCTCCG	360
	CTOCTCACCC ATGGGATCGC TAGATGCCCA GCATGAGACT GITCAGGITA GGCAGGTGIT	420
20	GTATGCGCCG CCAGAGGGAA ACCCAATGAC TTTGCATAGA ACAAACCGGC CATCACCCAT	480
	GICTIOCOCT GIATAGAGAC TAAGGIATCT GACGATCCCT TAGCGACTCT CTCCACCGCT	540
25	CGACGAGGCC ATTGAAGCTC TTACGAACTG CACAAACCTA CTCGAACTCT GTTTCCAGAC	600
	TICTTICIGI TIGICTICAA CIGCTTICOC ATGAAGTACC CCCCAGOCTA TTITTCTTAC	660
30	CCGCCTGGTG TTTGTCTATA TACCCGGTTG TATTTTTTCA TAAAAAA	707
	(2) INFORMATION FOR SEQ ID NO:594:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 571 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1407UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:594:	
	GATCGTCGAA TTTGGGTATA GGGGCGAAAG ACTAATCGAA CCATCTAGTA GCTGGTTCCT	
<i>55</i>	ACCIONAL CONTRACTOR CO	60

CCCGAAGTTT CCCTCACGAT ACCAGAAGCT CCTATCACTT TTATCACCTA AACCGAATCA	120
TTACAGGTAC COGGGTTGAA ATGACCTTGA CCTATTCTCA AACTTTAAAT ATGTAAGAAG	180
TOCTIGITION THANTIGARE GROGACATAT GRATGARGAS CITITAGIOG GOCATTITIG	240
GTAAGCAGAA CTGGCGATGC GGGATGAACC GAACGTGGAG TTAAGGTGCC AGAATACACG	300
CTCATCAGAC ACCACAAAAG GTGTTAGTTC ATCTAGACAG CCGGACGGTG GYCATGGAAG	360
TCGGAATCCG CTAAGGAGTG TGTAACAACT CACCGGCCGA ATGAACTACC CCTGAAAATG	420
GATGGCCCTC AAGCGTGTTA CCTATACTCC ACCGTCAGGG CAAATATGAC GCCCTGACGA	480
GIAGGCAGGC GIGGAGGTCA GIGACAAGGC TTAGGCTGTA AAGCTGGGTC GAACGGCCTC	540
TAGTGCAGAT CTTGGTGGTA GTAGCAAATA T	571
(2) INFORMATION FOR SEQ ID NO:595:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 658 base pairs	
(B) TYPE: nucleic acid	
(C) SIRANDEINESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: DNA (genomic)	
(vi) ORIGINAL SOURCE:	
(A) ORGANISM: PAG1408RP	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:	
GATCCCCCTT ACCAAGCAAT TACAGGAGAC AGAAAAGAAG GATAATAATT TACCACAGAA	60
CICCAAGCCT GACAGAGCAG CGATTTACAT TCTGAGTCAC ATGACAGCAG ACTCTCTTTG	120
CTTTGGAGCT TCAATAAGCA CCAATATGAA TATGAATAGT TTTAGATGCT TTGTATAATT	180
ACCACTATTA ACTITATOTI GATTAATATT TATTATTITG TTATTTATT ATTITATTAT	240
	TEMPOSTIAC COSSISTICIAA ATGACCTICA CCIATTCICA AACTITAAAT ATGIAAGAAG  TCCTTGTTGC TTAATTCAAC GTGCACATAT GAATGAAGAG CTTTTAGTGG GCCATTTTTG  GTAAGCAGAA CTGGCCATGC GCCATGAACC GAACGTGGAG TTAAGGTGCC AGAATACACG  CTCATCACAC ACCACAAAAG GTGTTAGTTC ATCTAGAACAG CCGGACGGGG GYCATGGAAG  TCCGAATCCG CTAAGGAGTG TGTAACAACT CACCGCCCGA ATGAACTTACC CCTGAAAATG  GAIGGCCCTC AAGCGTGTTA CCTATACTCC ACCGTCAGGG CAAATATGAC GCCCTCACGA  GTAGGCACAC CTTGGTGGTA GTAACAACC TTAGGCTGTA AACCTGCGTC GAACGCCCTC  TAGTGCACACT CTTGGTGGTA GTAGCAAATA T  (2) INFORMATION FOR SEQ ID NO:595:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 658 base pairs  (B) TYPE: INcleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MCLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1408RP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:595:  GATCCGCCTT ACCAAGCAAT TACAGGAGAC AGAAAAGAAG GATAATAATT TACCACAGAA  CTCCAAGCCT GACAGACCAG CCATTTACAT TCTGAGTCAC ATGACAGCAG ACTCTCTTTG  CTTTGGACCT TCAATAACCA CCAATATGAA TATGAATAGT TTTAGATGCT TTGTATAATT

	TATTATTITA TETRATET TATTATETTA TIATTETALE ATTECHTATIAT TETATEATIN	300
5	TTATTTATT ATTATTTAT TEATTATT TATTATTAT TATTATTTA TTATTTAT	360
	TGITTGITTG TITATTATT TTTTATTIAT TACCTITTTA TTTTATGITA TTTTATTTTA	420
10	TITTATTITT ACTIVACIATA TAATATTATA TIATATCATA GIATAGITAT ATTATGGIGA	480
	CTITATICAT TATATAGATT GIATTITGIG AACATAATAT ATATOCTATT TCTATTICTA	540
15	ATTITATITI ATTITATITI ATTITATITI ATTITATITI ATTITATITI ATTITATITI	600
	TTTTATTTA TITTATTTA TTTTATTTA TTTTATTTA TTTTATTTA	658
20	(2) INFORMATION FOR SEQ ID NO:596:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 722 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) Original Source:  (A) Organism: Pagl408UP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:596:	
	GATCCGCCTT CCATCGAAGA GOGTACTGTT TGATTATGGT GATTTCTTGG TGTGGGTTCG	60
45	ACATTCAAGT GCATAGTTGG AGGTTACCGA TAACTTAGAT TTTCTTATAA ACGGTTACCC	120
-	TACGTCTTCG COGTTGGCCG ATATACTGAT TAACAGTTGG AGAGCCTTGG CGGCATACTG	180
50	TGAATGCCTT CTCTTCAACA TTATTTGAAT ATGCAAACGT TATTTAAATT AAGTAACACA	240
	CTTGTGCTTA TATATTCAAT TGTTCCAAGC GCGCCATCCA ACATGGCCAT TCTCATCTAG	300
55	TTIGAGAACT TOCGICTATT CITATTCIGT GTACOOCAAC OGTATTAGGA GAGACTICGA	360

	GITTITICAA CITCAAAGTC AATACTICAT CATCGTAAGT AGCAGTTACT TOOCCTAAAC	420
5	CAGTGCCCAC CTTTGTAGGG AGCCTGATTG TTCGCCGAAA CTCCGGGTTT GTGGGTTCTC	480
	CAGTAGTCCA COCCTCTGTA TICTCATCCG TATTAATGGC TGGCACGACA ATAGAAAGAA	540
10	CIGCATCATT CATGICICGA TOCAGGGCAA TATCTATGIG GICTIGAGAC ATTACGCCAG	600
	GAACTICTICAT GIGGATICTICA TAGGOGTICOG AACGCTICCAA AATTAATAAT GAAGGAAGAA	660
15	CGICAGAATT TGCCCCCGAG AGCTTGTATT CTGAACTAGC TGCCACACTC TCAGCTTTGT	720
	GT	722
20	(2) INFORMATION FOR SEQ ID NO:597:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
25	(B) TYPE: nucleic acid	
25	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1409RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:597:	
40	CATCCTOGCT ATCTACCTOC TOCTOGGCCC OCTOCACGCC ATACTAGGGC GCACATTCAG	60
	COCATTAATG TATGTOCAAT ATOCOCCAGT AGAAAACOCA COTKCATGTG ACAACAAGOC	120
45	CACCOGACTA ACCAATTTAC AGAACOGCCG CTATTTACAG GOCTGCCCTG ATCOCGATGA	180
	GIACITOGAT TOCOCTIOCA TOCOCAGTOG TACAGGOCCT GTACCTOCTA TOCOCAGCAT	240
50	TTGTGGCACA ATCCAAGCTG ATATAGGATA CAGACATCCA GCAAGACGCT GGATGGATCG	300
55	GITGIATCCC TCTGCTGCAT CAATACGCTA TCGCGGGCCG GCAGCTTATT GTCACGTGAT	360
55		

	TOCCIATORY GIOGAGCACC CAGACATATG TICCIGAGCC TOCCICAGCI ATATAAGCGI	420
5	CGAAGAAGG COCCAGTOGA ATACATOTOT CTOOCGCTGT GTOCCTCGTG CAGTCCTCCG	480
	CGATGICGIC AACTUICATA AACCGITCCT TGGCAACTAT CCGTACAGAG CTTGCCTITIT	540
10	TOGTTCATTC COORDICATT ACOCORCASC AGTCAGASCA GATTGAATCT AATCTTCCAA	600
	ACCCTAACGA ACCCCTCCGT GGCGCTCCCG CAAATAACGC AGGGCCTGTG GAGTIATGTGG	660
15	AGGCACTITTA TGCGTTTCAG GCGCAACAGC CTGGTTGAGC TAGACTTCAA	710
	(2) INFORMATION FOR SEQ ID NO:598:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1409UP	
	1.2140502	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:598:	
40	GATCOGOGIAC CAGAAAACCA CACAACTOGT CCTTGAGOCG GOOGTGGOCG TATTACOCTOC	60
	TACTOTOTOT TOTTOTOGIA OCTOTOCCOT ACCOCTOTOC GTOCGTAACC OCTOCCATGT	120
45	GOCTICATICAC CAGAAAATAT GATGTCTCAA COGAAGTTGC AATATTGTCC TGTTCCCTGG	180
	TOGITICTOGG CTACOGIGIT GGACAGCIGG TITIGGGGGGC TCTGTCAGAC CTGTACOGGC	240
50	GOCGCATAAC GTACTICACA TCTCTATICC TITACGTGGT ATTTAATATT CCATGTGCGG	300
	TESCTCCCAA CATCCAGACG CTTTTGGTTT GCAGGTTTAT TTGCCGGGGTC CTGTCGTCGT	360
55	CTOGACTATE CCTAGTOGGC GOCTCTCTCG CCCATATGTT TCCAGCCCAC CTGCGTGGGT	420

	IGACCAICGC GITCTITIGCA TITIGCACCAT AIGCAGGICC GGIATTIGCG CCACTIATAA	480
5	ACCIGATICAT COCTIGICCOC ACAGAGACOC TIGACCITIAT CITITOCGIC AACATCOCCIT	540
	TAGCCOGAGC TGITTGGCTG TTAGTCGCAC TGGTGCCCCGA AACATATGCG CCAATTATTT	600
10	TGAAACGGCG CGCAGAGAAG CTCAGGAAAC TAACAGGCAA CCAGAATATA ATGACAGAAC	660
	AGGAAGCACA GGGACTICTCC CTGTCGGCAT GGTGCACACT TGTCTACTGA GACCG	715
15	(2) INFORMATION FOR SEQ ID NO:599:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 709 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1410RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:599:	
35	GATCAATTOG TCACATTTOG CGTATOCAAT TTCTACCATC TCCTCTTTOG TAGCCTTTAA	60
40	TICCACTCCT GGIGTAACAT CACTAATGCC AATAGAAAAG CCTCTATTTC CCAGATAGCG	120
	COCACAAAGC TITOCCATCC TAITCATAGC CTGCGTTGCT TCTTGTGGCC CGAAATCTCT	180
45	CAGAATAGTA TAGAATACOG AATGITTCTT ACCATCACCA AGCACAGACT TATCCATGAC	240
	ACCAGACAGA ATATTAGAGC CTCTGATAAC TACATAACCA TCATTAGCAG ACATCTCATT	300
50	TOGATAGGCC TTATTCTTAG GCGCAATATA AACCITATTC TTTGCATCCA AATTAATAAT	360
	AACGGGAGAT TICTIGTICG GTTITATCAA TAGAGAGAAG AGCTGTTTIC CAGTCCATAA	420
55	GIAGIGIGGT COCATAATIG CAGOCGGCG TAIGICAAAC TOCAGGITOC CGICAGACAT	480

	CATAGAAAGC ATITIOGACAA AAGTIOOOGC GIOGAAGAAG GAGICITTIGI GAGAAATCAA	540
5	ATATGATCCA GTGATGAAAT CCTGGGTAGC TGCAATGATC GGTTCACCGG ATTTCGGAGT	600
	CAATAAATIG TITTIGACAC CCATAAGGIT GATIGCTICC GGGCGAGCCT CTICCGTTIG	660
10	AGGAACATOC AAGTTCATTT CGTCACCATC AAAATCGGCG TTGTAGGGG	709
	(2) INFORMATION FOR SEQ ID NO:600:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 727 base pairs	
	(B) TYPE: nucleic acid	
20	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1410UP	
	(ii) Garater. resigioup	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:600:	
35	GATCTGAGCC CTAGCATCIT COGTTGGAAG CGGGAACTCT ATTTTCCTAT CCAAACGACC	60
	GGAACGCAGA AGCGCTGGAT CAAGGACATC GACTCTATTC GTAGCAGCCA AGACTTTTAC	120
40	CCTATOGICA GAACCAAAGC CATCTAGTIG GITTAGCAAC TCAAGCATGG TICTCTGCAC	180
	CTCTCTATCA CCGGACTTCT CCGAGTCAAA ACGCTTAGTT CCAATAGCAT CCAACTCATC	240
45	GATGAAGATA ATGGTAGGTG CCTTTTCCTT CGCCAAGGCA AAGGCGTCGC GGACCAGCTT	300
	COCACCTICA CCTATGAACA TCTOGACCAA CTGCOGGAGCG CCCAGCTICA AAAAAGTCGC	360
50	ATTOCTOTICA OCOOCACAGE CTICTTOCCAS AAGOSTICTIG CCOGTACCOG GTOCACCATA	420
	CATCAGAGCA CCTTTCGGTG CCCTAATACC CATATCCTTG AACTTGTCTG CCTGCTTCAT	480
55	GGGTAACACG ATTGCTTCGA CTAGTTCCTC GATCTGCTTG TCTAGCCCAC CAACGTCGCA	540

	GIAIGITICC GIACOCTIGI CATOCACTIC CATAGCITIC ACTOTAGAGI CAAACTOOGA	600
5	AGGAAGOGTA TOCAAGATCA GGTACGAGTC CTTGTTCACA CCCACCAGGT CGTTCGGCTT	660
	CAACTOCTTA AGGGTCCACT AGCCCAACCA TGGGGAGAAA AACGGTTTGT CGGGACGAAG	720
10	TITCACA	727
	(2) INFORMATION FOR SEQ ID NO:601:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1411RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:601:	
35	GATCAAATOC CCTTCCCTTT CAACAATTTC ACGTACTTTT TCACTCTCTT TTCAAAGTTC	60
	TTTTCATCTT TCCATCACTG TACTTGTTCG CTATCGGTCT CTCGCCAATA TTTAGCTTTA	120
40	GATGGAATTT ACCACCCACT TAGAGCTGCA TTCCCAAACA ACTGGACTGG	180
40	CTTAGATGGC ACTAGCACCC CCGCCAGACG GGATTCTCAC CCTCTATGAC GTCCTGTTCC	240
	AAGGAACATA GACAGGGACT AGCAACCAAG GTACTTTCTT CAAATTACAA CTCGGACGCC	300
45	GAAGGCCCA GATTICAAAT TIGAGCITTIT GCCCCTTCAC TCGCCGTTAC TAAGGCAATC	360
	COGGITGGIT TCTTTTCCTC CGCTTATTGA TATGCTTAAG TTCAGCGGGT AATCCTACCT	420
50	GATTIGAGGI CAAACTITIGG GAATACTATT COCCTGGAAG GOCTTGTTTG TCGTACGTTC	480
	TTCAAGCCCC ACCTCCACTC CACGATCTGG TCGAAACCTA ATTACCCAGTG TAGAAACTAG	540
55		

	CICALACUSE ABICEGEGEA AGIICEGECE ATGGOCAGEA TUTTECAAGUT AACCUTGUET	600
5	TACGACCCAG TATCACTCAT TACCAAACCC GAGGGTTTGA GAAGGAAATG ACGCTCAAAC	660
	AGGCATGCCC CTGGAATACC AGAGGACGCA ATGTGCGTTC AAAGATTGGA TGATTCACGA	720
10		
	(2) INFORMATION FOR SEQ ID NO:602:	
	(1) SEQUENCE CHARACTERISTICS:	
15	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1411UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:602:	
	CATCCTCACA TACCTTAGIC TCTATACAGC GCAAGACATG CGTGATGGCG GGTTTGTTCT	60
35	ATGCAAAGTC ATTGGGTTTC CCTCTGGCGG CGCATACAAC ACCTGCCTAA CCTGAACAGT	120
	CTCATCCTOG GCATCTAGCG ATCCCATGGG TGAGCAGCGG AGGATTTGGT GCATTACTAG	180
40	CCAATGGCAA TCCAAACCAA AGAAACCGAC TTGGGGGAAT GCCTCATTGA ATAGCCGGTG	240
	TTTCCACACT CTCATTCTCT CACTGTAACC TCCTCTTTGC TTGCCCATAT TAAACCTGTT	300
45	CTGTGAAACA TCGGAGCGGT GTTTAGTGGA AAGCAACTAG AGGAACTCAA AGAGTGCTAT	360
	GOCATGGGGG CAGCTGTTGC GAAGGTGTAA AAACCCCGAGC TCCGGTTCGC TTGACACAGA	420
50	AGITACITIC TGIATCICTA TCAGICTATC ACCGAAGGAC CGIGGIGIGC TTIGCGCATT	480
	TICCOCITGI TCTTTAAGAT ACTIATCIGG TIGATCCTGC CACTAGICAT ATGCTTGICT	540
55	CAAAGATTAA GCCATGCATG TCTAAGTATA AGCAATTTAT ACAGTGAAAC TGCGAATGGC	600

	TCATTAAATC AGITATCGIT TATTICATAG TICCTITIACT ACATGGATAT CIGIOGIAAT	660
5	TCTAGAGCTA ATACATGCTT AAAATCTCAC CTTTTGGAAG AGATGTATTA TAGAATA	717
	(2) INFORMATION FOR SEQ ID NO:603:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1412RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:603:	
	The same beautiful. SEQ ID NO. 805:	
30	GATCTCGAAC CAGGATGACT GICTCCCAGT TAACTCCCCC GACCAGATTC GCTTCCTACA	60
	CAACTICIOC TCCGGIGGCC ACGGIATTIC CATCGGGICT GITGGCCACA AGAAGGGCGA	120
35	CTCAGTCACC AACTTCCTCG CACAGGACAA CCAGGTCGTC GAGTCGGACA ACGGTCTAAG	180
	AATCAAGACT TTCGTGGGGG CCATTGGCAA GGTCGACAAC ATCAAGTTCA TCAACAACAA	240
40	GGTCAAGAAC ATCCGCAAGT TCGCTATCGT CATCCAGGGC GACTACAAGG ACGGCACCAC	300
40	CACCOCCACC CCAACCOCCG GCTGCCCAAT CACCAACCTA GAGGTCAGAG GCAACACCGG	360
	TAACACCGTC GGCAAGCGCA GCAAGCTCAA GATTCTCGTC AAGAATGCGT CTAAGTGGAC	420
45	CTTCGCCGAC AACAACATTT TGGGCAAGAC CTTCCCAGGC TGCTCTGGCG CACCTAACGG	480
	CATCAAGIGC TAAGCGCCTT TTTTTTTTTT GGCTGCGCCT CGAAACTATT ACTATGAACA	540
50		340
	TTGGCGTCCA CCGCCACTAC AAAAGCATCG GGTCTATCCC ATTATAACAT TAAAATCTCA	600
55	GITGATATTA TATTITACAT TCGAATGICC TTAGGGCTIT TTITATATTAT ATAAACITTA	660

	GATTAAAAAA ACGAGGTACA ACCAGATCAA CGAAGCTTTT CGCCCACCCA	710
5	(2) INFORMATION FOR SEQ ID NO:604:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 728 base pairs	
10	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG141ZUP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:604:	
20	GATOGAACGA GATAAACAGA GGIATTGGIT GITATCACAA ACATATAATC CTGGGGATAC	60
30	AACOCIGICA AACICIOOOC CITCIOCITT GIGICIAGAT TOOTITIOCA GOCTIGAGAA	120
	TRACCIGIAC ARTITITIGA TGIGGITAGI AAGAGACGCA TCAACGATAT CATOGCACAA	180
35	AGTICOGITT CITICCCCIG CAAGCGGGAA TGCGCCTICA TIACTICCCG AATCTICICC	240
	ATGAGTCGAT GGTCTCGGCG TTGAAGCTTG TAGTGTCAAA GGTTCTATTC TTGGAGAAGG	300
40	TICTATCICT ATTITITICIC CCCAGAAAGA ATCATTIGAC ATCCAATATC TIGIAACTIC	360
	CCTGGGATGT AATCTTTGAA TAGCGGGGTT TCGGTACAAG CTGCTACCTG CCAGATTATT	420
45	ATTIAACCAT TCTTCTCGTC CGTCAACGTG ACGTATAACG TCGACCCTAT TCCGTTTCTT	480
	TICCAACATA GETTETTCAT CAAATGAGAG GTAAAATGGT TCCTGCTGGG AACGCGACGA	540
50	AGGCTOCTTT ACTITIAAGIC TTAACAAGGC GICAACATAT ICTTITIGAA TOGTICTAGA	600
	AGTOGITACA AAATCCATAT TOCGICTTAG ATCICACICC TGAACOCCIT TGICTAGITT	660
55	CTCATCCCCC AGTGGTAAAT CTGAACGAGG GACAAAGTAC ATGCAACTGT CCTCATCATT	720

	GTAAGTCA	728
5	(2) INFORMATION FOR SEQ ID NO:605:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 732 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1413RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:605:	
	GATCTOCTOG GAGTGACTCA OGAAGCTTTG TCAGTACCTG GAATGAAAAA ACAGTCTCTG	60
30	ACAGAGOGG GAAGCTGGGC CTGATGGTCG TTACAGCGGA CCAGTTCAAA GAATATGAAC	120
	AATTCAACAC TCTCAGCCCC AAGCATCAAC TTCCTCAGCA GGCCAAGCAG CTACATATOG	180
35	TOCTAATIGA TOCTOCIGAA CIATACGAAT TAAGAAGCAA AGITICOGAT GGACTGICIG	240
	OCCATTICAA CTCTGACTTT GTCTTGAGCA AGGAGATCAT TCTTGAGAAT GCTCATAGTT	300
40	ATGGITTAAC GGITCTTCAA ACGGAAGAGT ATCTTCAATT ACAGAGTAGT TTGGAGAGAG	360
	AACAGGTAAC GTCCTACAAC ATTGCCGAGA AAGCAACTAC AATTGGCTAC GTTGCACTTC	420
45	CAAGAACCGA GTACGATGAA CTTGTAGCTT COCAAGCTTC TACGAAAGAA CAGAATTTTG	480
	AGGTATACOC OGOGGAAAAT GOCAAGGTCA TAGTOGATAA ATCTGAGTAT CACGATTTGA	540
50	AGATCAAAGC TATCCCAGIG ATTICACCAT TOCCTCAAAT GAGCAAAGAG CAGATGGTTG	600
	AAAAGGCCAA GGAACTTOGA ATGGTAGCTT TOCTCATTCA CGAGTATGAG AAGTTAAAGA	660
55	GCCCTATTIC CGATAACGCT TIGAATGCAA CAGCGAAGGG ACCGIGGAAA GCTIGITCIC	720

	CTAAAGGAGA GT	732
5	(2) INFORMATION FOR SEQ ID NO:606:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 721 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1413UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:606:	
	GATCCACTIT TAGGICCACT TCAAACIGGA TITICGGGIA CICCCGGCAC ACCACCGICA	60
30	AGTICATOGGC ATAGATGGAC TOAAGCACTT COAGCTOCTG CTTTTGCTCC TOCTGATAGT	120
	CCATACCTAT CCCCTCGACC AACTATGAGC CCACGCGCAG CTTAGGGCTA GACCGTTACA	180
35	OCTOCAGGIG ACCGICCOGG GCACCATOCG CIATOGCIGG CCAAAITITIT COCCIATACC	240
	ACCACITATE TTACCCOGTIC TATAGTICCTE CTCTCCCACC TCACTCATICG TCCTGTCCCC	300
40	COOCCENTICE TOCCTOCTICE COCCAAATOC CCACCOCTCT CAACCCTCGT TCCATCTCCG	360
	TCACGGGTTG ACCGAACGGG AATTGCGCGC GCCGAGAAAT CTTGGCGAAC CATGCTGCAC	420
45	GIAGOCITAC TOCCAAAATT AAGCCGICAA ATGCCTGGCT ATCCTTCCAC GCACGCCCAT	<b>4</b> 80
	AGTCACCTGA AGCTGGCTGG AACAGTGGTC ACGCAGCTTT CTGACGCATA CCAGGAACAG	540
50	GIGGCCCAGC CCCAGGCCAA CGGIGGGIGA TIAIGICAGC CACITITIGGI GGATTACGIA	600
	AATCIGGGIG CATGCCIGGC ACGACAGCGC GCATGGCACC CCAAGACAAA CGIGGCCACAC	660
55	CCATTCAATA TTAGAGGACT TTGCTGCACA CCCTAATCAT CCGTTGGGTT GTGAGATACG	720

	С	721
5	(2) INFORMATION FOR SEQ ID NO:607:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 729 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
00	(A) ORGANISM: PAG1414RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:607:	
	GATCCGTAAT CGAGTTTAGC TICCGTGTCG CATCATCGAC AGGTGGAAAT GCTCGCTTGT	60
30	COCCOGNICTIC AAAAACGAGTIC AGATGTOCAG AGACOCTIGAA GTCCAACATT TTAACCACCG	120
	CTGAAGACCG GGAATAGTAG GOCAACGTAG TTCCCCCGAAC TTCAGTTTTG TTTTCTTTTTA	180
35	ATTIAATIGGA CTACACCAAA AAAAGCTCAA CAACAGTCCC AATTIAGTTCT GCTIAGAAGAT	240
	GCAAACACGT TAGTGATCAG TAAGTATGTG TACTCGTGTA CTCGTCCTGC ACTGCAAAGT	300
40	TOGOGICACA ACTAGOTGIG AACCATGGIT TGAAAAAAAA TAATGATAAT GATTOCGOCC	360
	AGGATOGAAC TOGOGGACGIT CTGCGTGTTA AGCAGATGCC ATAACCGACT AGACCACGGA	420
45	ACCACCTATA ACCCCTTAAT TATACTCAGA TACTAGTGAC CATTITICTAG TCACATGATG	480
	CTAGTTICCT GAATAAAAGA TOCACGIGAT TACCAAATCT GTATTTACTA GGTAAAATOC	540
50	CTTOGICAAT AAGIACGIAG ATATTATATA TGIATACATA TOCATTITTAG ATOCAATAAA	600
	ACCICIATTA IGIATOCOCO COCAOCITTA ACCCAGIGIG TITITOCCATI GITTIGIOCA	660
55	TOCANTOGIC TITOCATAAA ACCCIGACIT TCATCITITIT CGIGCIIGGA TGITAACTIC	720

	CAACTCTGA	729
5	(2) INFORMATION FOR SEQ ID NO:608:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 639 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1414UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:608:	
	CATICTOCCC COCCOCCAA CCCCCCCCCAAAAAA CCACACCCCC CCCCCTTCCC	60
30	GCCGCCACTG CGGCGGTTGC ACAAGACATA TATGTCGGTA TATAAGACCG CGGGTGCCGC	120
	GIGGCTGCCG TGCAGAACCC GCCGIGCGCG CGCGGCCAGA GATTICIAAT ACICIGCGIT	180
35	TICITITICE AGCOCCIOGI ATATAAGITC COCCIGIGIC COCCCCGITC	240
	GCCAGGGACA TAGGGGAGCA TICCGCAGCA GCCGTCTGTA GCCGGACCAG TACGACAGGG	300
40	ACCCAGGACA CAAACCACCC GACCCCCAGT GCCCCCCATC AGCCACCCAC AGCCAGCCAG	360
	COSTATIVAÇÃ COCCOCUSTAC GACCOCCIG GIACCIATAG COCCACATOG ACCIGOSTOC	420
45	TAACGGGATT TTTCTGCACC AGAACGACTC TGCGGAGACG ATCAAGCTGG AGATGTCGCC	480
	TGTCGGCGGT TCGGGCAGCG CAGGCAGCGG CATCGGCATG GGCAGCGGGG ACGAGCAGCT	540
50	GACGAAGTOC ATCAGOGACC TGAACATCTT CGATCTOCTG CACAACAACC CGCCGTCGAG	600
	TICOGACGAC AACAAGGAGG GIGGGCGGGG GGCGGCTGC	639
55	(2) INFORMATION FOR SEQ ID NO:609:	

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1415RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:609:	
	CATCGIGGIT CIGITATOCA AACGITGGIT GCTAGAACAT TGCGCCAGGI TGAAAGIAGC	60
25	CAGAGCATGA TACGAATTCT GOGATTATCG GCTACATTAC CTAACTTCTT CGACGTCGCA	120
	GACTITITIGG GGGITAACAG ACATGIGGGA ATGITITIATT TIGATCAAIC GITCCGICCA	180
30	AAACCCTTAG AACAGCAGCT GCTTGGTTGC AGAGGCAAGG CGGGCAGCAA ACAAGGAAGG	240
	GAAAATATTG ATAAGGITTC ATATGAAAAG CITTATGAAC ATGICITAAA TGCCTCCCAG	300
35	GICATOGITT TIGIOCACIC AAGGAAGGAT ACIGIGOGCA CIGOGOGGAA TIACATTICT	360
	TITICCCCAAG CCAACCAACA GICCGATGIT TICCIAAGIA GCGATCAAAG CGITACCAAG	420
40	TITTCCCGAG ACATCTCCAA ACATAAGGAT AGAGATATGA AGGAGCTCTT CCAACATGGG	480
	TITIOGIATAC ATCATOCTOG TATOTCICOA TCTGATAGAA ATCTAACAGA AAAGATOTTC	540
45	AAAGAGGGAG CIATTAATGT GCTTATCTGT ACAGCGACGC TGGCCTGGGG TGTGAACTTA	600
	CCGCCIGATG TIGICITGAT AAAGGGAACT CAGATATMIG ACTCTAAAAA AGGIGGITTT	660
50	ATAGATTIGG GGATICIGAT GIGATACA	688
	(2) INFORMATION FOR SEQ ID NO:610:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGIH: 703 base pairs

	(B) TYPE: mucleic acid	
5	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
10		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1415UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:610:	
20	GATCATCAGG AGTICGICAC CTIGGAAACC AATIGCGAAC CACAATICCT TCIGAGCCTT	60
		• •
	TGGAAATTIG TCACACCAAA CTCTGAAACC GTCTTTGTAA CTTTCATTAT GGCGGAATGC	120
25	TACAAGTGIC AACTTATCAG GGITGGATTG GTCCTTAAAA TGTACCTTAT CCAGAACAGG	180
	AASCATOGAG GCTTCACGTA TAAACTTATC TTTCGCCCCT CCTTGAATGT TATGCACGCG	240
30	GCACACTGAG CACAACGCAG CATAGCCCAT CCGACCTAGC TTCTCCAACG TCAGCATCTC	300
	OCCACTATAC TCATAGOGAA AGCCATCATC CCCGAATAAT TCOOGGTCTA AGCGTTGTAG	360
35	CGIAATTCCA GOCAAACCAG TCACCGGGIT GTCCTCATAC CATGITCCCT GCTTAATGCA	420
	CTGCATGGCT TTAATCATAG TCATAACTGT CCTGAGGTAC CCAGATTCGC TTGCAATATC	480
	Charles come	
40	GATATAGGCC TGTAGAATAC GTAGCGCCTG GTCGAGAACT GAGATCGTAT CTTGGTAATA	540
	ATTOTICAL ACTION	
	ATCIGCAATT OCTAAGICAG CICTACTTAG GIAAGCTIGI AAAAGCAAAA AGOCTTIGAC	600
	MIXXXXIII CAMBURANA	
45	ATGGGGGTCC CATATTGGTA ACTCTTGTTC TCCTGTAAAA GTACTTTCAA CGGAATATCT	660
	AAGAGTTTCT GACATTTCAA CATTCATGAT AGTCTCCCCC CCC	
	THE STREET GREATITICAA CATTCAIGAT AGTOTOGCCC CCC	703
50	(2) INFORMATION FOR SEQ ID NO:611:	
50	== outliffed for SEQ ID NO:011:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
55	(B) TYPE: nucleic acid	
J <del>J</del>	(b) TITE. MIGHELC ACIA	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1416RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:611:	
	CATCATCATT ATTTCCTCCC TTCGTCCCCA CCATTCGAAG CCCCCCCTCC CTTTCTTCAA	60
20	GCATTICAGG CGIATGAATG TITGCTCTCAC CAGAGCAAAG GCCAGTCTCT GGATCCTGGG	120
	TCACCATAAA TCTTTATACA AGAACAAGCT ATGGATGCAT TTGATTTCAG ATGGGAAAGG	180
25	COSTGACTICC CTCCAAATICG CATGTCCCCCG CTTCCTTGAT CCACGGAACA GAGCCGCCCA	240
	GGATGCTCTT CATAGGTTCA AAAATCACCA TAATTATATC GAGAACGCAG ATGATTATGG	300
30	OCCIGARCOS GIGATGACTA ARTCARGAGO ACOCARTAGA TORTOCAGAA ARCOCARACA	360
	TATOGAAGAT AATOCAGATG ATAACTACGA TOOCGITIOCT GAATTCAAGA AGGAAAATCA	420
35	AAGAGAAAGC AACACAGGCA COGGTGGTTA COGTGGGGAT ACATCTAACC ACAGATTGGC	480
	ACCIGCTAGG AACGATAGCA AGAAGGCCAA GACGTGCTCC AATGCCGCCG GTATTTCCGA	540
40	GOCTACTICA GAGGATGGIG ATCGAGGICA GAAAGGACAT GGAACIAAGA AGAAGICITC	600
	CATATICOGO AATTITATOC COCCAGITICA TGACGOCACC CCTGCTGCCC ATGTGTACCA	660
<b>4</b> 5	CCCTAAGGAA CGCAAGCCCA AGAATGCTGC ATCCGCTTAA GCGGCTGGCC TTGGCAAC	718
	(2) INFORMATION FOR SEQ ID NO:612:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 712 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(b) Totolkol. Illian	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1416UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:612:	
4.5	GATCTIGCCC GGCAAGACCA GGAAGTCGTT GTACGTCAAC CCGCCCCGCG TCTTGGAGTC	60
15	CATCAACTOC TOCACOGGAC AGCCCGTCCT TCTCGGCCGIA CGTCGCCAGG TGCTCCAGTG	120
20	COGROSCIOC GICTOTOTAA GICATIOCOC TITIGITICOOC GIOCTATGAA GAGAACCAGT	180
	CAACACTAAA CCCAAGCTCT CAAGTTGACC CATCCATCAA GTAACTATCC CGAACAGACG	240
25	CCGGTAAACC CAGCTGGGAT TTGGCGCATC TAGAAAACCT ATTTATACTG CAGCTCATCG	300
	CTGCAAACIT TTCACGTAAA AGAAACGATG ATCCAGCGGG GOCCAAAAAG CAATGGGCCT	360
30	GCGCCGCACG ATGCGAGCCC TACCGGCGGC CAGCACCAGG TAGGAGCTGT CAGGGGCCTA	<b>4</b> 20
	GAACOCCOC ACOCTAGACG COCTOCTOGG COCCCCCC ACOCTTCCCA CCCCCCCCCC	480
35	GCAGCAGCAG GCGTGCCAGG CCGACCAAAA GACCGACCAG CCAGCGCAGC AGTCTGTAGA	540
	COOCOCCAGA CAGOCCAAACG GCCAGGAATA CAGTCCAGAG CACGOCGGAG AGCAGCAGGA	600
40	AGITGAACAC GCCGTCCATG CCCACGCGCG CACAAACGGG AACAGCGCCA GCGCGCGC	660
	GCAGAGCGC TGCAGGAATG CGACGACGGA CAGGAACGGC AGGATAGCAC TA	712
45	(2) INFORMATION FOR SEQ ID NO:613:	
	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
50	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGIN	AL SOURCE:
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(vi) ORIGINAL SOURCE:

(A)	ORGANISM:	PAG1417RP
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10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:613:	
	CATCCCCTTG OCCTCGTCGT TGACCAGGIA GCGGCGCTGT AGCCCGAAGA AGCCGGACAT	60
15	COORTICICAC GCGCTCGTGA GCGCACGCCC CATCATGCCC GCGCTACTGC AGATCACGCG	120
	COGGIACAGG GGCCAGICCT IGICGATICC GACGCCGGGC GCGTAGCGGC IGCCCAGCAC	180
20	CAACOGATGT GTGCGTAGTG AGTCCAGAAG CAGCGGTAGG CTCTCTGGCG GATGCTGCAG	240
	GTCCCCGTCC ATGCACACCA GGTACTCCCC CTTCCCCTCG TAGAAGCCCT TGAGCACCCC	300
25	ACTOGACAGE COGCOCTOGT COGTOCOCAE GATGATOCOC ACGITIGIAGE CCTOCTIOGC	360
	CAGGGCCTCC ACCTCTTCCA CAGACCCGTC CTGGGAGTTG TCGTCGACAA AGATCAGCTC	420
30	AGTOTTOTTG GAGTOCOCCT TACOGAGCOC GGCAAACAGC COCGTGGCAA GOOGOTTGAT	<b>4</b> 80
	GITGOSCCTT TOGTOGTAGG COGCACGAC CACAGAGTCT CGATOCTCAT GOCGCTOGTA	540
35	TOGICCITAA TGIAGIGAGI AGCGAACGIC GGIAGCIGIT TCGCAAATAA GIGAGGCCTG	600
	CCCCCCTAAT GTCGTGCCT TATCGTTGCT TTTTGGTTCG TGTCACGGGG TTACCCGGCC	660
40	ACCAGGCTAG ACAGCGAGAC CCGCGGTGAG CAGCCCACGA CCAAGAAGCG CTGTA	715
	(2) INFORMATION FOR SEQ ID NO:614:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

## (A) ORGANISM: PAG1417UP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:614:	
10	CATCTOCCTA OCTACTACAT CAATTCACCC TATACCCAAA ACTTTOCTOC CAACCCCAAC	60
	CACCOOCCET COCCCTTGTT GTAGTCOCCC TACTTCTCCC AAACCTTGAT CAAAGTTCTA	120
15	TOGATOCACO GGATGACGTO AGOGOCATOA TOGGAATOTG COTTATOGAC TGCAACACGO	180
	OCCATTAGTA CAGCAGOGOC CTOCTOGTCA AAGGAAGCAG CGATTGCCGG GTTACCGAAT	240
20	GOCAACATOT GETTAGCAAC TETAGTCACT CTGACACGET TOGTACCAGA TGCATOCTGG	300
	TATOCAGIAA TGAATTOOGT GTATOCCAAT TTTOGTCTGT CCCCCATGAG GCTGOCAGTT	360
25	GCAGCGGTAT TTGCAATCTC GAAAAAGATA GCGTAAGAGT GGTGAGGGCT CAAGCACGCC	420
	ATTITICCATE TAGAAGTIGOC COCAATACCE ATTICIGAAT COCTCACGIT CIGIOCATCA	<b>4</b> 80
30	ACGITAACCG GOGAAGCATG GOCAATCAGT COCTGCAGCT TTAGATCTGC ACTGGTTTTA	540
	ATGCACATGG AAGCATTGAA CGCCATGGTT AGGTACCCTC CTCATCTTTA GAAAACAGTC	600
35	TGATGAAAGA TTGCTTGAAG ATGGCCGTCG AGAATGCGTC AGTCAACAAC AAAACACCAC	660
	CAGIGGAGIC GGICAACITC TICATCICAG ACATACAACC IGGICGIAGC ATCCA	715
40	(2) INFORMATION FOR SEQ ID NO:615:	
45	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 728 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	

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(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1418RP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:615:			
5	CATCCCCCAG ATTCATCCTC CACCCCCCAC ACCCAATTAC TATAACAACA TCCTCCCCCTC	60		
	TTAAAGGACC TAACTCACGC TCAAGTATTT CAGGATGATA TCCTAGATGA AGAGCTGCGC	120		
10	CACACOCTOG TICOGITACA ATATTOCTCT CITCCOCAAA ATTTAAACAT GICTGTACTA	180		
	CAGCGAGCTG GTCAAGCACA ACAGATTTTG TCCTGTATTT TTGGGCGTAA CTCAGAGTAA	240		
15	GATCCGTCAC GAAAGATGTG CATAAAGAAG TAGCAACGCT TTTAGGATTC ATCGAAACGT	300		
	TOCTGCCCAG CAGCAAAGAT CTGTGCAAAA CCTCGCACCC CTCTGTTTCC ACTGCTACAA	360		
20	CAGGGATAGA GICTGCCAAA CCATGITTCT CCAGCCCATA TACAATCCCA TTATATAAACC	420		
25	CCCCCCCACC TACCCTCCAG ACGATACCTT TCACCCTCTC CAATTCCACG CCTTGGAGAT	480		
25	SCAGISCITC TACTACITCA TCTACCATTG TISCATSCCC TICCCAGATG AGISSGITGT	540		
30	CGAATGGATG TGCATATIATC GGAGGGACTT TTTCTAAATT CACATTCCCC ATCAACTCGG	600		
	AACCTAAGTA GICATCCCTC TCTTTCAATA CACTTCCCAT TCATATCACA TCTGCCCCCG	660		
35	TIGACCGIAT CCCCICTACC ATCCCCCGIC CAGTAGTTIC AGCCACTACC ACTGTCCAAG	720		
	GTATCCTA	728		
40	(2) INFORMATION FOR SEQ ID NO:616:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 713 base pairs			
	(B) TYPE: nucleic acid			
45	(C) STRANDEINESS: single			
	(D) TOPOLOGY: linear			
50	(ii) MOLECULE TYPE: DNA (genomic)			
	(vi) ORIGINAL SOURCE:			

(A) ORGANISM: PAG1418UP

5	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:616:	
	GATCATCTOC GTOCGATACT GOCAAAAAAT GAGAGACAGC ATGATGAAAA TATAGTTAAT	60
10	AAGATATTOC ATGATATAAG CACAGGGGG TITICGTCGAA GAGGAAAGGG TGCACTTGAT	120
	CTOGAAATGA GTGAAAATGA AGACCAAGAG TTACAACAGT TTAGACAGAA AAGACGAGAA	180
15	CTTTTGAAAC AAAAGATATT GGAAAATGGT GATACTAGCA AGCTGGTATC TAACCCCAAG	240
	TOATACOCCT TITTICAGAC GATGITGGAC GATGITACTG AAGCATCATT TOGAAATACA	300
20	TTTGATGCCA ATATAGATGA AAAAACAGAT CCATCTGCTG CAGGTCGGAA AATTGTCATA	360
	TCAGAACAAT TTGTAAAGGA AACCCTGTCA TTCTTGTCGA GCAAGAGTGG CGACTCAGAA	420
25	ATCCCTOCAG AAACTAAATC TATTTCATCC AGCACAGTTG AACGTGAAGA AATTCAAGAC	480
	CTTCCATACA TIGAAGCAAA ATAGTAACAT TAAACATITG AAAGGAATCT AGAACTTCCT	540
30	OCTCAGATOG CTGAACTCAG CAGTOGAGAT GAAGGTGATT ACGCCTTTTC TTTAGATAGA	600
	TICOCTCTOC GOCAAAAAGT TIAATAATOG AACTAACGTC GACGATAAGT TIAAAAGTOG	660
35	CACCAAGGCA GTGCGAATCT TAAAGGCAAT AAGACAATTG GCGGTCAAAA GCC	71
	(2) INFORMATION FOR SEQ ID NO:617:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 723 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1419RP	
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ı	(vi)	CENT IEMPE	DESCRIPTION:	CEN	TD	NO.617.
٦	ハルリ	SEQUENCE	DESCRIPTION:	250	$\omega$	NO: 01/:

5	GATICTOCOGA GTCTCATCCA AA	OGTATIOG ATGAGGCTTG	G10G109CAG 000	<b>33370070</b> 60
	OCTOGATIOG OGAGOTOGIG AT	GACTICGC ACTICICCGG	GCCCGGAAAAT TCC	FTGTCAGA 120
10	CAGICOOCCI TOOCCITICAA OC	TOCCOCTG TTOCTOCACA	CG1GG1GGCC CCC	ETTAGETG 180
	AATACGIAAC GCTGGCGCGG TG	TCCCGCGC ATCCAGGTAT	TCTTCGAGGC TIT	CTTCTTC 240
15	GGCGATGTCT GAGATATCTG GA	GCACCGCG AGCATTCTGA	TACACCTOSC CCC	PAACATGT 300
	THECHICOCC CHCAACHCIC CC	TCAAACCC GTAGAAGTCA	TCGCGGTATT CTC	CATCCGG 360
20	CATTIGICATT GTAGTAGTOG TO	TCCACATA GCGTACGCCA	TICATOTOCT TC	ACCGTCTG 420
	GOGAGTICACG GTCCGTGTAC GO	CCCTCCAG GICCTTCCTT	TCCCTCCTCT TC	ACCGITAT 480
25	CGTATTGCCA GCTGCGACAG CA	GCAGGGCC AAAGCCGTTG	TTOCTOCCIA OCC	PAATTOGC 540
	GOGIOGITIGO GAGOTOATAC TO	TAAGTCCG CGGAGGCGCA	CCCAGCTAGC TOC	93CCAGC 600
30	AGCTICCTAGC GACCGCGTCC GC	CCGIACCC AGICAGICAC	TGAGTCCCCC CCX	ATCCCAAC 660
	COCHOGNOTT COGRAGICACG CA	ACCGACGC CGCCGCAGAC	GACAAGCCGC TGC	CIGITGA 720
35	ATA			723

## (2) INFORMATION FOR SEQ ID NO:618:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 721 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1419UP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:618:			
5	CATCOSTOCG COCCTOCOTA COCCATAGOGG CGAGGTOCCC CCCCCCCCCC CAGGTCACTG	60		
	COCCCAAACC GCACCTGCAC CTGAACCGAG CCTGCAGCCC ACGAAGGAAC GCCACGCTAC	120		
10	ATGROCCOST GCAGAGCACC GCCCTTGTCT TGCGGGGCTG AAGTGACTGT GGCACGCTCC	180		
	GCAGGACATA TCTTTTTAAT GAGCTGTGTC ATGCGCACAT TCTCACCGTC GCGCTACCGT	240		
15	AGCGTCGCCC TCTGTCACCG TGTGAGCTGC TGCCAAAACA AACAAATCGG GACGGGCCCG	300		
	CATOCAGIAA TIACCICCIC CCCAAGOCAA COCCTIGGIT TIGITIACGI TGGCCAGAGA	360		
20	THICICITY GOOGIOGATY ACCYCACOCC TCATCCCCCCT GOCAGAGGIG CCTGCCCTGA	420		
	CAGITICTICG AATATTAGAT OCTOGTATOC GOOCACOCCT AGCOCAACCG ATTGTAGTTT	480		
25	ATTGITTCGT CACACCOSSC TAGAGGGCCG AGCTACAGGA TCGCCGATGT GCCGTGACGG	540		
20	ACACCETCAA CETTACCATC TCAACCETCG CTCGTCCCCC CCCCTCTGTC CTACCCGTTG	600		
30	AGATACOCTT AGGATGAAAG CACGAAAATT AAGGITGICG TAAAAACACA AAGTCAACTG	660		
35	COCTITICCCA ATCOCTITAÇA CTCCCATCCT AATCOCCCAC CCACACTCTC CATCCTCCCA	720		
33	G	721		
40	(2) INFORMATION FOR SEQ ID NO:619:			
	(i) SEQUENCE CHARACTERISTICS:			
	(A) LENGTH: 721 base pairs			
	(B) TYPE: nucleic acid			
45	(C) STRANDEDNESS: single			
	(D) TOPOLOGY: linear			
50	(ii) MOLECULE TYPE: DNA (genomic)			
	(vi) ORIGINAL SOURCE:			

(A) ORGANISM: PAG1420RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:619:	
5	GATCAATTCA AGGITGCTTT CCCAGACATC TACGCTGTTT TCCAAAAGAT CGCTCAGCAG	60
	CACCCCGACT ACGAAGTGAC TGTCACGGGT CACTCACTGG GTGGCGGTTA TGCCTACTTG	120
10	ATGOOCTIGG AGCTCCAGCT ACTTGOCCAC AAGCCACATG TGATCACCTA CGCCGGCCTG	180
	CGTATGGGTA ACGCTGACCT CAACAAATGG TACGACAAGG TGTTCGACAA CGTCAAGAAG	240
15	GTCGAGGACT TGAAAAACGG CGGAAACCCA AGAAACGCCT ACATCCGTGT GGTTCAGAGC	300
	CGTGACATTG TICCTATGGT TCCAACTGGC CCTATCTACA CGCACGCGGG TATCCTATTT	360
20	ACCATCACTG ACGTOGACAG CGAAGTACCT CTACAATCOG GCGTCAGACT TGATGGCTGT	420
	AACACCAAGC TAAAGGAGIT GGTGGGGGAC ATCCTCTTCA GCGGGAAGTT GCTAAGCTTG	480
25	GTOCGTCTCC TGAACCACAA CAAATTITTC AGAAGAATGG CTTTGCCATG CACTGATAAT	540
	TCCTTGAAGC TATAATTCCG AGGAAGTAAT GAATTTTAAG TACGGAACGT GCAGTCGCTG	600
30	CAGICTICIG CCICTICCIT ATOCCCTATA TAGITAATIT CATGITCIGI TCTATTTTTT	660
	TACATTITICC AAACACIGGG AATGCCACCT IGTAGATGIT GITCCCAAGA IGGATATITA	720
35	G	721
	(2) INFORMATION FOR SEQ ID NO:620:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 626 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1420UP

887

50

	(XL) SEQUENCE DESCRIPTION: SEQ ID NO:620:	
5	CATCOCTOCC CACCOCCCA CCAACCCCAA CTOCATOCTIC GTTGTGCCCC GCCTGCACCT	60
	CTTOGAGATT GACATGAAGA AGCTGGCGAA GACCTTCGCG TCCAAGTTCG CGACGGGTTG	120
10	CTCTGTGTCC AAGAACGTCG AGAAGAAAGA GCAGGTCGTG GTTCAAGGCG ACATCGCGGA	180
	CCACCTCCAC CCCTACATCC ACCCCCTCCT ACACCACAAG CCCATCAAGC CTCTCAAGCT	240
15	CGAGCAGATTA GACGCTGCCA AGAAGAAGAA GAAGACGCCG ACGACGACGA CGCCGCCGCCC	300
	GTCGTGAAGA GCGGGTCCGG ACATGTGTAT CAGATTCGTA TGTAGTGATT AATGATTGCC	360
20	GCGATTICCA GIGICITACC AGICCAAGAG GACAGGIGIC TGGCATGCIT GCACATTGCT	420
	GOOGTOTOGG TOGOGACCAT GAGOOTOGAG ATOGATOTAA TIGAATOOOC OCTTAACCTG	480
25	CGTOCTOCOG GACOCCOGGT ATTTOCCAGT GOCACCGAGG AATTGCACAG AGTOCTAAAA	540
	CTGCACTACC GAGTGACATA CCATGCGTTT GACCGGGGCA CCAAGCGGTC GGTGTGGGAA	600
30	GTCTGCTGGC GGAGGCCGAG AAGATC	626
	(2) INFORMATION FOR SEQ ID NO:621:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 582 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1421RP	
50		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:621:	
	GATCCCTCAG TTCCCCCATCT TGCCTTCACA GCCAGGATGG ACCATCCGTA ACTGGGAGTT	60

	ANGEOGRAPHIC ATTRICTUTE TRACTACTECT TOSTATIACA TECTACTICAT	120
5	TITATOGITA CITOGGIATG TATGGCATOT TAAATITTAT OGACTOTAGT ATTITTATGA	180
	CTGTGTAAAC TAATGAAAA TAATGAATCG AAGTCTCGTT TACCTAGAGC TGATTATGCC	240
10	ACATOCOTAC TATCOOCOTG CCACCOCAAT TATGTATCTA TCCTACAGAT AATCCTTTCT	300
	ATTAGCAGTT CTCACGAAAC GTCTCAGTTG CCACTCGACG TCAGCATCCT TGTTCTCCAA	360
15	GETGCCCAGT GTCAGCTCGT AGAGCTTCAT TTCGAACCGT GETCCCACCT CCGCCAATTC	420
	AACTCCATCT CTCGTCTTGA CGTATACGTG CTGCCGCACA CTAATGAAAT CGCCGCGGTT	480
20	COCAAATGTG ATGACCCTAG GOCTGTCTTT CTTGACTCCG GOCGGGAACA TGTGCTTCAG	540
	TATTITAACG ACCCGTTCCC CCAATCGAGT ATTGAAATTA TC	582
25	(2) INFORMATION FOR SEQ ID NO:622:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1152 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1421UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:622:	
45	GATCATCATA COGTGTCCAA CATCGCCCAC GGAACCACCA GTCACTTCAA GTGGAACGCA	60
	GETAACATAC GOGATGGOCT CCACGACGAC TTGGCCAGCT TCAAGGACGC AGTOGTGCAC	120
50	TETETCACET TOCOCAGOGG CCAGTOCOGC GACTACOGCC ACCAGTOGTC CATGTTOGGC	180
	AACOGTTICTG CTGGCAGTGC CAAGTCGGGG TCGTGGTTCG GTGGCGGGAC TGACTGGCGC	240
55		

	CATOCACTAC TOCACOCOCO COCCACACOC COCCACTOCA COCCACCTOC	300
5	TESTICCECE COCACASCOE CACOGASCAT TOSSECCET COTOCTTICE COCCCACCCC	360
	COCCACACOC COCACACTOS CTCOCACOC TOCTOCTTTTC CCCCCCACCC ACCCCACCC	420
10	COCACCGACG OCACCTOOCT CAACOGAGAG COCGACCOCT CGTOGTTCGG TCOCGAGAAA	480
	CACOCCACCC TOGACCACTC CCACCCTGTC TTCCCCCAATG GCGCCCGTCT CCCCCGTCCAC	540
15	ACCACGOOCT AGGOOCOGAC GOCCGCOGCA AGGTOGACGA CATCAAGCAG GCAGGTGCAG	600
	ACCTOGGCCG CTCCCCCACG GCCAAGGTCG ACGACTTCAA GCAGGCCGCC GCTGACCTCG	660
20	GTCGCTCTGC CCAGGACCGC CTCCAGCGGG GCCTTGCCGA CGCCAAGCAG ACGCTCTCAG	720
	COCCOCCTIC CACCICTICS COCCCCCCCC CCTCCCCTICS TOCCCCCTICT CCCCACCCCC	780
25	CCTCGTCCGC CGCCGACAAG ACCCAGTCCC TCTTCAACTG GGGCTACAAC AAGGCCGAAA	840
	AGTOGAAGGC CATOGCCATC GGCGAGTACG ACAAGGCCAA CAAGGACTAC CAGCAGGCCC	900
30	TOGACOCCTA CAACOOCTOC AAGOOCCTOC TOGOOCACOG CCACCAGCAC CTTCOCACOG	960
	COCTOCACAC COCCCACCOC CACCTCCCTC ACTGTCCCCA CAACCTCCAC GCCATCTCCC	1020
35	COGAGITOGA CCACTACOCC COCCAGAACA TCTCCGGACAT CTNCCGGGCGN CTGGACCACG	1080
	ACCACCOCCA TTCCCCCCCT TCCCCCCCTCT TTACCTCCTT CCCCTTCAAC CCCCCCCTCT	1140
40	CGAAATOGAC CT	1152
	(2) INFORMATION FOR SEQ ID NO:623:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

(A) ORGANISM: PAG1422RP

5	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:623:	
10	CATCCGTGTC CTGGGGGACAACAT GAGCGGCTTT GTGTGCCCAT CGTGCGAAAA	60
	CGAGTICGACC ATCTTCAAGC CAACAACAGG TOGTIGGTCOC GCCTTGTGCG AGGAGCTGGG	120
15	GATAAAGITC CTIGGAGCCG TGCCGATIGA TCCGCGAATT GGAAGATGCT GCGACTCTGG	180
	CGAAACCTTT TTGGACGCCT ATCCGGACAG TCCAGCGTCG ACCGCCATCA TGCATGTGGT	240
20	AGAGGCTCTC CGTGACGCCG TCGGCGACGT ATAACGCCCC TAGCAGTTCC TGCCAGTGAC	300
	AGACTGATAC CAGTITTATAC ATACATACAT ATTIGTAAAA AAGACGCTTA GIGTTACGIG	360
25	GATOCCAGOG CCCGTTTCAG GTAGATAGTT TOGGGCTGTC CCAGOGGCAA TOCAAGTAAT	420
	CIGICITIAA AAGACOOOT CICCAACOCT TOTCGATAAT TCTCAAGGAT GATATCACAG	480
30	ACAACTITICS ACATGACACA CCAAACGACG GAGACTICIC CCTCCCACCC CAAATCCCGTG	540
	GCCAGGACGG GCAGAACCCG GACCAGATCG GAAAGCAGCT CTTGGTTGTG GTTGTTGTCA	600
35	AGTOCTATICT GGAGGTACTT CTCAAATACC CCCAGGCCGT GAGTCCAAGT TTCCATCTGT	660
	TGTGCGGGGA AAGTCTCCAA TAATTGACGC AGTGTCTGCA AGTTAGCAGC TGA	713
40	(2) INFORMATION FOR SEQ ID NO:624:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 642 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
50	(2, 55152551, 221502	
	(ii) MOLECULE TYPE: DNA (genomic)	

- (vi) ORIGINAL SOURCE:
- 55 (A) ORGANISM: PAG1422UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:624:	
5	CATCTCCTAG OCCCCAAGTC CACGACTACA COCCCCCTTT TTCCCCCCAAA CACCGAACAG	60
	AACCCCCAG CCCCCCTTT CCCACAGAGT AGTCCCCCTC CCAATCCCAC TGCCCCCCT	120
10	OGTICTOTTOG CTAGCACGGG CAACAGCGGC AGCACCCAAT TGGGTGGGCT GTTGGGCAAC	180
	ACTOCTOCOG OCOGTOGTOG CACTCTTTTT GOCGCCOOCT COOCCOCCAA CAACAACOCA	240
15	TOCACCTOGT TOOGAAATCT CTTTGGGAAA CCTAATGACA CGGCACCGGC AGCTGGTGGA	300
	GGICTITICA GCAATOOGCC GAACACAGCC ACCACAAATA COGITTCTIC CACTAACAGT	360
20	CTTTTTAGCA ATAATCAGGG AAATGGTGCG CAGAATAATG GGGGGCTCTT TGGTGCGAAA	420
25	CCTACCISCIC GOCTCTTTGG AAACAGCACC GCTCAGCCAC AGTGCTCGCT TITTTGGAGCT	<b>4</b> 80
	TOCTOCTOAC AGAATAATOA GOAGCAGCAG CAGCAAACAC AGCAACTGTC CCTTCTGGGT	540
30	TCCAATCCAT ATGGCCTGAA TCTGACTGGT GTTCCTGTTA CTACCATGCC GGAATCTATA	600
	ACGOCAGCAA TIACGICTAA GAAGAAGACG AAGCCTACCG CT	642
35	(2) INFORMATION FOR SEQ ID NO:625:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(I) Islandi Illen	
45	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1423RP	
50		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:625:

892

	GATCGAACAC AAATTCATCT ACGAACACAA ACTTGGAGCG GTTCGTGTTG GTTATATTGG	60
5	ACAGGAACAT TGACCTACCT TCAATGITTG COCATTCGTG GATCTACCAA TGTTTAGTAT	120
	TIGACGTATT CAATCTCTCC AGAAATACGA TITCAGTACC GAATACTGAT GAAAAGGGAC	180
10	AACCCACATA TAAGAAGATG GATATTGAGC CTAAAGACTT CTTTTGGAGG ACAAATGCGC	240
	ACTIOCCGIT COCAGACOCA GIOGAGAATG TOGAAAATOC ATTOOCAGAC TATAAGOCCG	300
15	AGGCGGAAGC GATAACCAGG AAGACAGGCG TTGACAATAT AGGCGATTTA GATCCTAACT	360
	CTCAAAATGA TACTITIGCAA ATTCAGGAGG CAGTGAACAA GTTGCCGGAA CTGACTGCTA	<b>4</b> 20
20	GCAAGAATAT CATTGATACA CATATGAATG TTCTGGCTGC GTTGTTGAAA GAGCTAGAAA	480
	ATAAAGGGTT GGATTCGTTC TTTGAAATGG AGCAACAAAG TGACTCTGCT AAGGTGAGGC	540
25	AAGCATTCAT GGACGITTTIG AAAGATGGCA AGACCAATAA CCTCAAGGAC AAGTTAAGGA	600
	CATACATAAT CATCIATITG ACTAGITICOG AGAAGCITICC CGATCAATIC GTCCAACATG	660
30	TIGAGAGITA CITCCAAGAT AATAATTICG AAACGCCAGC GITGAAGIAC TCIATAAGI	719
	(2) INFORMATION FOR SEQ ID NO:626:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1423UP	
	(A) ONGANISM: PAGI423OP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:626:	
55	GATCATCCTG TTGAACTOCA TOCTCATGTC GTCCCATGAG TACACATGAT TGAAGTCAAA	60

	CAMADETTIE COCCACTICA COTTECCECC ACECAACCIC ECAAACAATC CETCECTEGA	120
5	COGANAGICT GOGATOCCTG CAGOCACAGA GATOCOCGCA COOGTGACCA COACGATGTC	180
	COGACTOTOC TOGAGOSCAT ACCGAATGAA GICGOCOTOC COCOGCOCTCA CCAGCTCCGG	240
10	GTCACTGACG TAATGOOCTA GCTCAAATAC CGAGTTCGTC GCAGGCCTGT ACGTCAGCCG	300
	CGGCTTCCTC CGCACCGGAG CCCGGGGCCTT GCGCAGCGGC GGTAACAGCT CCTTCGGTGT	360
15	CACCICCICG CACACCCICG CCCCCCIGIC CCACCCCICI GICICCITICI TITIGACCCI	420
	CCACCCCC CTCATCCCCA CCTTCACCTT CATCCCCCAC CCCTACCCCT TCACACCCAT	480
20	ACCACCAGTA GOCTOCGTCA TOCCGCACGT TOCACAAACC TOTGCCGCTT GOTGCACTCG	540
	TOSTTOCCCC OCTOCCTOOC GTGTAGCOGA CATGAAATGA GTGACGGCGG GCCCAATTITT	600
25	OCCOSCUTTO GCTTTOGACC AATCCOGAAA ACTTATCCCC CGTAAAACAA AGGCAGGACT	660
	TCCGGTGTGG CGATACCGCC TTTTGTCGCA TGCGCTCCTG GTCCCGTTAC GCCTACATT	719
30	(2) INFORMATION FOR SEQ ID NO:627:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1424RP	
45		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:627:	
	GATCTCATCT GTATTTGGAA GGGAACGCAC CAGACGGGG TGACTCGCAG AAGCTGCCAG	60
55	AGGAGAGA AAACATAGAA AATATATTTA TATTATCTAT ATTCAGTTTA CATAAGAATG	120

	IOICAIMIT TIMIOTTIT IMMITTECH CHOCCHDIO CCCIOCAIMI CHEIMICCTI	100
5	TTATTCTAGA TTCAGTGCTA GCTAGTCGCA AGGAAATCGA TATCGTAATT CCCATTTAGA	240
	ACAAGATACA AATTAGCGAA TTTCCCGGAA AAACCGGTCT TATAATACAG CATCATTGCC	300
10	GAATCCATAC CAGTCCTTCA ATTAAACTTC CGAATCAAAA AAGOCCCGGC GCGGTCTCAA	360
15	GAATCTTTTC GCCAGTACTC GAATGGTGAC TATCAGCAAG CGACTCTTCA CTACCCGAAA	420
	CGACCAGTAT ATTIGTGTGC AGCAAATGAT TTAAGGCTCT CGAGACACCT CTTATTGGCG	480
	TOCTATGIGT TOTGTGCACG COCTGGCCCC GATAAAGAAT GCAGGTCGCC TAATAGTAAT	540
20	TACTAACCGT TTTTTAAATC GCCGTCTTGG TTGAGACCTG TGAAACGATA ATCCCATTTA	600
25	TACCAGATGA ACTOGOCOGCA CTATAGTGTC CGTAATTCAG CACTGTGGAT TCCGAGTTAG	660
	GGTGCGCGAA GTAGCAAATT TGTGTATCCT CCATAATAAG GATATCCAAT GCCAGTATAA	720
30	TAGT	724
	(2) INFORMATION FOR SEQ ID NO:628:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 720 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1424UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:628:	
	GATCATCGIA TOCACTCAGI TGTATTCTAG CATAGCCCGT GCGATTCCCG TGATTTCGAA	60
55	CCATGATCAC AGGCAAATCA CCATGAGGAG COGAGGATTC TCCGCTAAAT TCAGCTGCAT	120

	TIGLAALAAA GATGOOGIGT TICIATGOGA GOOCCITCAC ACGOOCGIAA AACATGITGG	180
5	AAATOCTOCT COCTCTOCCT TOCOCTOCCT GTGCCCTCAG CCAGACOGTC TGTTTCCTTC	240
	TAATGTGGGG GAGAGTGGTT CTACTCACGT GTTCAGCGTG CTGAATAACT TGCCTATCCT	300
10	TACASCIOCI GACCIGAGO: AATOCACGIT TOCAAGICCA ATAGICTACG GOCCCGAAGG	360
	TIGICOCGAA TOCACAGIGA TOOGIAATCI ATTACTACAG COCACTOCAA GOGIACAGAC	420
15	AACCTACAAT GACGGCGCT TGTACAATAA AATCAATTCC GCTTGCTCGA COGTTAACCC	480
	AAAGCTATAC CGTACCTTGT GTCCTTCCCT GTTTCCATTA GCCGTTGCAT GTGCTTTTTT	540
20	ACTIGIGATTA CAGAGCCTTT CTIGIAGAATG TIGIACGTGAA TITAATACTA GAGAGCTATA	600
	AAGCICICIT GITCITGIAA TGICIGITTC AGAAGATAAA AGGIAACACC AGAAAAACGAG	660
25	GTACGACCCA ACCOCTATTG GACTACGAAC TOGACAAAAA CTAAGAGTCG TAAGTAAGAA	720
30	(2) INFORMATION FOR SEQ ID NO:629:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
35	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1425RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:629:	
50	GATCACCICC CACTIOGITG CAACAGIATI OCIGAGACIA ICATICITGI AGACCGATIC	60
	TIGIGAAGCA GITGGCCCGG TGIATGAAAC CGCGIGTTTA CCAAGIGGAG GCCTFIGITC	120
55	AGAAATTTTA GITCCITCTC GAACGTATTC GTGGTCCTGG AGAATAAAGT TTTGTTGCTC	180

	GACATAGTCA GOGTCAAAAA CATTCACAGG TGTGTCATCA TATGGCGGCC GGCTGCCGGA	240
5	OGITIGIOGGA TOAGOCCITTIC TOTTOOCCITIC CGAGTICTOCCA ACCUTOGAGA TAGCTITTIGA	300
	TAAGTTGTAG AAGTCGTCCA AAATATCGTC TTCGCCGAGA GGAGCAACGC TCGAGCCCCT	360
10	GAACAGIGAT CCACTAGAAC TICITOCAGT ACCCTCOCCG TCACCATTAT TOCTATIGIG	420
	TGTACTOCTC GAGTTGCGCA GATTAGATAT ATCAAACTGT TTCGATTGTG TGGAACCTTT	480
15	ATATTCATCA TATOCTCCAA AAGAATCTCT OCTTTOCOGA GAGCCTCOCG CTOCATGAGG	540
	AGGAGGAGCC ATRAAAAGATG AATCCCTGCC AGGAGAGTTIG TGTAACCGCC CAAATGGTGA	600
20	TOCAGOGIAG TIGICATAAA TIIGAACCAG ATCIGCACOC GACTIGIACA GGICCCTGGG	660
	GITGIATOCT GCCTTGGGGT CGCCAACTIC TTTAATGGAC CCGAAGAAGC	710
25	(2) INFORMATION FOR SEQ ID NO:630:	
	(i) SEQUENCE CHARACTERISTICS:	
30	(A) LENGTH: 711 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1425UP	
40	(A) ORGANISM: PASI4250P	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:630:	
	GATCATACAC GCGCTGCGCA TACAGTTGGC CAGCACCAGC ACCCGCGACA GCCTCCAACG	60
50	OCTAGAGACG GACACCOCAG GOCTTGTCOC CCACGACCTT TCCCOCTGGG CCGACAGCAC	120
	CAATGCATAC ATAAACGGCA CAGAGGCCTC CGTAAATGCC GGCCTCCTCG GCTGGGTTAC	180
55	CACAGCCACT ACAGCCCTCA ATACCACCGT COCCGCCCTG CTCGCCCACA TOGATTCCAC	240

	CONCORCO CONTROCAS ALACOCCACT TOACOCCCC ATOSTICACOS TIGICTOCTIC	300
5	TGTAATCGGG AACAAGTTGC GOGCCATOGA GGCAGGCCTC ACCTGGACCC ACGACCACGT	360
	ACGCATCGCC CTGCCGCGCA TCCATACCGC CCGCCTTCGC GACGCTGTGG CAGAACCAGA	420
10	CCTTCCAACC CATCCCGCCT ACACAGCCGT GCTCCAGTCC CTCAGTGACC GCTTACGTCA	480
	TICOGITICAC COTOTOCTAC ATCACTOCTO TOCCOCOGCIC COCATTICAAC TCTACGTATC	540
15	CONTROCCCIG CICCOCCCICI CONTROCA CACACCTCIC COCTICOCA TOCTOCIATI	600
	CAAGTOGCAC TOCCGTOGCA GGAACCTOGG CCGCAGAATG CCTTGAGCCT AATTCTTACA	660
20	TAATCITAAT TOGOCATTOT GOTOCTOGAA CAOGAACTOC GOGITAGOOG G	711
	(2) INFORMATION FOR SEQ ID NO:631:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(Vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1426RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:631:	
45	CATCTTCTCT COGCTOGACG TCACTGGCGG CATGCACGAC GCCATGAACT GCTGCTGCCG	60
	CICCIGATOG CCCTOGTICCA CTICCTAGCOG CGACTICCCC TCCAGAAAACC CCCCCATCTT	120
50	CITICOCATCC TOCACCACCAC CCACCACATG COCAAACCACC COCTOCCTOC CTOCTTTCCC	180
	TAGCTGAAAC GAAACAAGAC GCCCTATAGG CGCGCTGCCT AGCATATACA CCCACGGGAC	240
55	ACCCATAACA GCCCTTCTAA CCCTCAACCG AGTCACTGAG AACTGGGGTA GTGCGCATCA	300

	TOGACCTOCC GATTITICAT TOTAGTGAAT AATOCTTACA COGCCAACAC AAAGGCAGCT	360
5	TCACCACCAT TCTGGCTCAA CTAGGAGGGG TGTCGGGGGGA ACCAGGAACG CGTTACTCGG	420
	TAAGCGGGCA TCTAGTCAAG TGGGCAGTTG CAGGCGACTT CTTTTTGTGT GTTATTCAGG	480
10	GIGTAGGATG CITGITATAG GGTTGACAGG AGGTATTGCA TGCGGCAAGT CGACGGTGTC	540
	OCCEPACITY CACCACCAT ACCOCATICCC GETCATOCAT COCCATICCA TTGCCCCCCA	600
15	CATTATOCOG CCOSOSCACC GOCCTIACCA CGOCTOCTOG AACOCTITICA GCAACOGCTIC	660
	CCGCAACTGG TGCAGGCGAA CGGGGAGCTG AACCGCGGGG CGCTGGGGGC GTGGATCTTC	720
20	CA	722
	(2) INFORMATION FOR SEQ ID NO:632:	
25	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1426UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:632:	
45	GATCTOCTOC ACCOCCTOCT TGAACCAATC TCCAGAAGAG TGTCCCCCTC GTCAAGAACC	60
	TIGAACICAA CCTCGGIAAA GIACTITIGGA CCGCAAGCCT CGAGCATGTC GATCAACCGG	120
50	CCGGGCGTGG CAACCACGAT ATTGGGCCTC CTGCGCTCTA GGGATCTGAA AGTTTCAGTC	180
	COCCAGCACC COCCCATCAT CACAACCOCA TICAAACCOC CAACCTICCT GITGOCOTIG	240
55	COCATCTCCT TGATCTCGTT GAAGATCTCC CCCCCCAAGT CCCTCGTTCG TCCAATCACA	300

	ALAGCCITGA CATTITUTGA AGGAGGCCCC TOCAAGAGCC GCTGGAACAG CGGCATCAGA	360
5	AACGCAAGTG TCTTACCTGT TCCAGTTTTC GCCCGTGCCA CCACATCGTG CTCCGTCTGC	420
	AGGATCOOCT TCAGCGTCTT CTGCTGCACC GGTGTTAGTT TATCGAAGCC GCGTGACTGC	480
10	AGCATCTOGT ACAGCTOGIT GOTGAGCACG COCTOCTOCA COAAGGTCCG CGGTGTGCTT	540
	TOGACCOCCG CAGCITOGIC GOCCACACGO ACCACCITOGG TGITGGGGCC GAGGCTGAAT	600
15	COCTOBOBOG COCOCCGTC TGTACOSCOC CGTCTGCCCT GTGGCTTCCG CCACATGCCC	660
	CCGCGGGGGAC CACGCTCACC ATCCTCCCTG TCGCTGCCCG GCT	703
20	(2) INFORMATION FOR SEQ ID NO:633:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 711 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
	(b) 1010boll. Illient	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1427RP	
35		
<b>4</b> 0	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:633:	
	CATCTITICTA TCCCCCAAAG ACTCCATCCA ATACAAGGIG CITCTAGAAG COCCCTATOG	60
45	AAACACCATT CCGCGGCTTG CTGCTCCTGA CCGGCGCTAC GTGGGGGCCA GCGCAGGTCT	120
	TOCCTIAGCA COCCICTACC CACACTICCT CICICIGITIC CACAACCAAA COCACTICAC	180
50	CCATTCATTC TACTOGATTA TAAATGACCT TTCATATCTG CATTGGFFTT COCATGAGCT	240
50	THE TAXABLET TRAINING CATTOSTTT COCATOASCT	240
50	CAGGTACCTG GCGGACCGGA ACTGCGACAT CAAAATTATT TACACGAGGA GCAATGAGTC	300

TGACCATTTC COCTATGCTG TGAAATCTAG CATCACGGC AAACTCCAG? GTCATGTCGA  CCTACAGGAG GAAACCTACA CCTGGTNGAT AGATACCATC TTATTAGTTA ATTGTACTTA  TTTATTCCTC TTCCTGTATC TTAAGCAAAT CCCGCCATGT CTCAACCACC TTCTGCATGC  (2) INFORMATION FOR SEQ ID NO:634:  (3) SEQUENCE CHARACTERISTICS:  (A) LENSTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTTG TCCATGCCCT TGGGGCCCAG CGACGGTTCT GACGAGGGG CGACTGCTCT  GGCAGCAATA ATGTTCGCCT TGGGGCCCAG CGACGGTTCT TGGAGGTGC CGACTGCTCT  ATTGCTGCCA CTGACCTTCG GTGGCCATCT AATATACCTTC CTGATTCCCC GCCCCAGAAG  CCTTACTTGC TGCTAGAGGAA GTTAAACGTTG TTTGTTTATG CTGACAACCC CTAAGTTACC  GTCAAAACGAT CACATTTTTG CCACTGCGAAT TTCCCTTCGT ACAAAACGGAT ACTTGATCCT  TTGATCTCCA AGACCTGTTC CATCGCGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT  TTGATCTCCA AGACCTGTTC CATCGCGAAT TTCCCTTCGT TATGTCCCGGG TTGAAACGGAA  AND TTCAAACCAT CACATTTTTG CCACTCCGAAT TTCCCTTCGT ACAAAACGGAT ACTTGAAACGAA  AND TTCAACCTCCA AGACCTGTTC CATCGCGAAT TTCCCTTCGT TATGTCCCGGG TTCAAAACGGAA  AND TTCAACCACATTCTC CATCGCGAAT TTCCCTTCGT TATGTCCCGGG TTCAAAACGGAA  AND TTCAAACCAT CACATTTTTG CCACTCCGAAT TTCCCTTCGT TATGTCCCGGGGAT ACTTGAAACGGAA  AND TTCAAACCAT CACATTTTTG CCACTCCGAAT TTCCCTTCGT TATGTCCCGGGG TTCAAAACGGAA  AND TTCAAACCAT CACATTTTTG CCACTCCGGAAT TTCCCTTCGT TATGTCCCGGGGAT TTCAAACGGAAA  AND TTCAAACCAT CACATTTTTG CCACTCCGGAGT TTCAAACGGAAA  AND TTCAACCACATTCTCAATTTTTG CCCACCGGAGGTTC TATGTCCCACACCC CTAAGTTCCCACACCC CTAAGTTCCCACACCC CTAAGTTCCCACACCCACACCCACACCCACACCACCACACCCACACCACCACA		GCATATCTGC AGGCTCCTCC TGCGCCCAGA TCTCAAAGAG ATGGTGGAAG AGCAGATCCT	420
TITATICCTC TECCTORIAC CETGGINEAT ACATACCATC TEATRAGITA ATTGIACTEA  TITATICCTC TECCTORIAC TEAACCAAAT CCCGCCATGT CTCAACCACC TECTGCATCC  661  TITATICCTC TECCTGTATC TEAACCAAAT CCCGCCATGT CTCAACCACC TECTGCATCC  661  15 TITECCGATT CACCCTGCC TCGACCACGT CCAGAGGIAC CTGGITTICC G  (1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STANDEDINESS: single  (D) TOPOLOGY: linear  (ii) NOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP  16  GATCATCTIG TCCATGCCCT TGGGGCCCAG CCACGTTCTG ATCGCATCCG CCACTGCTCT  60  GGCACCAATA ATGTTCGCCT TGGGGCCACG CCACGTTCTG CCCCCACAAG 180  45  ATTGCTGCCA CTGACCTTCG GTGCCATCTT AATATACTTC CTCACTCCC CCCCCCACAG 180  CCTTACTTGC TCCTACACCAA GTTAACGTTG TTTGTTTATG CTCACAACGC CTAAGTTACC 240  50  GTCAAACCAT CACATTTTTG CCACTGCAAT TTCCCTTCGT ACAAACGCAT ACTTGATCCT 300  TTGATCTCCA AGACCTGTC CATCGGGAT TCCCTTCGT ACAAACGCAT ACTTGATCCT 300  AATCGCGCACAACTTC CATCGGGAT TCCCCTTCGT ACAAACGCAT ACTTGATCCT 300  TTGATCTCCA AGACCTGTC CATCGGGAT TCCCCTTCGT ACAAACGCAT ACTTGATCCT 300  AATCGCGCCACACTTG GGAAATGTC ACCCTGCAG TAGTGCCCGGG TTGAAGCGAAA 360  AATCGCGCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	5	OCTOTOGTOT AACCAGOCAC AGGACGTCAC GITTATTAGC AGCGGCCCTT CGACCTTTAA	480
TITATICCTC TROUTGIATE TRANSCAAAT COCCCATGT CTCAACCAC TROTCCATCC  15  TITACCGATT GACCCTCC TOGACCACGT CCAGAGGTAC CTGATTTCC G  (2) INFORMATION FOR SEQ ID NO:634:  (2) INFORMATION FOR SEQ ID NO:634:  (3) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STRANDENNESS: single  (D) TOFOLOGY: linear  (11) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAGI427UP  35  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCAGCCCT TOGGCCCAG CGACGTTCTG ATGCATCCG CGACTGCTCT  GGCAGCAAATA ATGTTCCCCT TICTCACTTC CTGCGGCTTC TOGGGTTTT TGAAGGTCCC  ATTOCTGCCA CTGACCTTCG GTGCCATCTT AATATACTTC CTGATTCCCC GCCCCAGAG 186  CCTTACTTCC TOCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACCC CTAAGTTACC  46  GTCAAACCAT CACATTTTTG CCACTGCAAT TCCCCTTCGT ACAAACCGAT ACTTGATCCT  30  TTGATCTCCA AGACCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGGAT  AATGCGGGGCT CGACAACTTC GGAAATGTCT ACGGATGTGGC GCCCGGGAA ACACGGAT ACTTGATCCT  AATGCGGGGCT CGACAACTTG GGAAATGTCT ACGGATGTGGC GCCCGGGAA ACACGGAT ACTTGATCCT  AATGCGGGGCT CGACAACTTG GGAAATGTCT ACGGATGGGGG GCCTGCTGAG TAGTGCCGGGAT ACTTGATCCT  AATGCGGGGCT CGACAACTTG GGAAATGTCT ACGGATGGGGG GCCTGCTGAG TAGTGCCGGGAT ACTTGATCCT  AATGCGGGGCT CGACAACTTG GGAAATGTCT ACGGATGGGGGGGGGG		TGACCATTTC COCTATOCTG TGAAATCTAG CATCACOOOC AAACTCCAGT GTGATGTCGA	540
15  TITGOGGAPT GAGCCCIGCC TUGACCAGGI CCAGAGGIAC CIGGITITICC G  (2) INFORMATION FOR SEQ ID NO:634:  (3) SEQUENCE CHARACTERISTICS:  (A) LENGIH: 718 base pairs  (B) TYPE: Incleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) CRIGINAL SOURCE:  (A) CRCANISM: PAGI427UP  36  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATOCCCT TOGGGCCCAG CGACGITCTG ATCOCATCCG CGACTOCTCT  GCCAGCCATA ATGITCCCCT TUCCACTTC CTCCGGCTTC TUGACGGTTCT TUGAACGTCGC  ATTGCTGGCA CTGACCTTCG GIGGCCATCTT ANTATACTTC CTGATTCCCC CGCCCAGAAG  ATTGCTGGCA CTGACCTTCG GIGGCCATCTT ANTATACTTC CTGATTCCCC CCCCCAGAAG  CCTTACTTCC TGCTAGAGAA GITAACGTTG TTTGCTTCGT ACAAACGGAT ACTTGATCCT  30  GTCAAAACGAT CAGATTTTTG CCACTGCGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT  30  TTGATCTCCA AGACCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGAA  AATCGGGGCT CGACAACTTTG GGAAAATGTCT AAGGGAGGACG GGGCGTTTAAC ACGGATTCCG  AATCGGGGCT CGACAACTTTG GGAAAATGTCT AAGGGAGGACG GGGCGTTTAAC ACGGATTCCG	10	CCTAGAGGAG GAAAGCTACA CCTGGTAGAT AGATACCATC TTATTAGTTA ATTGTACTTA	600
(2) INFORMATION FOR SEQ ID NO:634:  (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 718 base pairs (B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1427UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATOCCCT TOGGGCCAG CGACGITCTG ATCGCATCCG CGACTGCTCT (GCACCAATA ATGTTCCCCT TOGGGCCAG CGACGITCTT CGACGGCCC CTAACTTACC  AFTICCTOCCA CTGACCTTCG GTGCCATCTT AATATACTTC CTGATTCCCC GCCCCAGAAG  CCTTACTTGC TCCTAGACAAA GTTAACGTTG TTTGTTTTATG CTGACAACCC CTAACTTACCC  GTCAAAACCAT CAGATTTTTG CCACTGCGAAT TTCCCTTCCGT TACACACCC CTAACTTACCC 300  TTGATCTCCA AGACCTGTC CATCGGCATG GCCTCCTCAG TACTGCCCCCCAAAA  AATUGGGCCCT CCACACCTTC CATCGGCATG GCCTCCTCAG TACTGCCCCCCAAAAAAAAACCCAT ACTTCATCCCT 300  TTGATCTCCA AGACCTGTC CATCGGCATG GCCTCCTCAG TACTGCCCCCCAAAAACCCAAAACCCCC AAAACCCCAAAACCCCC TTCAACCCCCCAAAACCCCCCCC		TITATICCIC TICCIGIATC TIAAGCAAAT CCCCCCAIGT CICAACCAGC TICTGCAIGC	660
(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STRANDENESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: INA (genomic)  (vi) CRIGINAL SOURCE:  (A) CREANISM: PAG1427UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (GATCATCTIG TOCATCCCCT TESCRIPTION: SEQ ID NO:634:  40 GENACAATA ANGITECCCT TECCRICTIC CICCOCCTIC TECCRITICT TEAACGICGC  ATTOCTOCA CICACCTICG GIOSCATCTI AATATACTIC CICATCCCC GECCCAGAAG  ATTOCTOCA CICACCTICG GIOSCATCTI AATATACTIC CICACAACCC CTAAGITACC  45 GICAAACGAT CACATTITIG CEACTGCAAT TECCTICGT ACAAACGGAT ACTICATCCT  50 GICAAACGAT CACATTITIG CEACTGCGAAT TECCTICGT ACAAACGGAT ACTICATCCT  TIGAICTCCA AGACCTGTC CATCGGGATG GECTGCTGAG TAGTGCCGGG TICAAACGGAA  AAIUGGGGCT CGACAACTTG GGAAATGGCT ACGGGGGG GGGGGTGTAAC ACGGATTTGCG	15	TITIGOGGATT GAGOCCTIGOC TOGACCACGT CCAGAGGTAC CTGGTTTTCC G	711
(A) LENGTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATGCCCT TOGGGCCCAG CCACGTTCTG ATCCCATCCG CGACTGCTCT  (GCCACCAATA ATGTTCGCCT TICTCACTTC CTGCGGCTTC TCGCGGTTTT TGAAGGTCGC  ATTGCTGGCA CTGACCTTCG GTGGCATCTT AATATACTTC CTGATCCGC GCCCCAGAAG  CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAAGGC CTAAGTTACC  GTCAAACCAT CACATTTTTG CCACTGCAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT  GTCAAACCAT CACATTTTTG CCACTGCAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGAGG CGGCGTTAACGCAA  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGAGG CGGCGTTAACGCAA		(2) INFORMATION FOR SEQ ID NO:634:	
(A) LENGTH: 718 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (SEQUENCE DESCRIPTION: SEQ ID NO:634:  (SEQUENCE TOCATOCCCT TOCCCCANGE CONCEPTED ATCOCATOCG CONCENTED 120  GOCAGOLARIA ATGITICOCCT TICTICACTIC CICCOCCTIC TOCCCGITTT TOCACGICOC 120  ATTICCTOCCA CIGACCTICG GIGGOCATCTT ANTATACTIC CICCATOCCC GOCCCAGAAG 180  CCTTACTIGC TOCTAGAGAA GITAAGGTIG TITGITTATIG CICACAAGGC CITAAGITACC 240  GICAAACCAT CACATTITTIG COACTOCAAT TICCCTICGT ACAAACCGAT ACTICATOCCT 300  TIGAICTICA AGACCIGITC CATCOCGATG GCCTOCTCAG TAGICCCCCCC 300  AATCOCCCC COACAACTIC GCAAACTGCT ACGCAGGACG GCCCUTTAAC ACGCATTCCCC 420	20	(i) SEQUENCE CHARACTERISTICS:	
(C) STRANDEINESS: single (D) TOPOLOGY: linear  (iii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1427UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (SI) SEQUENCE DESCRIPTIO			
(ii) MOLECULE TYPE: DNA (genomic)  (vi) CRIGINAL SOURCE: (A) ORGANISM: PAG1427UP  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIC TOCATGOCOT TOCACCOCAG COACGITUTE ATCOCATOCG COACGICCTOT  GOCCACCAATA ATGITOCCCT TICTCACTIC CTGCGGCTTC TOCACGITTT TOCACGICGC 120  ATTICCTOCCA CTGACCTTCG GIGGCATCTT AATATACTTC CTGATTCCCC GCCCCAGAAG 180  CCTTACTTCC TOCTAGAGAA GITAAGGTTG TITGITTATG CTGACAAGGC CTAAGTTACC 240  GTCAAACCAT CAGATTTTTG CCACTGGAAT TICCCTTCGT ACAAAGGGAT ACTTGATCCT 300  TTGATCTCCA AGACCTGTC CATCGGGATG GCCTGCTGA TAGTGCCGGG TTGAAGGGAA 360  AATCGGGCCT CGACAACTTG GGAAATGTCT ACGGAGGACG CGGCGTTAAC AGGGATTCCGG			
(ii) MOLECULE TYPE: INA (genomic)  (vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1427UP  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATGCCCT TOCGGCCCAG CCACGITCTG ATCGCATCCG CGACTGCTCT 6(  GCCAGCAATA ATGTTCCCCT TTCTCACTTC CTGCGGCTTT TGAACGTCGC 12(  ATTGCTGGCA CTGACCTTCG GTGCCATCTT AATATACTTC CTGATTCCGC GCCCCAGAAG 18(  CCTTACTTGC TGCTAGAGAA GTTAACGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 24(  GTCAAACCAT CACATTTTTG CCACTGCAAT TTCCCTTCGT ACAAACGCAT ACTTGATCCT 30(  TTGATCTCCA AGACCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGCAA 36(  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGGACG GGCGGTTAAC AGGGATTGCGG 420		(C) STRANDEDNESS: single	
(VI) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (XI) SEQUENCE DESCRI	25	(D) TOPOLOGY: linear	
(VI) ORIGINAL SOURCE:  (A) ORGANISM: PAG1427UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:634:  (XI) SEQUENCE DESCRI		(ii) MOLECULE TYPE: DNA (genomic)	
(A) ORGANISM: PAGI427UP  (XI) SEQUENCE DESCRIPTION: SEQ ID NO:634:	30	(vi) ORIGINAL SOURCE	
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATGCCCT TGGGGCCCAG CGACGTTCTG ATCGCATCCG CGACTGCTCT 6( GGCAGCAATA ATGTTCGCCT TTCTCACTTC CTGCGGCTTC TCGCGGTTTT TGAAGGTCGC 12( ATTGCTGGCA CTGACCTTCG GTGGCATCTT AATATACTTC CTGATTCCGC GCCCCAGAAG 18( CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 24( GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT 30( TTGATCTCCA AGAGCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGCAAA 36( AATCGGGCCT CGACAACTTG GGAAATGTCT ACGGAGGACG CGCCGTTTAAC ACGGATTCCGG 420			
(XI) SEQUENCE DESCRIPTION: SEQ ID NO:634:  GATCATCTIG TOCATGCCCT TGGGGGCCCAG CGACGITCTG ATCGCATCCG CGACTGCTCT 6( GGCAGCAATA ATGITCGCCT TTCTCACTTC CTGCGGCTTC TCGCGGTTTT TGAACGICGC 12( ATTGCTGGCA CTGACCTTCG GTGGCATCTT AATATACTTC CTGATTCCCC GCCCCAGAAG 18( CCTTACTTCC TGCTAGACAA GITAACGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 24( GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT 30( TTGATCTCCA AGACCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA 36( AATCGGGGCT CGACAACTTG GGAAATGTCT ACGCAGGACG CGCCGGTTAAC ACGCATCGGG		(ii) GREATER PROTECTOR	
GATCATCTTG TCCATGCCCT TGGGGGCCAG CGACGTTCTG ATGGCATGCG CGACTGCTCT 60  GGCAGCAATA ATGTTCGCCT TTCTCACTTC CTGCGGCTTC TCGCGGTTTT TGAACGTCGC 120  ATTGCTGGCA CTGACCTTCG GTGGCATCTT AATATACTTC CTGATTCCGC GCCCCAGAAG 180  CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 240  GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT 300  TTGATCTCCA AGACCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA 360  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGGGG GCCCGTTAAC AGGGATTCCG 420	35		
GCCACCAATA ATCITCCCCT TICTCACTIC CIGCOCCTIC TCGCGGTTTT TGAACGICGC 120  ATTICCIGGCA CIGACCTICG GIGGCATCTT AATATACTIC CIGATTCCCC GCCCCAGAAG 180  CCTTACTICC TCCTAGAGAA GITAAGGITG TITGITTTATG CIGACAACGC CTAAGTTACC 240  GICAAACGAT CAGATTTTIG CCACTGGAAT TICCCTICGT ACAAACGGAT ACTIGATCCT 300  TIGATCTCCA AGACCTGTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA 360  AATCGGGGCT CGACAACTTG GCAAATGTCT ACGGAGACG CGCCGTTAAC ACGGATTCCG 420		(xi) SEQUENCE DESCRIPTION: SEQ ID NO:634:	
ATTOCTOSCA CTGACCTTCG GTGGCATCTT AATATACTTC CTGATTCCGC GCCCCAGAAG 180  CCTTACTTGC TGCTAGAGAA GTTAAGGTTG TTTGTTTATG CTGACAACGC CTAAGTTACC 240  GTCAAACGAT CAGATTTTTG CCACTGGAAT TTCCCTTCGT ACAAACGGAT ACTTGATCCT 300  TTGATCTCCA AGAGCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA 360  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGGACG CGCCGTTAAC ACGGATTCCG 420	40	CATCATCTTG TOCATGCCCT TGGGGCCCAG CGACGTTCTG ATCGCATCCG CGACTGCTCT	60
CCTTACTICC TECTAGAGAA GITAAGGITG TITGITTATG CIGACAAGGC CTAAGITACC 240  GICAAACGAT CAGATTITIG CCACTGGAAT TICCCTICGT ACAAACGGAT ACTIGATCCT 300  TIGATCTICCA AGAGCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TIGAAGGGAA 360  AATCGGGGCT CGACAACTIG GGAAATGICT ACGGAGGACG CGCCGTTAAC ACGGATTCCG 420		GGCAGCAATA ATGITCGCCT TICICACTIC CIGCGGCTIC TCGCGGTTTT TGAACGICGC	120
GTCAAACGAT CAGATTTTG CCACTGGAAT TICCCTTCGT ACAAACGGAT ACTTGATCCT 300  TIGATCTCCA AGAGCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA 360  AATCGGGGCT CGACAACTTG GGAAATGTCT ACGGAGGACG CGGCGTTAAC ACGGATTTCG 420	45	ATTOCTOCCA CTGACCTTCG GTCCCATCTT AATATACTTC CTGATTCCCC GCCCCAGAAG	180
TIGATOTICA AGAGOTIGITO CATOGGGATG GOOTICAG TAGTIGOCOGG TIGAAGOGAA 360  AATOGGGGT CGACAACTIG GGAAATGTOT ACGGAGGACG (CGCGTTAAC ACGGATCCCC 420		CCTTACTTGC TGCTAGAGAA GITAAGGTTG TITGTTTATG CTGACAAGGC CTAAGTTACC	240
AATCOOCCT CGACAACTTG CGAAAATGTCT ACCGACGACG (CCCCGTTIAAC ACCGATCCCC 420	50	GICAAACGAT CAGATTTTIG CCACTGGAAT TICCCTICGT ACAAACGGAT ACTIGATCCT	300
AATCGGGGCT CGACAACTTG GGAAAATGTCT ACGGAGGACG CGGCGTTAAC AGGGATCGCG 420		TIGATCTCCA AGAGCTGTTC CATCGGGATG GCCTGCTGAG TAGTGCCGGG TTGAAGGGAA	360
	55	AATCOOOCT CGACAACTTG GGAAATGTCT ACOCAGGACG COOCGTTAAC ACOCGATCOCG	420

	CICALCOCAD ADCICAAAAA AAAAIGCOCG TITIICCADCI GGIATGAGGC GITCAAGGC	480
5	CACACTOGGC GGGCGGAGGT GATTICGGCCG CTIGCCCCGAGG AGTTGGTGAG CTIACGTGGAT	540
	CAGCOCGGGA TCAGGCTGGC GCGCGAAGAA GGCTCGAAGT ATTTCTACGG CCAGGAATGG	600
10	ACCUTACCAC GCACGGACAG TACAGCGACT GOCAAGGGGG CGACAGCGGC AGTGAGCGGT	660
	CGITCGTGCC GCTGCACCGG TGGCGCACTT CCCGCAAGTG CACGCGCGGG TGAAGCAG	718
15	(2) INFORMATION FOR SEQ ID NO:635:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 723 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1428RP	
	(wi) officers are also as a second of the se	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:635:	
	GATCATACAC GCATTGCAGG TATACATTAT AGTGCTCATA ATTATCGGAT TGCAAATAGA	60
40	ATGGGGCCCT TACCGTAGTA CTGTCTTGGT AATGCAGCGA CGCTCAGGCT TAAGAAGCTT	120
	TITGITCTCC GIGTATTACT AACAAAATAA TITCCTCGAG CACAGGGAGT AGAGATGAAT	180
45	TACATAATOC ATATOGACAC CIOGICACCT TCCAGOGACA TTAACATTIC CITATGAATG	240
	CCCAATAATG GTOCCTAAAT GATGTOCTTG GTGTAATOCG CATTATAAAA TGTATGTOCA	300
50	TTATATATIG TITGIAGCAT CTAGTAGAAC CATGGTAGCG AGGICTITGG CCATACCCTT	360
	CTGAAGAGAG ACATAGCAAC AGTGTCTTGT GCAGACAGTC TGCCGTCGAA TGTTGCCTTG	<b>4</b> 20
55	AAGTAACCAT GAGTACCAAG ACTICTICCTTA ATGAAGCCAG AGCGTCCAGA TTTCGTGAAT	480

	AGTGGGATGG ACTTGAACCA CTCGACATCT TCTGGCCTAA AGAACATATA GCGCACTGTG	540
5	ACCACGCCCT TGTGGAACTT GAATGGATGG CCAGTTAATA TGATTCTCTT GGCCAATATC	600
	CONTRIBUTE CHOOCHTCAG GAACOTOCCG TOOCCCACGA ACGICAGOCC CTTTOCATCA	660
10	GAGGOGITTT CITTGAAGTA GATGOCCGGT GACTGGGTCA GGTCCAAGGG AAGCATGCAT	720
	GTC	723
15	(2) INFORMATION FOR SEQ ID NO:636:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 726 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1428UP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:636:	
	GATCAAACCA GAGTGOGAAG COCACACGCG GCACTGGCGG GAGCCCTTAC CGTAGTTTCT	60
40	TOOGTOOGAG AACCAAACGT TTTCGTGAGC CATCTTGTCT GCAATGCGTT AGTACTCTGT	120
	CTGACCGCTT GGAAGCGCTC CGGCCCTCGT GAGCTGCCCA CACGCTCGGC GTCTGCGGGC	180
45	TOCTICATIFIC COGCACOGTA TICTOCTCOC ACOGACAGOT CTAGACCACA CTITOGCCCCA	240
	TOCTOTOCAC ATACGATTAT GCTTTGTCTC TTOGTATTAT CCTTAGATTC GCTAGACTTC	300
50	GACACTATOG TTATCACCAC TGTTGAAGTC TGCTTCGGTT GGCACCCAAA GTCTCGGGAC	360
	TGTAG:TGGA AAGCGCAGTT CGCGGCAAAT CAAGCATCTC ATAATGTGTG GGTGCAACCG	420
55	TIGANIGIGI GOGIOCAACA GICANITGIA ATTICITITI TIGAICGAGA GATGOGATGC	480

	GAIGHECTAG TIGAAAAATT TTAGTATOOC AAAACTOOCA TOCATATCTG AGATOOCCA	540
5	TCAATTGCGG CAGCTTAGTG TTAGACGACC AATCCAGAGG TGGTAATTGG GCTATGGCAG	600
	GICACTOGCA CAGGTOGTOG GTAAAAAAGG GCCACAAAAC GTTCAAGTOG AAGCATGOGA	660
10	GCAAGGGGG GITIGAAACGG CTGCACAAGG GCAAAGTGGA ACAGGAGACC GCTGCTGGGG	720
	TGAAGG	726
15	(2) INFORMATION FOR SEQ ID NO:637:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1429RP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:637:	
	CATCAAAGIT TAGCATGIAA ATGIGCAACA AACTATTTAT TACCTCTGCA CTGCCCATGI	60
40	CGCTTGAAAC CGCCGAGGAT CCAAACCAGT GCTTTCATAA TGGAATTGCA AAATTGAGTG	120
	CAGIAATIGA TAAGIATCITI GAGAAAAGCC CICCOGACIT TACOCIAGAT GATICCITAA	180
45	TATGITCAAA AGCCTCCGAG TTAATAAAAA GGCTTGCTAC ATCCAAGGTG CATATAGATG	240
	TGATAGATGA GACTAACAGC ACCATTCATA AAAAGCGGAA GCGCAATTTT CGAATCACAT	300
50	CACCCAGAGC AGTATACACA TCCATTTOGA ATGTCGTATT AAGAAAGTTG GATAGCGTTG	360
	TOGACCAAGG AAAGGTAGAA ACCGTOCAAT COTTTGATCA GATACTTGAG AATTTCCTTA	420
55	TTAACTIGAA AGAAGTCGAC TTTACTCTAT C10000TTGC TCTGATGTAT ACCACTATIG	480

	ACTACTOGRA CCCCCACATG ATCCCAGGCT ACGGCAAAGT TACGACTGTA GAGCATTTCC	540
5	TOSTOCASTA TATCTTACAT CGATATGAGG TATTATATGT GOCCOGCGAT GAAAGCCTAC	600
	TAGATAGICT GGTIGGIGCC ACTATICGGA AGCTATITGA ATGCATGCAG TCACAGCATG	660
10	ACCACCAGAG CCTGGTAGCG AATAGCCAGG CTGATACCGC ACGAAGAGAT AT	712
	(2) INFORMATION FOR SEQ ID NO:638:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1429UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:638:	
35	GATCAACCGA TAGCGGAAGG CGGACGAGCC TCGGAAATAG TACTAGGCAG TGGTTGGCTT	60
	TIGITITIAG CIGIGITICA ACATGICAGO GAGAACAAGO AGGGAGGCAG GCGCCICCAG	120
40	GGIGATGGGA GGTCGGAGTA GTATGGATGG AAAGTCCGGG ACAGGAACAG GGTATTTGGA	180
	ACAGCIGAAC TCGCCAAGCA TICAGAAGCT CATGCACTCG GACGCTTCCA CGACAGCACT	240
45	ATTOGAGAGG TIGAAGATGT COCTAGTGAC TTGCGTGGAG TTCACGAAGT TCATAAGAAA	300
	GAAATACTIG CTAGAAGAGG GCCATGCGCA GGAGATGGGC AAGGCTTATA AGAACTICTT	360
50	TCCGGAGGGC GGTGAGTGCA GCTTGCAGAA TAGCATACAT AAGGTTTTGG AGTATGACGG	420
	AAAACITGCG CAGGIGAAAC TITCATATGT TGCTGCGITG CAGAAGATGT ACGATGAGTT	480
55	AACGTOOCTT CTTOCATOCA TGACTAAAAT GOOCAAATOC CTCAAGGAGA GCAGTOOGOG	540

	GIIGGAAAAA GAAGICGCAG AIGCTATACA TAGCGCCGAA AAGGCAAAGG CAAGATATAT	600
5	GTCCTTGTGC ATGGATTGGG AGAAGCTCAA GCTTGTAGAT CCTGCAAAGA CGAAGTTGAC	660
	ATTOCOGOC TCAAAGACCA CTCGAGACCA GCAAGAGGAC TTATTAGAAA GATTGATA	718
10	(2) INFORMATION FOR SEQ ID NO:639:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 730 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1430RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:639:	
30	GATCOCAGAG AGACACAATG TCCCTGTOCC CACTITIGICT ATOCTITATIC ATTITATICAT	60
35	TCTTGTGCAG GGGAAAACTG AAGGCCCAAC AGGGAATTGT CAACCATGTT TAAACTTTTC	120
	CATGIGCATG GAGCICCGIA TGTAGCAATA TATTCTCATA GCTAGAGATC TCACTATATA	180
40	TRACCITIOSC ACATITATOS CATATOGACO TROGITITIO TACACCITIO TOSCAGOSTAG	240
	CAGGGGCCGC ACATAACTAG TTATAAAAAC GATGCCGCCG GAGAACGAGA TCTACTATCT	300
45	CTCTGAGTAG GCACAGTTTC CAACGTATTA GTCCTTAATG AGCAAGCGAA TCATTCAACT	360
	CATACTICIC TCIGCCTTIG COCGAGCTAA TTACGIGGAG CCCTICAAAT CAAATCCATA	420
50	CATTOCTTOC TCAGAGGCAA GCCATTGCCC AAAGGAATGG CCATGCTGCT CGCAATATGG	480
	ACAATGCGGG AGTGGGCCGC TATGCATTAG TGGCTGCAAC CCAAAATTCT CGCATAGCCC	540
55	TGAGAGCTOC GTGCCAGTOC COOCCCTACT ACCGCAATTG GAGATAGTGG CCAGCGATGA	600

	TAMAGAGIA TACCTAGAGA TGTCGGGTCA GCCTGCCTTG GTCACAAAGI TCCACCCAA	660
5	GASCICOSCO CAGTIGITICS ASSTACATCA CGASCAACAG CAGTATOGIC IGICOCCAIT	720
	AGAGCAGGAC	730
10	(2) INFORMATION FOR SEQ ID NO:640:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1430UP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:640:	
	CATCGATTIC GITACCITCT TGTCCAACCC ACGIACTICA ACACATTCCC ACCCACACIT	60
35	GTAGACAGCG TACCTATTCC GAGCGACAAA AGTCGCAAAG CTTCCCTTAT CCTCAACTAT	120
	ATTTGTGGCA TCAACAGCAC CGCTAGCCTG TTTTGGAAGC AGGCAAAGAG CATACCTATC	180
40	OCCATOCOTIG CTACTICAGT TOACGAGGAG AGAGTGTTGC GAGGGATTAT AAGAGATGGA	240
	CTIGAACACG TTATATGGCT TTCCAAAGTT TTTTAGAGAA ACAAATGGCA GAGAGGACAC	300
45	CTTCTTTTCA TAGTCAAACA TTTGGACCTG CTTCTCTTTG TTGACAAAGT AAAGCTGGTT	360
	CTOGTTCACA GCCACAGGIG GICTCTCACG GTCCAGTTTA AAGACCATGA TACCOGAGTC	420
50	ATGCGCCGCG CCAAAGAGGT TCACATTAGG GTGCGCCCTA ATCCGACCAGA ATCTGTCCTG	480
	TTCTCTTTTG AACTGTTTTA CAGGAGTGCG CTTGTCTAGA TCCCAGACCC TAATGGTAGA	540
55	ATCCTCGCCC ACAGAGATAA TTAGGTTTTC AAATGGGTCA AATAITTACAC TGTCGACGTT	600

	GITOGIATCA COCTOCACTT GICCACCTCC CACGCTTTGG TGGAGCTCAT ACGCCACAAC	660
5	TIGACCIGIC IGICTICAGA ACCOGAGACA ATCAAGGGCA GAATCOGATG GAACGAAGG	719
	(2) INFORMATION FOR SEQ ID NO:641:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 730 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1431RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:641:	
30	GATCATGTTA TACAGACCTT CAAAGTTGAT ACCAAAACCC TCAATGGACT COCTGACCAT	60
	ACTIGGIACT TOCTGITTAG AGGCCCTGCG GCACACTTAC TGCCTCTACA AGAAAAAACT	120
35	GITGCCTCTG AATTGGATCA CCCTTTTTCG GACACTAACC ATTTGCAATA CAATGCTATA	180
	TIGOCTICTAT CAATOGTCTA TIGACCTTGT TGAATCCAAG CTCGAAATCC AGCAATGTGT	240
40	AGAGATACTIG CAGCATTTICG GTGAGAAATG GGTTTTTIGCC AAGGAGTGTG COGTCGTCTT	300
	TCAAAATATT GGAAATGCGA TACTAGATAT AAGTCTCTCC CGAGGACAGG TAGAAAACGT	360
45	TGATAAATTG ACTAGGGAGC TATTITGGAGC TAGCAATGAA TACCAAGATA TATTOGACGA	420
	AAATAACGTA GATATATCCT GGATTGACCT GOCTATCTAA TTTCTGAAAC CATTGAGAAC	480
50	CTGTTTAAAC TATTTGGCAG TAATTCATAA TGTATTGGTT GTTCCATAGC TGAATTGCTA	540
	TIGOCOCIAT GGAGITOCTI ATGCAATACA COOSTIAGIG GGIGATIGIC GIGITCITAT	600
55	ACCCAAACTA ACCCAATCCG GTCTTAATCG ACTCCGGTAG ACTTTGTCAT CCAGTAAGAC	660

	AIGICITACA COCCCGATTA AIGGITGIAA TCTTTAATCG ATGAATGAGA AATGGIATAT	720
5	GTATGIGACT	730
	(2) INFORMATION FOR SEQ ID NO:642:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1431UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:642:	
30	GATCTCCTGT ACCATCATGA AAGTCTTTTT ATCACGGGAA AACCGGTTTC TCAGGCACAT	60
	CTGACGCAGT GCTTGTCGCA CATCAAAGGT CAAGTTCCGA TCCCTTGTGA GCGCTTCCAA	120
35	CTCCCAGAAC TCCTTCTGCA GATTTTTTAC TGGGCGGGGGC ACAACTTCTG CCTGCCTCTG	180
	GGCACATAT TICITTAACA CCTCCTTCGG AATCITAAAG TOCTTCACAT TATAGCGACT	240
40	TACGAGACCT TOGAATAAGA AGAGGCACTT TATATATAGG TITIGACATAT CCAGTTTCAT	300
	CTCGCACCCC CGCACGATCA GGTCCCGGTA GTCCAAGTGC GCCTTTCTTC TTGAATTCGT	360
45	AGAGCTCCCC CCCCAGGATG AGCCTCCCTG ATCAGAGGTG CCTGTCTTCA CCGAGAGCTG	420
	TOGCATACTO GOCTIGTICTOG CAAGCTOCAC CTTCACCTGC TTGGCAAAGT TCACATTTAG	480
50	GCCCTGCGCA AACGCCTCCA GTCGAGCGAA GATATGGTTC ACCAGCTCGA GTGGCATCGC	540
	CATCHTGITC ACGICCAGIG ACACGITCCC TTGGCCTAGC TGGTGCACTA GGGCCGCCCT	600
5 <b>5</b>	CIGIGIGAGT TGICOCTOCC ACACAGAGTC CAATTCCACT COCATCATGC GCATCGCGTG	660

	CITCAACCCA COCTCACTGA TCTCCCCTCG CTCAGGCATC TGTGGAGCCT CTTCTCGCCT	720
5	TC	722
	(2) INFORMATION FOR SEQ ID NO:643:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1432RP	
25	(asi ) (Taylor and a second	
	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:643:	
30	GATCCAGGAC TOCCGTOCTT GGTTGCGCTC AAGGCAGACT TAGAAATGAG GTGTTGCGCC	60
	GCATTCTGCG CTGCAGATAG AAACGAAGAC AAGATGCCAC CGTTACCCAA TTCCTCAGCC	120
35	CCAGAGAAAA AATTCCCGTA CCGGTGCTTC CCAGTACCAT CCTGGTCAAA GGGTGTGATA	180
	TCCCAAAATT TATCCTCAGT GTCCTCCTTG TATCCTGCAT CCCAGCGCGT GCTTTGGCCC	240
40	GCCCCCGGGG GCTCGCCGCC GGGGCCAGAC CGCACATGCG AGTGGGGGC GCTCATCTCA	300
	ATTOOCATOC TGAOCGACGA CGAATTOCTG TGCCCCCCCC TATGCCAGCT GGCGGCGTCC	360
45	COSCCACCCC ACCCCACGGG GAGCGACGAG TITIGTICCTGT TOOCGTAAAC CACCGGTCGC	420
	GACATGAGCC ACGATTICTGC TCCTGACACC CCCCTCTCCA CATCCGAGCC CTCCCCCCCC	480
50	OCCACCICGA CATCACCOCC CICCOSCCCC GICCOCCOCT CCCCATICCG OGICGCIACC	540
	CGICTITIOG CACIOCICOC GCGCCCCTIC CGCCGCCCT CCCCCGIAIG CT:CTIGAAA	600
55	AGTOCOGOGO GCTCTCTCTG AGCGACCOGG ACCCCTTCCG CTGCTCTGCC ATCCTTGCTA	660

	SCCTCTGCCT GAGAAGAGCA TCTACCTCTC CTCCCTGTTT ATTCCGCCGC CTTTTTGCGA	720
5	AACA	724
	(2) INFORMATION FOR SEQ ID NO:644:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 615 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1432UP	
25	(vi) SECUENCE DESCRIPTION, COO TO NO. CAA.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:644:	
00	CATCCCCGCIC CCCCCCCCTCCT CCTCCCAACAT GICCIGIACC CCCCCCCACCCC CCTCCCAACAT	60
30	CCCCCCCACC CCACCGTACT CCCCCCCCAA CAACTGTGTG TOCACCAGCT GTTCGTGCCG	120
35	CCCCTOGTICC GGCGCCCCCA TATTICTCCTC CTCCTGGTIAA GCCTCCTGCT GCAGAGACTC	180
35	CCCCAACTIC TOGICGICGT ACTOCGCGGC CGGCCGCGGG CTTGCAGGCC CACTGCGTGC	240
40	CCCACCCIGC GIGICOCCCC CGIGCICGAA GIACACCCAG ATTIGCCGITT CCACGICCCC	300
	ACCIOCCATA TCCAGGAACT GCCGCGCCAG CTCGGCGTCG GCCAGACGCC AGATGCTTTG	360
45	GAATACGCCG AGCIGCTIGI CIGAACTCAT GCTCCTACTT TCTGGCGCTG CCGTGCTGTG	420
	TOSCACACTC ASCACTTTGT CTCACGTTGT CSCTOSCTCC ASCCTTTTAT ACCOSCGGT	480
50	OCCACACATG COCCOCCCC AAACOCTTAT ACATATACAT OCTACTTAGT CCGCCGCTTG	540
	GTCACCOGCC CGTCCTCCAA GCGCGTGTGC GTGCCCTGGA AGTGCACCGG CTGATCGCCG	600
55	COCOCTOGGG COCCG	615

none en merconto La

	(2) INFORMATION FOR SEQ ID NO:645:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 688 base pairs  (B) TYPE: nucleic acid  (C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1433RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:645:	
25	GATCCATOCC CACCACCGTC COCAGCACCA TATOCAGTTT CCCCCCCTCA	60
	GCGCGCCAT TTCGAGAGCT CGCGGGTCCG CTGGCGTGCC CGCTTCGGCGC AGCCACGGAA	120
<i>30</i>	CCACCIGACE CCACGIGICI CCCCCCCCCC TGCCCGITIE CCCCACACAGIG CICCCCCCT	180
	OCTACTICIC TACCCCACCC COCCCCTTAA TCTCCCCCAT TACCTACCCC ACCATCTCCA	240
35	CGASCAGCOG CGACTCGCOC ATCITCTGTA TTTTCAGCAG CTCGCGCTCG ACCITCTCGT	300
	CLEGGLEGOC CYLCLOCOCC CCCYCCCCCL YCLCLLCCLC CYCLCCYCCC LCLCLCCYCCL	360
40	ACCGTOCTAT TIOCCOCTCG TICAGCACTT CGICATTCTC AGCCACCOGT ATTCCCAGGA	420
	OCTIOCATAT TOCCOOCCET TICTGIAGGA GAACGIGGTA GCGCCGGATG ACCTTACGIG	480
45	CITTOGATOG TITGATTOCC GOCGIATGIT TGACGCCCT CITGCCCGIA ATOCTICITC	540
	GCTTCCTGGC CAGCATGTAT GAAAGTTAAA CCGCAGTTAC TACTGGTACT AGATATGCCC	600
50	TOGGAATGOC ACCOGATIGAC CTOCTOGTIGT ACCTTOCTITT TGTCATCACG ATGCTTCGAG	660
	CTGAATOGIT GAAGAATITIC GAGTGAAA	688
55	(2) INFORMATION FOR SEQ ID NO:646:	

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 712 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1433UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:646:	
	GATCACOGAA GAAGOCAAGG TCAAGAAGGT TACATTTGAT ATCGAGCCGT ACAAGCCCAT	60
25	CAACACTAAG CTATACAAGT GTGACAATAA GTTCCGGACG GAGGTGCTCT CGGAGCTGCT	120
	GCAGGCTGAC GAGAAGTTCG GGTTCATTGT GATGGATGGT CAGGGGTGTC TTTTCGGTAT	180
30	GITGTCCGGT AACACCCGGA CTGTTCTACA AAAGTTCACT GTGGACTTGC CGAAGAAGCA	240
	COGTAGAGGT GGTCAATCCG COGTGCGTTT COCCCGTTTG AGAGAGGAGA AGAGACACAA	300
35	CTATGTGCGC AAGGTCGCTG AGGTGGCAGT GCAGAACTTC ATCACAAACG ACAAAGTTAA	360
	TGITAAGGGG CTAATTTTGG CTGGTTCTGC GGACTTCAAG ACGGACTTGG CCAAGTCTGA	420
40	ACTOTTICAC CICACOTTOG CACCCAACAT TOTCAACATT CTACATOTAT COTACOCTAC	480
	TGAAAATGGT TTCAACCAGG CTATTGAGCT GTCCGCCGAG GCGCTGGCCCA ACGTTAAGTT	540
45	CATTCAGGAG AAGAAGITGC TCACCGAGIA CITTGATGAA ATTTCCCAGG ATTCGGGCAA	600
	ATTOTOCIAC GGIGITGACG ATACTOTGAA AGOGCTAGAT TGGGTGCGGT GGAGAAATTG	660
50	ATTGTGTTTG AAAATCTAGA GATTGTTCCG GTACGTGTTT AAGACTTCTG AA	712
	(2) INFORMATION FOR SEQ ID NO:647:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 716 base pairs

	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) Original source:	
	(A) ORGANISM: PAG1434RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:647:	
20	GATCAGATOC TICTOTOGIC CTAGAGAAGA CTOCTATICT TAACCCTICG TCAACGAATA	60
	TAGCCCAGGA CGAGTITIGIC GATOCCATAG CGGAACCTCC ATCGGCGTCC GTGGATAGTA	120
25	CCCCTTATICT CACCCCCCC CCCCATTATT CCTCCCAACA CACCCCCCAA CCTTCTGAAC	180
	CTACAATAAC GGAATACAAA ACTGCAATTG AATCACCATC CACCTITIGOC GACGATAACG	240
30	AGAGIGIAIT TOTTGIAACT TOTGOGGACC TGCATCCATC GGIGICCTCT GCGAGICAAA	300
	CATTAACAAC GGAAGAGCTT CAAGCCGTTG CGAACAGCCA CCAATATAAG ACCCAGGTGC	360
35	AGATTOTIANA ACANGACCAN GATCANGTING AGCATOTTCT AGAATTOCAC TCGCCACCAG	<b>4</b> 20
	CATCTCTGTA TCATCGTCAT GTTTTGAACG ACCCACAGAA AAATCATAGT ACCAATGTTA	480
40	TICCIGATGA TICCATAGAT ATCGATGAAT ACCICGATGA AAACTICGIT AAAAACTICA	540
	CATTOGAAAA COCTCTTTCT TIAGATGAAA TCTTCGACGA TGATAATGIA GITTITOGAG	600
45	AAGAGAAGCT GCTTGTGGAT CCAGACCTAG AATTCCCCGGA ATTAACTGGA ATGGAACAAG	660
	ATATGGAATC TGACTATCIG CCGCTGATTG AAAATGGTAC GGAGGCTGTT CTACAA	716
50	(2) INFORMATION FOR SEQ ID NO:648:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 715 base pairs	
55	(B) TYPE: nucleic acid	

	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1434UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:648:	
	CATCAGGITT TOCCGTACGT GAGAACGTAT CTAAGGCACA AAGGGCTTTG GGCGACTGTG	60
20	COGACOCTTG ACTTOCGAGA TACAGGACAA ACCTGTTACG GCGGCAACTG GTGCAGCACG	120
	ACCACTANGE CACCAMINATION CONTRACTOR ACCAMINATION ACCAMINA	
	ACCAGCOGAG GAGOGATTCT GOGOGAAGOG ACGGTGAATT OGAGOCAGCT GGTAGCAGGA	180
25	GROCOGGATIC GICTATTIAG TIGOGACGGG CGICGCAACA GCATGCACGT AAACGTTGCG	240
	GTAACACGCG ACGCTCACGC GACGGCTGCT ACGCCCATAG CACGGGAGCG CAAACGACGG	300
30		
50	CAGCCGCTGT CGCCAGAGAT GTCTTCACCA CTGCCCCGGTA GCAAGCTGCA GCGGCGGAAG	360
	CAGACACTTG AGGCCGGTCC GGGTCGCGCC AGTGGGACAC ACACGGTGGA CGAGCTGGCC	420
35	COCCACCTOC ACCOCCCTC CCACCACCCC TCCCACCCCA ACCCCCCCTA CTCCTATCCC	
	The second districts and second and second and second companions	480
	GTGCTGATCG GCGTTGCGAT CCTACAGTCG CAGGAGGGCA AGCTGACCTG TCGCAGATAT	540
40	ACCOGNOCAT CYCGNOCYTC TYCCCTTACT ACCOGCNGIG TGACCCCCCC TGCCAGAACA	600
	GCATCCGGCA CAACTTGTCG CTGAACGAAG CGTTTGTCAA GGGCGGCAAA TCGCTCGATG	660
45	GCAAGGCCCA CITICIGGGAG ATICAAGGCAC TIGTIGAAGGGG CITICTCCGGG ATIGGG	715
	(2) INFORMATION FOR SEQ ID NO:649:	
50		
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 538 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: INA (genomic)	
5		
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1435UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:649:	
15	CATTOTATO TACOTOTATA	
	GATCCCATOC TACCOGICOC CCTOCCAACC CGITCOCCIA GCGITCACOC CTAGGICICA	60
	AACTGAACAA CAGGTGGCAT TGTGGGGGGGG CCAGCAGGCC CTGGGGGGGAC CATGCCGGCA	120
	The state of the s	120
20	TOOCCOCCA ATAATACCAC CAGITGICAA OCCCAGGIGT CTGTAATCIG CACCGAACAT	180
	CITTATCTAC CAAGGAGGAG CCTTGAAAAT TATATATCTA CCCCTCCCCC TAATATATTT	240
25	GACCAATTCG CTCTCCCCAA ACCCAATCAT CCAAGACCCC ATCAGGCCAG CCGACACCAC	7.00
	THE POST OF THE PARTY OF THE	300
	AGGAAGTGAG GAGTGATCTC GCAGGTACGA TGGAAGCACA GTCTATACAG TCTATTCGGT	360
<i>30</i>		
	CGAACCAAAG CGTACGGAGC ATCSCGAGCA CGAGCGGAAC CGCAGACGAG TCGCTAATCT	420
	TICAACGEAG CGITICAGCAT CGITTIGGCCC CGTGAAGCAC GCCAAGGGTT GCAGCCTGTG	400
35	to the contract of the contrac	480
	TEGRICICO CAGECAGGET CTCTECACEC CESSGTATCG CCCACTEGGG CCCCGTCT	538
	(2)	
	(2) INFORMATION FOR SEQ ID NO:650:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) NOV POTE TO THE TOTAL OF THE POTE TO	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1436RP	

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:650:	
5	GATCAACCTC GGAAACGTAT TTAAAAGCTT GTACTCGACA TCATTAAGTC TTCTCCTCGT	60
	TTCCTTTOGT AAAGTATWAG CATCCAGTAA AGTAACAACG AAATOCAATG CTGAAAGATC	120
10	CTATACCCTA GACGACCTAA ATGOOGTATT TTGATCATCC ATACTAGCTT GAAGATCAAT	180
	GAAGICAATA ATAGIGITGA CAGACTCAGG GGAGAGTTTG GACTTGATGT ATTCCTCAAA	240
15	OCCAGIOCAT COCACCTICC TAGCACTAGG AGTAATCTIC AGCGATICTT TAAACGGAAT	300
	ACTICICATA AAATOCIOCA GCITTITITIC CICGIAAAGG ATCIGIACAA AATTAGCAAG	360
20	CGCCCTCCTA TCCTTCTTAA TTATCATTCT TCCAACTTCA ATCACCTTCT CCTTCCCCAT	420
	TTTCTTGATA AGCTCACCAA ATACCATCGG AGATTTTTCA AATACTTGGA CCATTAGAGT	480
25	GACCAATAGT TOGITAATAA TOGOCTTATT TICAACCATA AGACTGAAAT GCTTCGTTTC	540
30	TGAGATCAAA GTCAAGOCCA AATATTCGGG AACAATATTG TAATCATCGA AGAAACAATC	600
30	ATOGAATAAT TOGAACATAG GACTOGAGOC AAACTOCTCT CTTGATAAGA ACAGTTCAAT	660
35	ATCGAGCITC GATACCGATG TCAGATATAA CAAGGAGITC TTTCAGTTTG GCAGTACTTT	720
	AGAGACTT	728
40	(2) INFORMATION FOR SEQ ID NO:651:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 713 base pairs	
	(B) TYPE: nucleic acid	
45	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1436UP	

	(MI) SEQUENCE DESCRIPTION: SEQ ID NO:651:	
5	GATCCAGAAG ATTATCCGAC AATATTAGTG ATATCAAGGC ACAGATCGCT GCCAACACTA	60
	GAGGIATICA ATIGCITAAC CAACTOGITG ACGITTICOG TCTAGOCACT GITACAAGGI	120
10	ACATOGACOC AATTCAOGAA AATOCAOCTC TTACTGTAAA GAATGTCTTG CGAAAGATTA	180
	CCAAGCATTT TOGCAAAACC GTCTATTCGG CCCAGGATTA TATGGATGAT GGCTCTGTTA	240
15	TAAAACITAG GGIGGAGCIA AATOCTAAGG AAGATAAGTA TATIIITIGAT TITACGGGGA	300
	CTTCTCCACA GGTCCACGGT AACCTCAATG CACCTGTTGC TATTACCAAC TCTGCCATCT	360
20	TATACTOCTT ACGITGITIT GIAGACGAAG AGATTCCOCT CAACCAGGGC TGCCTAAAGC	420
	CCATTACTGT TATTATTCCA GAGACCTCTA TCCTATGCCC GACCAAGGGT GTCGCGGTAG	480
25	TOOGNOGIAA TGICATGACG TCTCAGOGIG TAACTGACGT AATTCTCAAA ACTTTTAAAG	540
	TCATGGCGGA CTCCCAAGGA GACTGCAATA ACTTTACTTT	600
80	CITCTACCOG TGAATATACT CAGOGITTIG GATATTATGA AACCATATGT GGCGGCATG	660
35	GIGCAGGIGG AGATCATGGC GIGGICCGGG GIGGCATGGA ACACATCCIG TIC	713
,,	(2) INFORMATION FOR SEQ ID NO:652:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGIH: 587 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) Original source:	
50	(A) ORGANISM: PAG1437RP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:652:

55

	GATCOCOCOC CAGCTATCOC TICCOCCOGT CAAGCTOCAC TGTAGTATOC TCOCOCAGGA	60
5	COCCATCAAG GCCGCCATCA AGGACTACCG CAGCAAGCGC AAGGCGACCG AGCTGCGCTG	120
	AGCGCAGGCC GCCGCAGCCT GTCGGCGGCCC GGCCGGCGCC AGCCGCAGAG GGACGTCCGC	180
10	GGGCCGGCGA GAGCCGCCCG TTTTCTATGT AGCGACTCKA GCATCTAATA GACATGGTAA	240
	TAGCTICTCG TTTTCTACGT TTGCACACAG TATACAAAAT TTTCACGCAG CTCATCGCCA	300
15	CTICCACTIG CTGAAGCGCA GGTACGGCAC CAAGACCTCG GCTATGTCCT CGACTCTCTT	360
	TGACGACATC TTCACGATCC AGGAAGTGGA CCAGGGACGG TACAATAAGG TATCGCCGAT	420
20	TGAGGCCATC TCCACGTCGC AGGACACGTG CAAGCTGACG CTGGATGTGA ACACAGAGCT	480
	CTTCCCGCTG CAACCACAAC AGCAGCTAAC GGTGATGCTG GCGACGACAC TCAACCTCGA	540
25	COCAMICACAE CACACACACE CELECTICACAE CCCICACACC CCIACACE	587
	(2) INFORMATION FOR SEQ ID NO:653:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 260 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1437UP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:653:	
50	GATCCGGCGG GACCGCTACA ATATTCCCCAT ATGTATTAYA GGCAACTTTA TACCCATCTC	60
	CTAAGTGCAG TACGTACTGT TTGTCAGTCT AGOGTCTCGC TCGCGGTGAG CCCCGTGTTG	120
55	222222222 222222222	180

	GCC19CACCE CCG19CG9CA GOC19CGACG AACTCGACCA CG1TCG19CT CCAOCGCACG	240
5	AACTICICCA COOCCACGIC	260
	(2) INFORMATION FOR SEQ ID NO:654:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1438RP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:654:	
	GATCTCTTTT TAACGGCTGT TACCAATAAC GATACCGCAG CTACATCTGG AGAATAGTCT	
30	CHACATORIC PALACTORICAL GALACTORICA GOALTAGTOT	60
	OCATOCCATG COTOCAAGIT COTGTGAACA TACTOCTOGG GATOGACCTO GAAGCTCTOC	120
	AAGGICICIT COCTAGGACA AAGAAGCOGG AAGATAACAT GITCCAAAAT GGTTGCATAA	180
35	TGTGGGTCAA CTATCGGCCA AGTAGACTTT TGGACCACTG TTTGTTCAAT GAACTCCAAT	240
	ATGTAATATA GOGACTCCTT GCTTAACCAC AATTCGCCTG CACCCCACCT TTCAATCTGC	300
40	TOGAAATGCA ACTOCAATAG TTGCGGCAGA AACTGCTCCA CATACAGCAT TTTAAATTCA	360
	GTGTACTCAA ACTITITIGCT GAGAGATTCT GAGGCATAAC GTTGGAATAA TCGATACATG	420
45	THAGCATATG CCCACTITIT GOCTCTGACC CATOGATGCG CCCGCCTATC ATCGACCGCC	480
50	AGCGCCATCA CATGCTCCGG CAGCTGGCTT TGTATCACAG AAACATGGAA GTTGGCCCAC	540
	GCAATGAAGT TITICCGACCG TIGGAGAGTG AACGGCAGGT CATTATATGT CACAAACTTG	600
	TAGATOTTOA GCACAAGOTT CAACATATTO COCACGATOT COTTGTGCTT TOOTGGCTGT	
55	Grammie Container Christich Techtocier	660

	ACAAAAGOGC GITTIGOGTAG TIGCAGCAAGT CTIGGGAAATA TICTICATIGATIC AGCATICTICCA	720
5	GCTCCTGA	728
	(2) INFORMATION FOR SEQ ID NO:655:	
10	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 774 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1438UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:655:	
	GATCOSCAAA CCTAATOCGT CTOGACGTAA TGTAATCCAA CAGCGACTGT AGAGCTGCCT	60
30	GOOGTITETICE GACAGAAATE AGCTCATETG COCGCTITCAA GOOGTITTICA GOOCGAAAA	120
	CAGGIGGAGC CAUGCIGAAT TAGAGCIATT TOGICACCIG TITICAGIAGT GIOGACTICC	180
35	TITCAATGIG GIGAACTITG AAGIAGGITA TICAACIAGA AAATTITICA COCAGAAGGA	240
	TOCCCTICTAT CAGCOGCCGT GICTGACGAT GATCTCAACC GCGTAAAGGA CGAGAAGTCG	300
40	TAGGTCGAGT CTAATCTACT ATTOGTACTG ATGAACGGGA CTGGCCAGCT AACGTGAAGG	360
	CACTIGTICTICC GOCCATICAGGC CCCCACCGCCA GCGCACGGGCC CCTGGGGATGA GCACAGGTTG	420
45	CCTCCACACG ATTCCCATCG CCTCACCCCA ACCCACGCTT CCACACCCTT CCCCACACCCTT	480
	CGTCGTCAGG CTGCAACTGT AGAAGGGTTG TCTTGAGCTC CGCGCACGCC GCACGCTGCC	540
50	CAGGIAGCIG GCGGGCCGIG TICATCGCGC ACAGCGGIGG GCTCGCIGIC ACGIGGCATC	600
	GAATATUTCA OUTGATTACA OUCAGCAGOG CATOUCAGAC AATOOOCAAG CAGCAACAGG	660
55		

	ACCACOGICT CATCOCTICGT CICCCTTTAA CAGTATGTCA CCTGTCCACC TCCCTCCCCA	720
5	TCTCTGGGTT TACTCGTACC TGTGCGCTTA TATAGGCATT GCCAAAAGGT TTCC	774
	(2) INFORMATION FOR SEQ ID NO:656:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1439RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:656:	
30	GATCCIGITG GACGICITGC AAAGTCGIGG TCACCCCGAC CAACITCICC TCTGTAATAC	60
	COCTOTACTT COTTAAGTAG TCCACAATOG OCTCATCTOG CTTGACAAAC TTGTCATAAA	120
35	CTAAGTTACA ATCAAAATCG ACGACGCTCA CACGCGTCAA CACGTATCCG TTTTTTGAAA	180
	GOCACATOTO ACAGTOCATG GCAAACGTGT GAGAACCGTC GTGTTOCAAA CTGACAGTGT	240
40	CCACCCACCC ACTIGIACTIC TOCTTATTCT GATACTITAG CAACAAAGCC TTTTGGTACT	300
	CCTCCGATAA GCCAGGTGTG TTTAGATGGA TGGGGTACTC ATTATGCAAT AAGTCATCAA	360
45	COGICATTAG CAAATCAAGC AAAGTGATTT CCTTTTTGTT CAATTGTTCC ACCTTTCCCA	420
	TCTTCTCCTT TTTTGACAAG CCTACATTGA CAAAAGAATT GTATGCAGAA AATAGGGAAT	480
50	TETTIGATEC COGCOCTIGAT AACGOCAAGA TACACATTIG CTIGCACATE TGTICATTIT	540
	CACTAATOGA GITTAGATGT OCGICTTOCA ATTTCOGAAT ATTTTTATGA AACAATGAAT	600
55	CCTTCGGTAG ACTGAAGTCC TCGGGTAAAA GGCCTGCAGT GAATAAGACG ACCACCTTCT	660

	TCAAAGAGGC CTATTTTCTA TCGTAATCCA GTTCGGAGAG TTGTTCGTAT CGTGGAATAT	720
5	GTACTOGA	728
	(2) INFORMATION FOR SEQ ID NO:657:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 694 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1440RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:657:	
	GATCTATTCT TCATTCAGCA ATCAACAAGA GCTGGTGAAA CTTGGGCAAG AAGCTGAGCA	60
30	AAGCGGTAAA TACAACTTGG CATTCAATGC ATACTGGATT GCAGGAGATA TCAACAAGGC	120
35	CAGOGACGIG CITTICGAAGA GCOGACGCCA THOOGAGOCT GTOCTTICTOG CATCCACATA	180
	CACCTCAGAC AATGACGCCA TCAACGCTGC TGTAGAAAAA TGGAAGGAAC AACTGAACTC	240
40	AGCTOGAAGA GTATCTATCG CAGAAAGAAT TATACTTTCC GGAGAAGACG ACTTCCCTGC	300
	AGCTCCCCAG ACTITIGGTCG AAATGGATGA CGGATCAGAG TCCGCGTCTA AATAAACTAT	360
45	AATTITAAAG ATAACAGCAG GAATAAATTA ATTACCACGA AGGAAATTITG TATGTACATT	420
	CTAACTAGAC CCAATGGTAG AATTICATTG CGIAAACACG GCAACCTTAT CAATATCTTT	480
50	CCGIPTIGTCC AGICCGACAA AGIAAAGITC TITIGGATTCA GATOGGCATG CPTCCGGCTT	540
	AAAACGCCGC ACTITGGTGA ATACCTTTCG CAGACGCCGT TCTAATAGCT GGTCTTCCTT	600
55	GCCAGTGTAT AACTTGCAAA CGAATGAGCC ACCGGGCCTC AACAATGCAA TTGCACATAG	660

	CAGTOCTOCG TICACACAG TCCATCGACA TGTA	694
5	(2) INFORMATION FOR SEQ ID NO:658:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1440UP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:658:	
	GATCCIACAG AAATAATCCA GIACAAGGIA CCICIAAICI ACIGIGIIAA CAIGGAAAAAC	60
30	ATTICGCCTT TAGGCTTTTT CTTTTCACCG AAAAGGTAAC GIGITGGAAA CATATATCAC	120
	GOGTTCGAAA CTGACTAAGG TTGCTCATGC CTAAACCAGA TAGGCAGCAA TGGCAAGGGG	180
35	CTTGAGGIGG TACCAGAAAA GCTGCCACCT CCTGCTGCGT GCTTACTCTC GCAAACGGTG	240
	TATACTATTA GIGITGGAGT ATTTATTGCT TATTAAATAA COGAATTGTG GOCCTAGAAG	300
40	TOSCCATTAT CACTGAGCAG CAGCGGCTGG CAGCGCAGAC TGCTCGCCAA GCCCAGCACG	360
	TOCGITTICAG OCAGOGITTA CAGCITOCAGO OGITCACOATO AAACOCTOGO OGOGGAGGAC	420
45	CACTATCAGG GCTAGCTOGA GGOGCATCAA GAGCTTCTTC GATATGCCGC AGACCTTGCT	480
	GAAATACTCG TOOGAGTOCA COGTGTCTTC CACAATCTTG GTTGAGACAC GTATCAAGGC	540
50	CACTATGAAG CGATGCACAT ACCTCTCGGC GATGGGCCCAG CGGATCTGCA CCGGACCGGT	600
	TICCGAAGGA GOCCATITTA GOGIGAGGOG GAGTAACAAG CAGCCCGOGG TCTGGTAGAC	660
55	TATGGGGGCA AACATGCATT TGGGGTTGAT GCCGTCTAGG TACTGGGTAT AC	712

	(2) INFORMATION FOR SEQ ID NO:659:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1441RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:659:	
	CATCETTAAT TOTAGCAAGC CACCACCAGA CATGETCTAC CAAGGCCGTC TACCACAGG	60
25	CACGCAAGCA GTCCGTCCCC AGGAGCAAGC CCCCGAGGAC AGACCACAAG CACACTTGCC	120
	GOGTCTICACO AAGGOCCTICA CTACCOGATIC CTTAGAGOCA ATOCTTATOC CGAAGITTACG	180
30	GATCHATTIT GCCGACTICC CTHATCHACA THATTCHATC AACHAGAGGC TGHTCACCHT	240
	GCACACCIGC TGCGGITATC AGTACGACCT GGCATGAAAA CTATTCCTTC CTGTGGATTT	300
35	TCAAGGGCCG TCGTAAGCGC ACCGGACCCA GCATAGATGC TGGGCTCTTC CAGCCATAAG	360
	ACCCCATCTC COGATAAACC AATTCCCCCC TGATAACCTG TTAACAACAA AAGATAACTC	420
40	CTCCCAGGC TCACCCCGAC GTCTCCACAC TCAGTTACGT TGCCGTGAAG AATCCATATC	480
	CAGGITICCOG AATATTAACC GGATTCCCTT TOGATGGTGG CCTGGAAAAT CAGGCCTTTG	540
45	AAACGGACTT CCCCATCTCT TAGGATCGAC TAACCCACGT CCAACTGCTG TTGACGTGGA	600
	ACCITICCCC ACTICAGICT TCAAAGITCT CATITGAATA TITGCTACTA CCACCAAGAT	660
50	CTGCACTAGA GGCCGITCGA CCCAGCTITA CAGCCTAGGG CTTCGTCACT GA	712
	(2) INFORMATION FOR SEQ ID NO:660:	
55		

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 718 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genamic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1441UP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:660:	
20	GATCCAACCG AACCTITCCT TCTGGCTAAC CTAGGGTACT TGTACTCTAG GCGAACCAGG	60
25	ACTITIACIT TGAAAAAATT AGAGTGTTCA AAGCAGGGG AAGCTGGAAT ATATTAGCAT	120
	GGAATAATGG AATAGGACGT TIQGITCIAT TTTGTTQGTT TCTAGGACCA TCGTAATGAT	180
30	TAATAGGGAC GGTCGGGGGC ATCAGTATTC AATTGTCAGA GGTGAAATTC TTGGATTTAT	240
	TGAAGACTAA CTACTOCGAA AGCATTTGCC AAGGACGTTT TCATTAATCA AGAACGAAAG	300
35	TTAGOGGATC GAAGATGATC AGATACOGTC GTAGTCTTAA CCATAAACTA TGCOGACTAG	360
	GGATCGGGIG GIGITITCIT ATGACCCACT CGGCACCTTA CGAAAAATCA AAGICITTGG	420
40	GITCT0000G GAGTATOGTC OCAACOCTGA AACTTAAAGG AATTGACOGA AGGOCACCAC	480
	CAGGAGTOGA GCCTGCGGCT TAATTTGACT CAACACGGGG AAACTCACCA GGTCCAGACA	540
45	CAATAAGGAT TGACAGATTG AGAGCTCTTT CTTGATTTTG TGGGTGGTGG TGCATGGCCG	600
	TICTTAGITG GIOGAGIGAT TIGICIOCIT AATTOCGATA ACGAACGAGA CCTTAACCTA	660
50	CTAAATAGIG CIGCTAGCAT TIGCIGGIIG CGCACITCIT AGAAGGACTA TCGGIITC	718
	(2) INFORMATION FOR SEQ ID NO:661:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 722 base pairs	

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5	(B) TYPE: nucleic acid (C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1442RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:661:	
	GATCAATTOC GTCTTCATCC GATGAGACAT TTTGAAAAATT GTTGGAATAT TOOGCAACAT	60
20	CAGOGTATOG TAACACCTCC GGTTCTAAAC TTCTAATCOG TAGOCTCGTC GCOCGTGTAA	120
	COCATOGATO ATCAATOGAC OCTOCTOCOG GCCATCTAGA CACOCCCGAA TTOCCOCTTG	180
25	GIGIGAGGIT TICGICCOGA CITCICACTI TATCAGGIAT GACTATCACT TGATGATTCA	240
	TTAGATTCCG TGTATCCACA ACATGGACGT GOCTTTGGTG TTCCGAGATA AATAGTAGGT	300
30	CATCAAACGA GCGGCTAAAC TTGCACACCC TAAAGGACCC GTTCTGTGCA TGTCTTCGAG	360
	TIGAAGGIAT CICCOCAAGA GOCGIGICCA TITTICICAT ATCGIACACC AGACAGAGGC	420
35	OGITTIOGAA TATOGIAGOC AIGIOCACGI OGITTIOGCI ATAGCTIGIG TAAAAGCCGI	480
	TATCACCACC AGGCGAATCG TAAATACCAT CTAGGACTTC GGATCTATCG ACCCCGCAT	540
40	ACCITICGAAC GCACITIGIG CGCGACCATT TIGAACCCCA CICAGGAGCG GCGICATATT	600
45	GTAATGAAAA ACAACCOCTT AGTTCATCTG TCTATAGACC GCAAACTTGC TGGAATCTCC	660
45	CGAAACCACC ATCGTCTTCC CATCGTGTGA TATTGCCCGAG CAGTTTAAAG CAAATTTTAA	720
50	GT	722
<b>70</b>	(2) INFORMATION FOR SEQ ID NO:662:	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGIH: 720 base pairs

5**5** 

(B) TYPE: nucleic acid

	(C) STRANDEINESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1442UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:662:	
20	GATCAAGRET GREAACTIGE CETTGACTIGE CTTGGCCTGC GCAGRETICTC TGTTGCCCGCT	60
	CITECCECCT CIGITECCEC CETTECCECC TETTTIGTIG TETETEGT COCCAGACTT	120
25	AGGAGCAAAG GACTOOGTIGC CATCAAACTC TAGGAACTIGC TTGGCCTTCA AGTIGCTTCGT	180
	CITICACCITIC TICACCITICS TACCCICCAT CAACACCICC TGCTTCTTAA CGAACAACTC	240
30	AGCGTCGTCG AACTTCTCGA CCTTTCTCGC GACAGGGCC TTGTTCAGGT CGGAGTTCTG	300
	CTOCTOCAAG TACOCCTOCA AGGIGACGOC AGCTGCAGTG GCCTGCTCCT CCTCGGCAGC	360
35	GTCGGCGGCC AACTCCGCCT CGGCAACAGC GGCACCAGGC TCCTCATGGG CCTGCTCCTT	420
	CTOSTIGIOS COCCACOCCI OCTIGATOTT CITIOGOAGAG TOAGTOTTOC COGTICIOGA	480
40	GTGGCGGTCA AAGGTCTTTC TGCTGTCCTT GGCTGGCTTG CCTGGCGCAA GAGGGTCCTT	540
	GCACTIGITC TGCGAACGGC CGGCCTGCTT GTCTCTGAAC GCAGCCTCGT TGCCGGTTGG	600
45	CTTTGGTCTG TTGTTCTTGG CACGCGATGG GTCGGCAGAT GGAGCAGGCA CGTCCGCCTT	660
	CTTGGAAGAG GTGGTCTTCT TCACAAGCTC CTTTGGAGGA GACACAACAA CGGTGGCGTC	720
50		
••	(2) INFORMATION FOR SEQ ID NO:663:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 716 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genemic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1443RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:663:	
	GATICTIATIGOG GIGCTIGTOGG OGTIGCATICGA CCAGCACAAG AGCTTOGAAT TOGATAGOGG	60
20	GAGCITCITC TITICAGTACG TOGAAGGCAT CIACTOGTAC AGGACTOCGA GCCTTCTTGC	120
	GOGCTATICTIC COGRACOCACT COGTIOCOGAC GOCCAGOCCAG TACOCCAAGG TICTTOCTIAGA	180
25	CCGCGCGCCC TCGCCACGIC ACGCCCACGI GCIGCTGCTG GGCATAGITG CGCATGCCCA	240
	COCCATOCAG COCCTAGTOC ACCAGTOCAA AACCAGTOGA COCGTGACAT CTGCGACCTT	300
30	CICOCTICIC ACAGAGIOCC TOGACATATA CCIGIOGIAT GIGAACGATA COGITTIOCT	360
	GOCCCCAAG ACCAACTICC COCTICAAGA TCTOGTOGTG TITTIOCAACT TOGTOCGTGA	420
35	COCCATATOT CAGOCTITIOC GTOCTGAGCA TGATTATGAG GTGAACAAGA TGCGCCGCCC	480
	OCTOTOCITÀ CTOCAAAAGC TGTATATTAG GGATAGAAGG ACCAATTTOC TCTCCGCGGC	540
40	CAACCCCCAC GACTTCTGCG TCATTGCCGCA TACCACGGTG AAAAAACTGCG ACATTACATC	600
	TOTOCTTOTT TACTITICATE AGITCTACAG AGAACAGITE CATTTETTCC TESCOCAGOG	660
45	CCGTGCTCGG CACGAGGTCC CAGCGGGGAT CTCGTIAGCGT GGGAAAAACGA TATAAA	716
	(2) INFORMATION FOR SEQ ID NO:664:	
50	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 711 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1443UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:664:	
15	GATCCOOCAT TEACATCTCA CATGIAACCG GGIGGITCTG TAGGIAGGGI GITCAATGIA	60
	AACTOGICOC AGITOGAAGT TOOOGTAGTA CTAAATTOGA ACCCOGGIGG COGTOGIAGA	120
20	AGATOSCCAT COTCAAGGIG TICCACAAAA CTATICGIIT CACCCTOGGA TACITICATCT	180
	TCATAACTOC TITICTAACAA TACATCICOG TCATAGTCTT CGTAGGCTGG TGGAGGCAGC	240
25	TTCATGCCGT TCAGCTTTGC ATATCCCCAT TTCTTTACGT TTGCTTCAAT GTAGACGAAT	300
	CCGTAGGTCC CGAAATTAAC GTGTATCTTG CATGGGACAT TCGCACCAAC AATCGGGTAA	360
30	ACATACTIAA TITTCCAGCC CITTATGIGG CCACCAATGC GITTCTCATT TAACTICTIG	420
	CCATTOCOCC TGAAGAAAAC TGTOCCOCTC CGAGTTCTGT ACCCAATCCC GATGACGTCG	480
35	CCCTTTTCGC AGCGGGGAA TAGTGAAGAG AGTTCCTGCG GGAGCTTAAA CCAGTTGTTT	540
	AACCTACGIG CICCATTAGA GICATATIGCA ACTGAGTGAT GGTGTCTGCC GGGAAGCCTA	600
40	AAATAGGGAT ACGGCGATGT AGCAAGACCA AAGGAAACTA TTTGGTTTTC TGAGAGATGG	660
	CTGACCGGGC GGCCAAGCCT GTCACAGAGT CGAAGATCTT GCACTCGAAG T	711
45	(2) INFORMATION FOR SEQ ID NO:665:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 736 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1444RP	
5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:665:	
10	GATCTOGTTT TATACCTTCA CGAACCCACT CTGGACCCGG ACCCTCCTGA AGTGTCCCAA	60
	CATOCTOTIAC TITOGTOCCCG TGATOCATTT CTIACGACCAC TACGACCACG COCCOGTACT	120
15	GAAGAACATT GOGTACTCGA TCTTTATTCT GAGCATTGGG ATGAATCAGG CACTGCATCA	180
	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	240
20	ATTIGIOCTG CAGCCCOCAC TATATATCAG CCAGTTCTAC CTGCTGCTAC TGAATGTACA	300
	GAACCCGAGC TITICATTICGA COCCGAAGCT TGACATAATT AATCOCACGG TGCTGGTGGC	360
25	CTACGIGCCC CTGGCGCTTIC ACTGCTTTCG TCGGCAGCTG ACGAGCTAAG TCACTCGGGC	420
	AGGAGCIGCT COGTGAGCTC GTGTGCTATG CGTGCGGCGT ATTCGTCAGC GGCATGAACA	480
30	TOTOTTATOT CTARATAGOG TICTOTAGOT TOOTTARTOC TOOTTACCAC ACTOTOGAGO	540
35	GETATATICTIC OCTOCAAGGE ATCCAGCTICT GOGAAGGCTIG CAGCOGTOGA CGOGTGCATA	600
35	COCAGCATAC GCTCGCTCCA GGGGATGGAT ATCCAGCAGC TCGCGCACAC TTCCCGCCCC	660
40	TOCTIGITICCC CCAGCTCGTT TGTGCCGCGCC TCGCGCCATC TGAGAAGCGC ACGTCGTGCA	720
<b>₩</b>	CTTCGACCCC ACCCTC	736
45	(2) INFORMATION FOR SEQ ID NO:666:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 709 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: ENA (genamic)

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931

	(vi) ORIGINAL SOURCE:	
5	(A) ORGANISM: PAG1444UP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:666:	
	GATOCAAATA CATOCOGTAT ATATOCTACT TGTGCCAGAA GACATGAAAA GCAAGCATCA	60
15	ACCCACCTAA TCACCATTCT ACACCAAAAAG CCCCAACAAT ACTACCTTCA TCAACTCAAA	120
	CCTATCCCAG AGACTGAACT CTTCAGCCAC AAAGAAGATG AAGAAGAACT ATCTGTCCAA	180
20	CAGCAGGTOC AGAAAGAGCT AGAGCAATTIG AAGAAAGGCA GTOGTCCTGT GGATACCAAA	240
	AAGAAACCGG TCCTGCAAGA GATTCAGITG GGATGTGAAT GTATGGTCTT CATCAAGACT	300
25	AGAAGACCAA TCAAGCCGGA ATGCTTTGTC AAACGCCTAG TACAGGAACT TGCATCGTCA	360
	GAAAATACTA CCAAGGITTC GOOGTAGGIC CAGAGATTGA CACCCATCAC TGATTCCTGC	420
30	AATOCTAGTC TAACAGAATT OGAAAAACTC TOCAGAAGOG TOCTTOCTCC TCATTTCCAT	480
	ACTGACAAAG AGATAAAGTA CAAGTTCOCG GTCGAGGTOG TAAAAAGGTAA CTTCAACAGG	540
35	ATAGACAAAA TOGATATCAT TAAACTIGIG GOGAAGGAGG TOGGIAAGAG TOGGGATTOG	600
	GGGCACTICTIC TOGACCTIANA GGACTACGAC ANGCTOGTICA TOGTICCAGTIC CTIATAAGAAC	660
40	AATATCOOCA TGTCTGTOGT GCACAAGGAT TACTCTGTOG CTCTTAAAA	709
	(2) INFORMATION FOR SEQ ID NO:667:	
45	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 717 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
50	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

**5** 

## (A) ORGANISM: PAG1445RP

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J

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:667:	
10	CATCATCITC CGAACATACT CGAGGGAGTT CGCGTTCGGG AAGITCTTGT ATCGTTGCAT	60
	GTAGIOGAAT TOCTCGTAAT CGTCTGTAAA TAGAAAATTG GCGTCAATCA TGTTGTCCCC	120
15	GITGGACGCG CCGGAAATGA ACATGAACGG TGGCAGCCG TAGCGCACCT TCTGGCCCCG	180
00	GCACGCGCC AGAATCGCAT CGTTGGTGCG CAAAATATCG CTGTACGCGA CCGGCATCTT	240
20	CICITCITCS ATGGGCTCCA ACACCGCCAT CITCAACAAC TCGCGCCCAT AGCTCATCTC	300
25	CATCTCCCCC GAGACGAGAT TGTAGTCCCC CTCCCCCCCCC CCACTCCTCC CCCACTCCTC	360
	CGAACGCAGC AACGTCGACG TGCTATTCAA GCTAGTGTTT GAAAAAGTGCA CATGCTCGTC	420
30	ATACGAGGAA CAGCTGAGCG CCATCTCGGT CACGCTGAGA AGGTACTGTT CTTCCCGGGT	480
	GTACAAAGAC CCCGCCTTGT ATGTCGAGCC TCTGGTGCAT TCCATTGGTG TCGCCATTGC	540
35	TCTGGCGCAG CCTGATACAC TCGCCGTCGA AATACTACCG CACCACCGCA CGAACGACCT TTCCGCCATT CTTTTGGTTT ATAAAACCCG ACTACGCATA TATTTCATCC TGCTCTGGCA	600
	TGTCCCCATG CCGTCCTCCG TGTCACATAG CTCCTTATTC ATCCTCCCCG TGCACATAG CTCCTTATTC ATCCTCCCCG TGCACATAG CTCCTTATTC ATCCTCCCCC TGCACATAG CTCCTTATTC ATCCTCCCCCC	660
40	(2) INFORMATION FOR SEO ID NO: 668:	717
	The second secon	

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 717 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1445UP

	(AI) SEQUENCE DESCRIPTION: SEQ ID NO:668:	
5	CATCCTTACT CACGAGGAAG AATCGAGCAA TAAAGTTCAC GCCGCTTCGA GCTCTAATAG	60
	COGTIAAGAGC ACCOCTIAGTA AACGTCCAGC CAAAACTIAGG AAGCCTIAAGG CTGACACTGC	120
10	GOCTACGAAA AKCOGAACCA CCTCCCCGCAT GCCCAACACT GCTGCTTTGC AGGCGCTGCT	180
	GAACAAGAAA AGGGGGCTT CGGCAGAATA GACTACTGGT AAACGTAAGT AATAGTATAA	240
15	ACTIGGITIT TITAATCCCIG GCTATCICAG ACTGCTAAAG CATGGCCGIT TAGGIGIGGC	300
20	CICCICGGIA GATGGITTOC ACCACGCAAG GIGAAAAAAA GATCACCAAC CCIGAAAAAAC	360
20	GITTAACACT TGTCAATCTC TAAAGGCGCT GCAATCAAGG CATATTACCA TTGTGCAGCC	420
25	ATGAATCTTG OCAATGAACC GAAGTTCCAA ATACAAGTTG ATGAAACAGA GGATACAGAG	480
	TOCAACGATA TITTICACOCA OCATOGIGIC ATCCCAGAAC GOCCACCITIC ACCGACCOCA	540
30	CAGCTOGAGG AAGOOCTOGA OGAAGTOCTA CAGAGACCAC ACGAGAATAG ATTAGAGAAC	600
	AAAGACTCTC TGAACTGGAG GACTGGAAGA TGAAGAAGAT GATGAATTTT TGGAGTTTTA	660
35	CCAACGIAAG ACAATGOCAG AAATGCAGAA GCAACAAAGA AGCGCAAGTA TGGGGAC	717
	(2) INFORMATION FOR SEQ ID NO:669:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 775 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
50	(A) ORGANISM: PAG1446RP	

{XI	SELUENCE	DESCRIPTION:	SEU	ш	: C00:UN

5	GATCTOCAGG CTOCTACOGA OGAACTCGTT TCCCAGGTTG CTCGCCTGAG TAAAGACCCA	60
	AACTITICCIA GCATTITICGC GCAGGAGCTA CAGAAGCTTA CTGGTGAGCC CCATATAGGC	120
10	OCCAROGIOG ATGATATAAC OCTAGTGATG GIGAAQGTAG ACTAGTAGAT TOCACATATG	180
	TAGAATTACT AATATCATTC GAATTTCTGG CTTAAGACAA TGTTCTTAAT CCGCTCTCTC	240
15	TOOCTOTTCA ATCTCTOCTC OCCUTCTAGT ACGTCATGAA CAAACTTGAC GTCGGTCGGC	300
	AGGCATATOG GGCGGAGTTG AGTCCGCTTT CCTGATTTGC TGAGAAACGT AAAGGGCACC	360
20	TIACCCOCTT CGACTITICA TGACAGAITG CIGITGACCT GIGIOCTGGI CCCAGAITCCA	420
	ACCATACCAA TGTTGTTCAT GOOCATTTTC TCATTCTTGC GOCATTCTAA ACATTGTTGC	480
25	ATCACAGCTT OGTACATCTT TTCCATTTCA TCTTCTGCTC TCCGCTCCTC CTCCGACTTT	540
	ASCUTTOUT OSTATUTUC GUTTATOUT TUGOSCUCTA GAUCUCUGUC AATAGIAAAC	600
30	ACCITCIGIGI CGTCGTCAGT ATCITCTTCA CTTTCACTCC TTGACCCCCA ATCACTATCC	660
	TOGICATOCT CATOGITATO TTOCTOTOAT AAGTOCTATT AAOGTOTTOT TOTTOTACOT	720
35	COCTOGAÇIC COCACTACTAC ACTOGIACOC ACTATCTICC TOCTO	775
	(2) INFORMATION FOR SEQ ID NO:670:	
40	(i) SECTION CHARACTERISTICS.	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 631 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1446UP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:670:	
5	GATCAATTAC ACTACTAGCA ATCTACTTTT CAACAATCTG ACTGTCCCCCG ACGTTAAACT	60
	CTACCGTGAA CAGCTGATGG TACTCAAAGA GCAGAGGTTT ATAGTGGAGG GCATGCTGGA	120
10	GAACGCCAAG AAACAGCGGC GTTTTGAAGA GGTTAATACG TTAAAGGAAA ATACCAAAGA	180
	GCTAGACAAT CAGATAGCCC AGCTCGAAGA AACCCTAGGC GACCAGGGTT TIGTTTAGTA	240
15	TCTAGCATGG AGITTITITGC TTAACTATAA TTACTGTGTA GATGCCGCAG ATAGCATGTC	300
	GIAGCATAAT TGCGAATITT CACCAACATG AAAAAGIGIA TGIGIATAAG GCATCCAGIG	360
20	AACTOCTAAC ATOCTGATGA OGTTTTAAGT AAAGATATCA CTAGCAATGA ACGTAAGTOC	420
	AGITITIGAG CITTATGICC TCTGTAGAAC ATAATATTAA CGACAGGGG ATAGGATGAA	480
25	AGAAGACAGC AGITATTIGA OCTGAACAGT GAAGOCTOGT CTOGAATTGA TOCGTTCCCG	540
	AATAAAACCA GCAAGCTTGA CTCAAGCATC AAGAGAAACA CAGGGTTTAT CAAAAAGCTG	600
30	AAACAGGIA TCACGAAAGA CTCGAAAGAT C	631
25	(2) INFORMATION FOR SEQ ID NO:671:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 703 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDELNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	
43	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1447RP	
	(11) CHARMATORY, FRESTARY/RE	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:671:	
55	GATCCAGGAT GATGAATTTG ACGAGGAGGG GGGTGCAGAA GAGAATGACG ACTACTICTICTACC	60

	GITTANAMA TOCTOCATOT COTOCCACOT COCCOCOTTO TAGTAGGCAT AGGOCTOGIG	120
5	GIACGERCA TOCGECATOG CERCECCAT GERCEGERCE CEATROSSEC ACCECETORE	180
	GTACATGTCG TACATCCCCC CCCCCCACCC GTCCCAAAACC ACCCCGTAGC CCTCGTTAAC	240
0	CASCITICAAG COCCOCAGOC CITICGTOCTIC ACCCAGCCCC TGTTGGGGCAG CCCCCGCCCT	300
	GICCOGGIGG TACAGCTTCG CGAGCTCGIG GTACCGCTTC TITTAGCTGCC GTGCATCGAC	360
5	OCCOGNICITIC ACCAGNOCCA GNACCIOGNA GGOCGNOGOC TOCTHOCCCT GGGGCCACCA	420
	TAGOCCCCCC TGCCACCCGG CGACGGTGCT AGCGCACCGC ACCGTACTCC GACCTGACGC	480
20	TGTAAGCGAG ACCGCCAACG TGCGCCAGTC CTGAGCAGTG CAGTCGGACG CGACAACATA	540
	ACACTTAAGC TCCTAGTTAA CGCTTTGGCG ATGGAGATCT TGTCGGTGCA TGCACATATC	600
?5	CAGGAGGGG CTCCGCCTCC GCTCGACTGC TGGCCGTCCA GGCTCCAGTT GGCGCGCTTA	660
	GCCATATOGG CGAAAAAATA AAGTCCTGCT CGAGGCGCGA TGA	703
30	(2) INFORMATION FOR SEQ ID NO:672:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 684 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1447UP	
45	(1.) (1.2.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:672:	
	GATICCASCAG ACCOTICOGGC TIGOCTICTTIGG ACATICCACTIG CCTICTTICCCG CCCCAGTICCCC	60
55	GBCAACGCGC CCGCCGGCGC AGACGCGCCC GCCGCCGCC CGTGCGGGTA CATCCGCACC	120

	AGGITICIOCA GCICAAACTC CAAGOCCAGC TIGITICIGI TCITICITOCG CITCOCCTIG	180
5	TACTICIACO COCCETACIT CITICOCCIOC TOCTOCIKCI CCACTICOCC CITICICCIOC	240
	CACTOCTTCT TCTCCTCCGC CGTCAGTTTT TTCCACTGGT AGCTGATGAT CTTGCTCACC	300
10	TOSCASTIST SCSSCATSTC CISSCOSCAC TECTTOCAST ASTOTISTCAS CASCITICISC	360
	TOGTOCCACC OCAACACCAT CAACOCCTTG COCOCCCCCG OCATGTOCTG CTTCTOCTTG	420
15	TAACCAGOOC GCCTCGCCGG CCTCGCCGTC CTCGTCCGCC ATCCTGGTGC	480
	GCTGCCACTC CTCGCCGCCG GGGGGCTGGT GCCAGAAAAA CTTCTGTGCC AGAGGCCCTG	540
20	COSCOCIOCO OCTOGOTICO COGOTICOTICO COCCOCOSCIG COCCITIGATI GOCTITOGICA	600
	AAGGCAACAA TIGCCCGGAT CICCCGCCGC TGCTGCCGCT GGTGTACGAT COGTGTGATG	660
25	GICAGCITICT GCTCCAATCA CAGA	684
	(2) INFORMATION FOR SEQ ID NO:673:	
30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
35	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1448RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:673:	
	- · · · · · · · · · · · · · · · · · · ·	
50	GATCCOCTAC GTATACAACG ACATATTOCT ACGTATCGAA TGTGATGTGA CAACATOCAA	60
	GATTOTOAAC AACAAGOGCA AGTOGTITTAG TOGTAAAATO CATOGTITOOC ATOGATOGGC	120
55	CCCCGGTTCG ATTCCGGGCT TGCGCATATT TTTCACAACA TGCACACACT GTGTGGCTAT	180

	COMPACOSAS ICCACIACOA GCAICOICAT TITIGICIAT AAITITACAAG CATATIGIAA	240
5	CTATIGIGIC ATTGATCTAA ATGTCGAGTC GATAGAATCC TTCAGCTCCT TGTAGCTAAT	300
	GATAATGCAG TICATCICGI COGGIGICAC CAAGATIATC TITICAGATA COCCOGIGIC	360
10	CACTITICTIC ACCCACCOCA CTACCTOCCT CACCCATC ACCCATTICC CCTTCTCCTC	420
	CACCTOGTOG AACACGTAAT CGTAGAACAG AATGATGGGG AACTTGTCCC CCGCCTCAGA	480
15	CCAGTOGATG TOCATOCTOG ATTOCATOCT ACCAAAGATG AAATTTAGCT TOCACATGAG	540
	CCTGAAGAGC CTGCCATTCT CTAACTCCCG CGACAAGTGC TGCTCGATGT TCTCCCAGTA	600
20	OSTOTOCCAC GAACTGATTA TGTCTAACAT CTTGTGGCTG AACAGGCCGG TGAACTCCGC	660
	AATOGICTIC TICTOGTOOG ACAAAAGGTA COCCAGCACC COCTTGAACA GOOGGTOG	718
25	(2) INFORMATION FOR SEQ ID NO:674:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(b) 10102001. Illand	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1448UP	
40		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:674:	
45	CATCTCCCCA CCCCTCCCAT CCCCCACCCCC CCCACCCCCCC CCCCCCCC	60
50	GCCACTGCGC CACAATGCTG TCCCATAGCC CTCAACATCC CAACTAGCTA GTCACCTTGT	120
	GCAATCGGTC TACCGATGGT GTGTGCGGCG GGGACAAAGC CGTGGTGAAA COGACACTTT	180
55	TCAAAATGGG CTGATCTGCA GCAGTACAGG ACCGATGAGC TGCGCGCACG GCGACAGCAG	240

	TCGCGGTTCG GCGCCTGGCT GCGCATAGGG AACTTACGTA TAGTATAGAA GGGCCGTCTA	300
5	CTTGCCGTAG GCAGCGAGGA TGTCGTCGTT GTAGCGGAGG TATTTGCCGT TCGCGCAGTC	360
	COCCATOCCT CTCACCOCCA COTTCCCCAA CATCCTCCCC GCCATCTCCC GCTCCACCAC	420
10	CTCGCTGTTC TTCTTGAGCT CCGTGAAGCG GCGCAGTGCC TCCGGCGCCA TGCGATGGCC	480
	CAACTITOTOC COCATICTOCI TOTOCATOTE OCTOTOCACO ACOCCOOCO OCACOCCACA	540
15	COCCOCCACC OCAGOCTCTT CCOCCOCCAG CGTCATCOCA AAGTGGTTCA CCGCCGCCTT	600
	CGACCACCCG TACGCCCCC ACGCGGACTG TCTCCCACTT ACTAGCTGCC CCTGCCCTGC	660
20	TCTGCGTCGT ACATACATAT GCCTTCGTGC TCGCGCCCGA GCTCACGAAC ACCACACTGC	720
	cocc	724
25	(2) INFORMATION FOR SEQ ID NO:675:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 697 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1449RP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:675:	
45	GATCCAAAGA COOCGIOCIC OCACTICCAC ATGICICCAA GCTGGACGOG AACAACGATA	60
	TOTTACTOOC OGTGAAAGAA AGCCCGAATC ACAAATGCCC ACGATGCTOG AAGCACGCAT	120
50	CTCCCGAGGC CGACGCTCTA TGTAATCGCT GCGCCAGAGT CCTCCAGTAA GCCAAACCTG	180
	AATTITICAA AAATTGAAAA CITCACCATG GCTCACATGC TGACTGCTTT AATATCCTGT	240
55		

	ANATACANCO GGACTOTOCA GGTOGATOCT COCTONOCTG GGCCCCCANC TCTCCCTTGT	300
5	ACCOCCTOCC GEOGROCOTE COTCATTCCC COTGCATOTC GOTTCCACAG GOSSOCOTTC	360
	TGGGGTGGGC GCGCGCCTGC CGGCATTCAT CGCGGGGCC TACGGCAGCC CACCGGGGA	420
10	CGCCGACCCAG ACCCGCCCCTT GCACGTACCT CCCCCCCTCC CCCCTCTTCC ACCCCCTTTA	480
	COCCCCCCT TOGTTCOCCC CGTACATCCA CCCTCTOCTC CCCAACCCCC CGGTCCCAAC	540
15	ACTOSCOSCO TITOCTISCTISC TOCATGAGGC CACOGCCATC SCITOCTOTISG COCTISCTISTS	600
	GIGGGGGGIC TACAGCIGGG ACGIGGIGGC GCIGITGCCG CAGGGCCIGC TICACTACCT	660
20	GOCCGAAGCA COCATCCTOC CGTCRAGAGG TTCGTGG	697
	(2) INFORMATION FOR SEQ ID NO:676:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 715 base pairs  (B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
30	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1449UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:676:	
45	CATCOOCTCA ATGOGITICCT CAAGCCGTGT CTTTCGTAAG ATGACCTCAA CTTAAAGGCA	60
	COCTOTOGAT ATCTOGTTTC TTTTTTTAAC AGGTGAGCTT TOGAAAATTT TTOGTTCTCA	120
50	CCTCATCTCA TCTACAATAG TATGTCTAGC ACCCCACCAA ACCTTGCGTA ACCCCTCTAT	180
	TCAATATGAG TAAGCAGGTA AATGATACTA GCAAGAATGG TCTTGACCTA AAGACGCTGT	240
<i>55</i>	TIGICCOGAA TATICCGITT GATOCTACOG ATOCAGAGCT GACAGACTIC TICICGCAGT	300

	PROCECULAR TRADICATOCIF GIGATICGIPAA AAGATAATIGO QOOCTOGAGO AGAGOGTTTIG	360
5	OCTITICICIC CITTOCTCTC CAAACTCATA CACACCCTCC ATTOCACAAG OCACCCAAAA	420
	CACAGITICAA GOCCGTCTT CTGAGGGTGG ATGTTGCCAA AAGAAGAGAA CGTTCGAAAA	480
10	AAGGCGATGA GOCCGAGGCA CAGACCTCCG CGGAGGACGC GGAGAAGCCG ACTACTGCTC	540
	CCCACOCTICA CCACCCCTC ATROCOGGOCA ACCCCAACCT GATCATTAGG AACATGCCGT	600
15	OGTOCTOCCO CGACCCGACC AAGCTGAAAA AGATCTTCGG TAAGTTCGGA GTGGTTGCGG	660
	AGOCTOCATO COGCOCAAAG COGATOGAAA COTGTGTOOG TTGCATTTGT CACGA	715
20	(2) INFORMATION FOR SEQ ID NO:677:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 705 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
35	(A) ORGANISM: PAG1450RP	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:677:	
	CATCAATTCT GICTTGAAGT AGGTATTAAT CAATGGGTCA GOCTGGGTGG AATTGCTTAC	60
45	AAAAATACCA ACCCAATCAT CTTGTAAGTT GGTGAGCGAT ACGTAGACAA TTTGCCTCAC	120
	ATCAATCITA TAATOGACAG CATAGGIGAG TIGATTATTA ACCAGIGICT TICCGATAAT	180
50	GIAGAAATOG GATGOCGIAA GIATAAAGGT TITIGOGTAGC CITTIGOGCCG ACCIACCAAA	240
	TITICAATGI AGCGCTTGCC CATTCATAGA GAATACGACA TGATCATTAA TTCCAGCTTT	300
55	CCTTTTGACA AACGCACCCT TCGATTTCAG CTCATTACAA GAAAGGTAGT CTCCCAGGAA	360

	TOCCCIGIAA CCIAACAAAG ACATTOCACG CCTCTCCTTT CTOCCACCCA ACAACTTGTT	<b>4</b> 20
5	ACCGTAATICC COGAGTTIGTT CGAATTIGGTT CCCATGTTTC ATCTCACGGA TAGCACGCTG	480
	GATACGAATC GCAGAATCGA TACGCCGTTG TAAAAAACCGC CGCCAGGCTC TCTGAATGCG	540
10	AGATGCCATA TTATGCCAAT ACTTATCCCT CATGTTTTCC AAAGCAAACA AGGTCTCAGG	600
	TGTTTAATA AATACCTTCG TTACACCCAA CTGATATTCA GTCACAGGAA TTGAAGTATC	660
15	TCTCAAAATT AAATTGACAG CATCTAAGGT ATTACCTTGC CATGT	705
	(2) INFORMATION FOR SEQ ID NO:678:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
	, , , , , , , , , , , , , , , , , , ,	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1450UP	
	(1)	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:678:	
40	GATCOCAAGT TOGAAGACCG AGTATCCATA TGATTACTCG COCGAGACCC COGGCTCGCG	60
	CATCAAGCCT CAGACAGTTA TCACTCGGCT CTCCGAAATC GCAAACGCCA CCGGAAAGGA	120
45	GGTCATCGTG ACGACCGGTG TAGGTCAGCA CCAAATGTGG GCCGCCCAGC ATTGGACGTG	180
	GAAGAAACCA COCACATTTA TCACATCAGG COOCCTCOGT ACCATGOGCT TTGGTCTACC	240
50	GOCGOCCATT GETGCCCAGG TAGCCAAACC CGATGCGAIT GTCATCGACA TCGATGCGGA	300
	COCCTCOCTC AACATGACCT TGATOGAGAT GTCCAGCCCG GTGCAGCCCG GCCCCCAGT	360
55	AAAGATATIG TIGITGAACA ACGAAGACA GOGAATOGIC ACTCAATOOC ACTCICIATT	420

	CTACGAGCAT CGITATTICTC ACACCCATCA GCTAAATCCG GACTTCGTCA AGTTGGCTGA	480
5	TOCANTOCOC TICANACICA TOCOCCTAGA COCOCAGTOG CACATOGACO CCATOCTOCA	540
	GGAGTITATT AATTGCAAGG AGCCCGTGTT ACTCGAAGTG GCCGTCGAGA AGAAGGTTCC	600
10	CGTCCTCCCG ATGGTCCCTG CCGGTAAGGC CTGCATGAGT TTATCTACTT CGACCCAGAG	660
	GTCAGCGACA GCAAGCGGAG CTTCGCAGCA GGCGTACGG	699
15	(2) INFORMATION FOR SEQ ID NO:679:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	THE STATE OF THE S	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1451RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:679:	
	CATCTICCTC CTACTACCAA ATATTCAAAT CACAACTTIC AACACTCAAC TCCCCAAACC	60
40	TTCCACGICA ACAGCAGITG GACGIGGGIT AGIGGATCCT AAGAGATGGG GAAGCTCCGT	120
		-20
	TICAAAGGCC TGATTITCCA GOCCACCATC GAAAGGGAAT CCGGTTAATA TICCGGAACC	180
45	TOGATATOGA TICTICACOG CAACGIAACT GAGIGIOGAG ACGIOGOCGI GAGCCCIOGG	240
	AGGAGITATO TUTTOTTOTT AACAGOTTAT CACCOGGAA TIGGITTATO COGAGATOGG	300
50	GICTTATOOC TOCAACACC CACCATCTAT OCTOGGTCCG GTOCGCTTAC CACCGCCCTT	360
	GAAAATCCAC AGGAAGGAAT AGTTTTCATG CCAGGTCGTA CTGATAACCG CAGCAGGTCT	420
55	CCAAGGTGAA CAGCCTCTAG TTGATAGAAT AATGTAGATA AGGGAAGTCG GCAAAATAGA	480

	TCCGTAACTT CGGCATAAGG ATTGGCTCTA AGGATCGGGT AGTGAGGGCC TTGGTCAGAC	540
5	OCCOCAAGIG TOCTIGICGT CIGICCTCOG GOOCTIGCTC CIGOOGACGG ACIGCTTCCG	600
	TOCTICTOG TAGACOOCCT TOGTAGACCA TCTICTOGTICG TCCCTTOCTA CAATTAACGA	660
10	TCAACITAGA ACTOGTACOG ACAAGOOGAA TCTGACTGTC TAATTAAA	708
	(2) INFORMATION FOR SEQ ID NO:680:	
15	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 722 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1451UP	
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:680:	
	GATCCCTTAG CGACTCTCTC CACCCCTCGA CGAGGCCATT GAGCTCTTAC GAACTCCACA	60
35	AACCIACIGG AACICIGITT CCACACITCT TICIGITTIGT CTICAACIGC TITCGCAIGA	120
40	AGIACCCCC AGGCIATITT TCTTACCCGC CTGGTGTTTG TCTATATACC CGGTTGTATT	180
40	TTTGATAAAA AACTCAGCTC TTCCTCTACG GCAGAAATAT ATATCCAGTC CTTAGCGCCA	240
45	TGCGAAAATC TGCCTTTTTA CCGCTGTTTC TCCCAGTCTT AGCACTGGCA GAAAAAAGAT	300
	GTATOCCGTA TAGCCCCCCC CCCCCCCGAA AAAAAAAAA AATAGAAAAAA TAGAAAAATA	360
50	AAAAGACGIG GGCCGCCCG CGGGCAGACG AAGAAAAAAT AGGCGCCAC CCCTCCAAGC	420
	AGACCACAGG CGAGACATAA TAAAATCCCA CACCAAGGGA AGAAAGTCTT GTGCACGCTC	480
55	CCGGCCTCAT ACGCTGCCAT TCTGTTCCAT CCGGCTTGCA AACCCAGTAG TGGCATGTCA	540

	AASCATTIGCT COGACGCTCC GCTGCCTTGC AGTCGACATC CTCTTCCTAA CCCCAGCCAG	600
5	ACTICCCATA CTTTOCACTT CACATAGCAT ATCACTITTC AGATCACTAC GTGACATTCG	660
	CTACOGAATG OCACTOCAAT GCCGACAAAC CTCTTCCTAC CCCGTGACTT ACCCCGATGT	720
10	OC	722
	(2) INFORMATION FOR SEQ ID NO:681:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 719 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1452RP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:681:	
35	CATCAAATGT GOCTCTACAA GOCCGCAAGT GOCAGAGAAT ATTAATGAAT CAGTTCCGCT	60
	CACATATTIC TATTCTCACG GTATTCCACA TICCTTTCAC TACCTATCTC CCTCTACCAA	120
40	TOSCIGOCIT AGTAAGOCIT AATAITAACI GAAAAGOOCA GCAGIGIAAT CCAICTAGIA	180
	ACTAACACAT ATOCATTAGC ACATGITICG TICAGIACIA CGICATICTT ACGCCGICCC	240
45	TACTOTGAAT TACACATOGT OCTOGAGAAG OCTCATAAGA TTCTTCACTA GOGATGAGAA	300
	GOCAGCTCCT CCATCOCTTC CGAGAGAAGA GCAGAAAGAG TTCCGAACGGC TTCAGAAGAT	360
50	TOCACAGTCA CAAGCTOCCA TOCACGAGTA CAACAGACAG TTOCACAATG ACCATACGAA	420
	GCAGTICAGOG AACTICTOCCA TOCTCAAGAC AGAAATAGGC TOGTTCTOAC COGAATTCAG	480
55	CAAGACGITG CCAGAGITOG AGGGCGACAA GAATCCCCGAG ACAGGGCAGA TTGGCCGGCC	540

	GCGCCAAGAC CCACTGCGGT ACGGGGACTA CTCATACAAC GGCCGCGTGA CGGACTTCTG	600
5	AGGIATAACT TGIGTTTATA TGITTGCAGG TTGGTTAAAT ACATAGCTTG COCTCCAACT	660
	CTCTCGCAGC TGCAGACAGG TTGTCGGTGC ACTCCGTGAT GAATTTCGAG TCCAGCTTT	719
10	(2) INFORMATION FOR SEQ ID NO:682:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1452UP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:682:	
30	GATCACCAAC TCTACAGCAA GAAATCCTAC GCCCAGCAAA AGCTGTCCTC GATGTTCTTC	60
35	TATTCTGTAA ACAGITTGTT ACTTCTGGTC OCTTGTATCT OCATOCOCTA TCATCTTTTC	120
	ATCIGGAGCG TTITICAGCCC GAAGTIGIGC TACCTICIGG GCTGGAACAT CCTCATCCAC	180
40	TTTCTCACTG AGACGGTGCT TGAACCTTTC TTGCTCATGG TGGCGGGCTG ACTGTCTCTA	240
	GFICCACTIG TATAATATIC CTICATCAGI GAGAATCICA TAGIATIGIC ATATATTAGA	300
45	TATTATCTAG GTCATGTTTT AGAGAATAGG TCTCTTCCGA AAAAATTGGC TACCACTGCC	360
	AATCATTACA TGTCAGAACC GACCATCTCC AAGTGTCGAA CCGTCCCCAC TGCAAATGCT	420
50	CTCACTTAGA TOCAGCTTCA GACGCTTATT TTCTGTTTCC TGCAGGGTTT ATGACCAGCA	480
	GOCGCAGAAG GCCGTGTCTT CCTGCCCCGC TGGCACACCG CTGAATCTGC TTATAAAGAA	540
55	CCCCCCAGGAG CACCCCTTCC CTCTCCAACA TCCCACTACC CCAGTCCTTA TCCAACGTCC	600

	TIGACCIGAG GCGCAAGCCG CAAAGCTGGC AGAGGACCCA TTAAAGCGCG GAAGAAGGCT	660
5	CTOCOGOGGA TGAACAGAGA ACACATOCAG CAGCAGAACT TCCTGGGGAA GATGTGAA	718
	(2) INFORMATION FOR SEQ ID NO:683:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 724 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDFINESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1453RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:683:	
30	GATCTTAATT TAAAATTTTA ATTAACTATT TATAATTTAG AAATATATAA TCTAGAGATA	60
	TATAATCTTA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
35	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITIG TOOCATCITA	180
	ATTTTATTA TITAATTGAT TATTATCTAT TITAACATAAA ACATTTTAAA ATGTTATAAA	240
40	ATAAATAAGA AATTACTTAT AGAATATTTA TTAAATAGIA TTTAATTTAA TTTTAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GIGATATATA	360
45	ATTTAATTTA TATAAATTAT TTAATTTACT TCATTGATAT ATATAATTAT TAAATGTACC	420
	TITCATAATA TITATITITA TTAGICTAGI AATATITCIA TITAATAGIC TACCCITTAA	480
50	TTOGATATTA CTACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	540
	TAATAATITA TTATCTAAAG TATATAAATT AATTAAATCT TITITATTAT TATTTAAATT	600
55	TATIAATAA DITITITAATA TAATITATIT TATITAATIAA TAATITATOA TAATAAATAA	660

	ATCATAATTA AATOGIAATT TATTAATAAT TATCTITAAT GAATTTAATG ATAAACCATT	720
5	ATTA	724
	(2) INFORMATION FOR SEQ ID NO:684:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 732 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) CRGANISM: PAG1453UP	
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:684:	
	(XI) SEQUENCE DESCRIPTION: SEQ ID NO:004:	
30	GATCAAAATT TCAACAATTT CCATTTCATT TAGTACTACC ATCACCATOG ACCAATTGIT	60
	ACATCATTTA GITTATTAGG TITACTATTA ACTITAGCIT TIACTATACA TOGIATTATT	120
35	GGIAATATIT ATCCTTTATT ATTATCTTTA TTAGEAGTIT TATTACTAAT AACTTEATGA	180
	TITAGAGATA TIGIAGCIGA ACTIACTIAT TIAGGIGATO ATACTITAGO IGIAAGAAAA	240
40	GGTATTAACT TAGGITICCT ATTATITGIT GTATCIGAAG TATTAATTIT TOCTICTITIA	300
	TTTTGAGCTT ACTTCCATTC AGCTATAAGT CCTGATATTC TATTAGGTAA TGTTTGACCA	360
45	CCAGTAGGIA TIGAAGCAGI TCAACCAACA GAATTACCAT TATTAAATAC TATTATTTTIA	<b>4</b> 20
	TTACCATCAG GICTAACTAT TACATATAGT CATCATGGTT TAATTGAAGG TAATAGAAAA	480
50	CATOCTITAT CAGGITTACT TATTACTITC TGATTAATIG TTACATTIGI ATTATGICAA	540
	TATATIGAAT ATAGTAATAC ATCATTTACA ATTACAGATG GTATTTATGG TTCAGTATTT	600
55	TTTOCTOGIA CTOGTTTACA TTTCTTACAT ATOGTTATGT TACTAATTAT GTTAGGTATT	660

	ASTIATIONS GRALAMOMMA TIMICATTIA ACATCAACAC TCATGIAGGA TATGAGACTA	720
5	CTACTATITA II	732
	(2) INFORMATION FOR SEQ ID NO:685:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 714 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1454RP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:685:	
30	CATCATOCCT CACCOOCGIG CAACATOCAG GICACOCGIA TGIACCCCAT GITOCCTTAT	60
	TITTICACCI GAAGCGGAIT GGCTCTTGIT TATACAGACT TITICTGCAIC CCTTGGGGCC	120
35	CAGAGCTAGG CCCTAGAATC CGTGTCGTAA GCGTTGGGCA CTGATTCAAC ACGAGCACAA	180
	TICCAGIGCT GCICGIAGAA ACGAGGCCCC TGAAGTATAT GGIGATATCC ACATTGCCGG	240
40	AGTATAGITIC TOTGT09999G CCACTTCATG CCATGTGCAT CTCCGGCCTTA CTCCACAGCC	300
	GCACACGCIG CATIGITITIG GGAACATCAT GIGAAATACT GGTATAGAGC GCATTICATA	360
45	GGGGGCCAG CAGCIGIAAT AGGGCGCAT ACCCCCCTCT ATTICATGIG TICATGIGCT	420
	AGITTAGAGG TATTTTTGAG GIOCATOGGT TATOGCTTAC TTTOCATATG GAGATCTCAT	480
50	TOGCTOGTAA OGTATATAAC TGAGGTAGCC GTAAACTTGC ACTGGTTCCC ATTGCCAGAG	540
	CGAACCTACA ATACCACCAT CIGOCTOCAA GITGTGAACA ATOCATTOCA ATCOCATACT	600
55	CITTIGGGGC TGIGGGCTTT TGCTGCAACA ATTAACAAAT GCCTTIGATG AAGGAGTGCT	660

	AAGGAAATGT TATGAATCTG GTGTATGCCA CCGGAACAGG CATTACGGAG AGAA	714
5	(2) INFORMATION FOR SEQ ID NO:686:	
	(i) SEQUENCE CHARACTERISTICS:	
10	(A) LENGTH: 720 base pairs	
10	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
20	(A) ORGANISM: PAG1454UP	
20		
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:686:	
25		
	GATCAAGOOC TGTATOGTTC CCOGCAGCOCC AGTAACAGCG GTCCTGTACG ATTTCAACGA	60
	TICCAACATG GACGATGATG GCTCCAAAGT TATGTTCCCG ACCACGCTTG AACTCAAAAA	120
30		-
	GETTITICAG GCTATICGIT TIGAGGCCAT CAAACGGGG CIGCAAGIGI TICCCATTAG	180
	GAATATTOCT CCTATCTTCC CACAGGTOGG ATTCAAGAAC GTAAAATATA COGTTCTGAC	240
35	CONTROL CONTROL GENERAL GIRAMINIA CONTROL	240
	ATTCAACCC COCCATTICG TCAATGAAAT COCCTTCGTG AACCACCTAC TIGCAACGTT	300
40	TCACTACGAT TITICIAGICC GAACCITTIT AACIGATOGI AGIAAGIATC CAGITGGAAC	360
	TGACCCACAG ACACTGCCGA GGAGGTACAT TGATGAGCAC ATGGGCCAAA TAGATGACAA	420
	TOTAL	420
45	TOCAGGATOC TTOCGTCTTA TTOCAATCAC GGCGGAAAAA CCAGAGTAGG TTTCCACCGT	480
	TOCTATIOCT ACCORDOCA ATTOTOCOGG TCATTATATA TGITAGCAGG TGICAATACC	540
	TCCTTACAAC CTAATATTTC AAAACCTAAT ATCTTCTGCT CCTTAGAAAG AGCCACTTCC	600
50		500
	TEATATGITA ATATCTACCG CTAGTICTAT CTAATAATTT TATAATTTTG ATAAATCTTG	660
55	ACGTACATOT TATCACTAAG GAAGATOTCA TOACAAACTO OGCAAAGTGT TICATATATA	720

(2) INFORMATION FOR SEQ ID NO:687:

5	(i) SEQUENCE CHARACTERISTICS:	
J	(A) LENGTH: 712 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1455RP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:687:	
25	GATCICTICG ACATAGIGIC TTAATAGGCC TGCTGAGGAC TTCACTGAGA AAGCTTCAAT	60
	AGCGGCAAT GGCCCATCTC ATCAACACTT AAAATTTTTC GTGGCAAAAG AAACAACACT	120
30	OCAATCACET GACCACACAA AACTCACCAT TTACTGITGA AGGGGAGCAG GCTACGACGA	180
	CTCTTCTTCG CATGGTAACT CGCTGCTGTC CACTTGCCGC TTGCCGAGCCT TCTTTGCTCA	240
35	COCTOCCTCT TICTCCTCTT CTAACAGCCT CTCCCGGTTA GCTGTGATGT AGTGGATGAA	300
	GAAGTOGCCA TOOTTGCTGC GITTOGCATC ACGCAGGAGC GTCTCGACAT CGTCGTATAT	360
40	ATCAATGOGT COCTTTCGCA GITGGTTTAG CAGCTTGTTA TCACGCCCTG CACATTGCAA	420
	CTTCGCCATG GCTTTGGTCG ACTTGAACGA CACCTCGCCC GGTTTCATAT ATCCACATTT	480
45	GCGCAGGITG TGCCCAGGGCG TGCTCACAAT GCTACATTGT GCCTGCTTGT TCCCTTGTAC	540
	AGACTICTIGAC TITOCACAACT GCAGGCAGGC ATTOCAGCACA TCCCGCGGCA CGTCGCTGGA	600
50	GCTCTGCTGC TTTGCATGTA ACTTGAGATA GACATGTGCG CTGGCATACT TGTCTACGTT	660
	GGAACCAGAA GIAGIITIAAT CCCGGIACCC GIOCTIGAAC AAAAGGICGI TC	712
55	(2) INFORMATION FOR SEQ ID NO:688:	

	(i) SEQUENCE CHARACTERISTICS:	
5	(A) LENGTH: 720 base pairs	
3	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
15	(A) ORGANISM: PAG1455UP	
,,		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:688:	
	GATCCCATCA CATGAAATGT CTAGAACTCC CTOCATGACG CGAATGAGGC CAAGAATGTC	60
25	TGGTGGGCTT GGCTAACCGA TGTTCGCAAC TGCAACAAGG GGTACCTGGT GTTTATAGCC	120
23	TOTOGOCTT GOTTACCON TOTTCOCKIC TOCKICHOO GOTACCIGGT GITTAINGCC	120
	GTATGTOGTC ATCCCCCATT CGTCCAACAG GAGAGAAGAA CGCGACCACA AGGAAACCCG	180
30	GTAAAGCATC TAGAATCAGC AACCCTAGAG AACGTTTGTT CGTCGTTGGC GCAAGAGCAC	240
	GCAGCGIAGG GGCTGGGAGI TGCCGTGGCT ATTCATGCGT GGGCACGCCG GGIATATAAG	300
35		
33	TAGGGTATGC GTCCGTTGAA CAGAATGGAT CCGTCTCAGA ACAATACCAA AATCGCATTT	360
	GGAAAAACAA CCACTAATAT GAAGTACACC TCCGCTATTC TACTCGCTCA AGTCGCTTTT	420
	COMMANN CONTINUES GENERALE ICCOLLETE TALICOCICA ASSOCITITE	420
40	GTTGCAGCAC AGTCATCCTC GGGGTCTGTT ACCGGCAGCG CTGCCCCCGC TCCGGGTTGCG	480
	COGTCOCCCC CAAGCATTTC TAGCACCACG ACAGTCACCG CCTCAGGTTC TGGACCAGGC	540
45		
45	GCCACCTCCC GTGCTAGCTC CGGTGCAGCA GGCGGGGCCG CTGGCGGGGCC CGCAGGTGGC	600
	OCCOCATOTO GCOCCOCAGO TOSCOCCCC GOTTCTAACT CCCGCAACTC TGGCTCCAAT	660
50	GGATCTGGCT CCCGGCCAGA ACACTCTGGA ACAGAACACT CCCGCCCCAGA ACACTCTGGA	720
	CHICACO COCCOND MARIETON MANAMARI COCCONDA MARIETOTORA	720
55	(2) INFORMATION FOR SEQ ID NO:689:	
95		

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 696 base pairs	
_	(B) TYPE: nucleic acid	
5	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1456RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:689:	
20	GATCCACOCC COCCTOCTGA CCAACGTCGT CATCATOGOC GOCCACCTCCC TGCTCCAGOG	60
25	CCTGGAGCAG CGCCTCGTCA ACGACCTCAG CCTGCAGTTC CCGCAGTACA AGGTCTCTAC	120
	CTACGCCACG CCCGCCCACG TCGACCGCCA GCTGCAGAGC TGGCAGGGC GCGTCAACAT	180
30	GIGCCACCIC CCGGACIGGA AGCICGGCIC CIGGGICACC AAGCAGGAGI ACCIGGAGIC	240
	CCICGACAAG TAGCIGIGIA GIATGIAACC GIATGCCGCG ACCCIGCGGI TICTTICCCG	300
35	CICCCCACC CCCATGACGC CCCCCGCCCC CTTCGCCCCC TCCCACGCC TGCCGCCCCC	360
	CGCGCCCGCC CGCGACACCG TCGACCTCTA CCTGGACTAC TGCTGCCCCT TCTCGCGCCC	<b>4</b> 20
40	CCTCTTCCTC GCCTGGCACG ACGCCCTTTT CCCCCGCCCG CGCGCCGACT CGCGCTTCCA	480
	GATOGICITO AACCACGICA TOCACCCTG GCACCCCCCC TOCCAGTACA TGCACGAGGC	540
45	COCCTORCE GROSCORCE TOGACCORC COCCTTOCTG COCTTOTOR COCAGCTOTT	600
	CCTCCACCAG GACCGCTGGT TOGACACGCG CACCGCCGAC AAGTCGGGCC ACGCCGTGTA	660
50	(2) INFORMATION FOR SECURITY AND COO	696
	(2) INFORMATION FOR SEQ ID NO:690:	
EE	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 739 base pairs	

(B)	TYPE: nucleic acid
(C)	STRANDEDNESS: single
(D)	TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

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(A) ORGANISM: PAG1456UP

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:690:

GATCTGGAAT ATTACCGGCA CAAACTTGGC GCTGTGCTTC CACACCAGCC TCCGGTACCG 60 CTTCACGGCC ACCAGCTCCT GCAGCAAGCG AATGCACACG TATGCCAGCT CCATGCGCTC 120 CAGATTAGTC AGAACCCGCA GGTAGTTGGG GTTCGACACC ABCGCCTCCA CCAGCTCCTC 180 CCTCTCCACC CCCTCCTGGA TCAGCACCGA GACAACGTTG AAGCACGACA GCAGCACGAA 240 CLOCLOCATION COCCOCCITAL COCACACACATA COCACACATA CANCALOCACA CANCALOCACA 300 CCCCTTCTTG AAGTACCGCA GCACCTCGTG CACGTACTTG TCGCTCGTGA ACAGCTCCCGA 360 CAGCAGGITIC AGCACGCCC GCTTCGCATC CAGGITGITIC GACGICGCCA GCAGGIGCAC 420 CACCCCTICC ACCCCTGIT CCACCGCAG ATCCAGCGCG CCGCCGCGCG CGTGTTTCAA 480 540 CAACGICGAC TOGAGCITCT TGGCAATCCC CGCGICAAAC TCGCTCAGCT CGGGCGAACG 600 CACCAGOGG TOCCAGOCA CATGOCTOGA GOTGATOGTA TIGOGGATAT COTTGAAGTG COTOCTATCA ACCAGAATCT TTTGAACCCC CTGAGCCACG GGCATCGTCA CAGCTAAGAT 660 720 CTACGCTTCC ACGCCACCGT ACTOCCCACT TTGAAACCCG TGGGACTAGT CAATATCTGG 739 CGTGGTCTGG CGGACTCCC

50

45

(2) INFORMATION FOR SEQ ID NO:691:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 688 base pairs

(B) TYPE: nucleic acid

	(C) STRANDEDNESS: single	
5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: INA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1457RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:691;	
	CATCAATATC COCACCAAAT CIGITGIATC TACTACCOCC ACCCCCACTG COCCCACCCC	60
20	ACCAGGATCT CAGGCTTCGT CAGCGAGTCC GGATTCGTCA GCTAAACAAA AGAAAGATTC	120
	ATCTCCACTA CCTCTTGACT TACCTCCACC GAAGGATTTT AGCAAAGAAA TCGAGGAGAT	180
25	TATAGAACAC GATTIGACTA AATTOOCCIT TOAGAATOCT CITTITIAAAG ATGAACTITOC	240
	ATATTOGTTA CAGOCCAAGA GOCCATTGAT CCAACCGTAC AGCACTATGT CTGAAAGAAT	300
30	GITGAAACAG CIGGAATOCT CATTACTIAA CIGCOCAGAT TOOCTIGACG CIGACACACC	360
	ACATCTCTAT CAACACCOC TCTCTTTACC GCATCCCACC TCCATTTTCT TCCCTAGTGA	420
35	ACCGATCAGG TICGIGGCTG CIGGCTGGAA TAACGATAAT ACGTCCACTA AAGATATCTA	480
	TOGAAAAACT TCTATOGTTC AGATAATGAC CAAGTTCGAT TTOGATACCC TGTTTTTTAT	540
40	CTTTTATCAT TATCAGOGAA CGTACGACCA ATTCCTAGCT GCCAGOGGAA CTAATCATCC	600
	GTGGGTGGAT ATTTAATAGA GTCAATCGGT GCTGGTTTTA CAAAGAAGTT GAAAAGCTGC	660
45	CCCCTGGAAT GGATCAAAAA GAAGAGGT	688
	(2) INFORMATION FOR SEQ ID NO:692:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 711 base pairs	
	(B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single	

(D) TOPOLOGY: linear

5	(ii) MOLECULE TYPE: DNA (genamic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1457UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:692:	
	GATICGAGGAC TIGAAGCAGT TCCGGCAGGT CGGGTCCAAG ACCCTGGGC ACCCTGAGTA	60
20	CCACCTTCCC GCCGTCCACG TCACCACCGC CCCTCTACGC CAGGCTATCT CCAACGCCGT	120
	TOGCTTOGOG ATCOCOCAGG CGAACTTOGC TOCCACTTAC AACAAGCCGG GTTACGAGTT	180
25	GTCGCACAAC TATACGTACG TGTTCTTGGG CGACGGCTGT TTACAGGAGG GTGTGTCCTC	240
	CGAGGCTTCC TCGCTTGCAG GCCATCIAAA GITGGGCAAT TTGATTGCGT TCTATGACGA	300
30	CAACAAGATC ACCATCGATG GCCACACTGA GGTGTCCTTC GACGAGGATG TCTTGAAGAG	360
	ATACGAAGCA TACGGGTGGG AGGTGTTGAA GGTTGGCCAAC GGTGAGGAGA ACTAGAAGAC	420
35	ATTICCCAGTG CCTTGGAGCA GOCCAAGAAG AACAAGGACA AGCCAACTTT GATCAAGTTG	480
	ACCACCACTA TROGGITTOG CTCCTTGAAT 90000CTCCC ACACTGTGCA 00000CCCA	540
40	TIGAAGOOGA TGATGICAAA CAGTIGAAGA CGAAGITGGG CITTAACCCA GATGAGICCT	600
	TCATTGTGCC TCAGGAGGIT TATGACCTCT ACCACAACAG CACTATCCAG CCAGGTGCCG	660
45	AGTCCCAAAA GGAGTGGAAC GCTCTACTCG AGAAGTATGC GGGTGAGTAC C	711
	(2) INFORMATION FOR SEQ ID NO:693:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 688 base pairs	
	(B) TYPE: nucleic acid	
	• •	
	(C) STRANDEDNESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1458RP	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:693:	
15	CATCCOCAGT AGCTGATTGT TCGGGTGGCC AGGCGAATAT TGCTGGAAGC GGTTCAGGCG	60
	CGTATATTIG CICIGOGGAC COCCAAAGTA CCCGCCGAGG TTACTCTTGC TGGTCGTACT	120
20	AGAGAAGITG COCACTOCCC TAGCAAGTOC GGTOCTAGGT ACCOGGATTTA GCTTCOCCAG	180
	TAATOGTGTG AAGACGTTGC GAAATGOCAC AGACGCCTGT ACTGGTCGCA CTTGCAAGTG	240
25	GATAGOGITG CTAAGAAAGA AACACOGOOC ATAGGAGOOC GTGAAGGIAG ATAAGCICAT	300
	GETCAGCAAT CAACAAGCCT AATGATGATC TTCCTTACAA AATGAGGTTC TAAAGCGACG	360
30	TTAAAAAGGG ATGCCCAACG CTATGTTCGA CACCTATGGA ATATCCGTAT GAATGACTGT	420
	GTATCATTAA CGACGGTACT TCCTTACAGG GCAATGGCAG GATGGTAACG CCGAGTAATG	480
35	TCCAATAATC ATCATATATA CTCTAGFTAT ACGCTATGAG GOGTCATTTG ATGTATTGTT	540
	CGPTCGCCTA TCGGCTATGC TTCAAATTCG ATGAGGTTGG GCAGCTCGCC ATTCGTACCT	600
40	OCCOGNICACI CICIAGICIC TITIGICOC CETIGICIC GICTICACICC	660
	ATGTCAAGGT CCAAGAGATC ACAGAAAA	688
45	(2) INFORMATION FOR SEQ ID NO:694:	
	(i) SEQUENCE CHARACTERISTICS:	
50	(A) LENGTH: 724 base pairs  (B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
55	(ii) MOLECULE TYPE: DNA (genomic)	

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(vi) ORIGINAL SOURCE
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(A) ORGANISM: PAG1458UP

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### (xi) SEQUENCE DESCRIPTION: SEQ ID NO:694:

	u

,	GATCIGITICC	ACCIGCTATT	TCAGGCAGAT	TIGICOCTOC	AGCAGCGCAT	GGCCATACTA
	TCTOCTTTOG	CGCICGCIGC	GCGCGAGITG	CGGGGGGCIGG	AAGACAAATA	CCTCCTCAAA

GAAAGCCGCG AATCCGGTAC AAGCTCCGAG GGGACCATCT CTGCACACCA CACCGTCTGG

COSTCOCOCA AACTTGACTC ACCOCCAGCA CCAGAACGTC CGAACGCCTT TCCGAAGCAT

SCACCISCST TITTCTTCCC SCTSSOSCAC SOSTSSCTGA ATGSCATOGA CCTSSSCACT

TITGACCCC TGITCAAAAA CCACTACCTA AGCACCCTGC GCCTTATTCT TGCAGCCGCC

AACCOGCATG CAGAATTTGA CCGGATGTCC GAACTCATGA GCTACGTTTT GCAGGACGCT

CAGGCGCACG ATATCAGCAT TCAGTAGCCC GTCGCGCATG TGTCAGCGCA TCTGTGGACA

ACTOCIGOTT GCAAACTGTA TOCOGACCAC TACCATGCAT TAGTATGAGA TOTATAGAGC

SCCAATIGCA COCCTAGAGA GATGTGAACC TCGCAATGCA TCTCTTGGGA GTCTCTGTGG

CCGCCAGTAT CTCCTAGTAC ATACTCTTG TAACTCTACA GAGATGTGAA GTCTTGTTAC

15

CCCGTCTTTG ATTTCCCCAC ACGCCGCCTG CCCAGAAATG ACGCACCATC AAGAGCCCTT

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(2) INFORMATION FOR SEQ ID NO:695:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 569 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

55

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1459RP

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	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:695:	
10	GATCATOCTG GOOCATATCT GAATGCTCTT GAACAACOGA CTAGATTAAT GCAGCCTTGC	61
15	ACTCAGAGGC TIGGGCAGGA TGCAGCTTAT GCGGGCAGCGG CTGTTGGAGC TTTACAATAC	120
,0	CAAGCAATAT GTGGTGCTGC CCCCAGATGA GACAGTAAAA CTGCAGCGAG AGGTGACGGC	180
20	GAGCCTGAAC TCAGCAGATC CAGGACTCAA GGACGTTGAC GGCATGGCCC TAATGGAGAT	240
	GAACITCIAT TIGITOGIGI ACATIGOGGA AGAAATAGAA GCAGACGIGC TCIACCGCAC	300
25	ACTIGITIGGA CGTATAGGIG AGAACTOGCC CCGGATGCAC CICATGAAGG CIACGTTACT	360
	OCAGGITACA GAAGGIGATC CCGCTGCCGC GAAGTACCTG AAGAACCTGC TTGAAAAAGCA	420
30	SCTTGAATAC GATACAGATT CCGTGGATTA CCTGCAGGIG GGCAAGAAGC TAATTGCGCT	480
	OGAACOOCCC OCCITICICCA CCCAOCTOTIC CATGAAAAAG CTOCTICTOCC CTOCTIAGAGA	540
35	AGITTCCACT GCACGCCGAA CTATGGTGG	569
	(2) INFORMATION FOR SEQ ID NO:696:	
40	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 572 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(VI) ORIGINAL SOURCE:  (A) ORGANISM: PAG1459UP	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:696:

55

	CATCACGTOC CTOCGACATG GOGACTTCAT CCACTGGCGC CCAGCTACGT GGTATATGAC	60
5	ATTATOCCCC AGACCITAAG CCGTGAGACT CGAACTAAAT TGACCGATCT CTTCCCCTCT	120
	GCCCCCCCCAG GITCGAATCC TOCTGATGTC GTTATTTTTT CCTTCCCCCG CCTACCCCCC	180
10	OCTIGITATITT OCTTIGITIOCT ATTITAGATAA ACGAGATAGC TAAACTATOG GTAGAACTCG	240
	COGTACTICC CGTAGTAGTA GOCTGTOCCG AAGCCCCCCGA GOOCGGTGAG CACCAGCCGC	300
15	ACGGGTTTGG CGAAACGCGA TGGCACGCCT CTGATGAGGC CGGTCAACAG CATCACGGAG	360
	CTOGOGOCAA GOGOGAGCTC GAGGOOGCCC TCTGCGTTCT TCCCGAGCAA GTACCCTGCT	420
20	ACAGOGTAGG TOCTACCAAA AACGAGACCT GCAGCCAGGG AGGGCACAGA CCCTTTACGC	480
	CAGTIAGOCCA TOGAGOCCACO GATIGACOGTIG AGOGOCOCCA GAGTIGAAAGA GOGATIGTTICO	540
25	CTTOCOGTOG TOCTGTOGGG AA	572
	(2) INFORMATION FOR SEQ ID NO:697:	
30	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 688 base pairs</li><li>(B) TYPE: nucleic acid</li></ul>	
35	(C) STRANDEINESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
40	(vi) ORIGINAL SOURCE: (A) ORGANISM: PAG1460RP	
45		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:697:	
50	GATCCGGGTG GAGACACGAA AGTAGACAGA CACGGACGGC TGTTGGGTTGG	60
	CTCGTGGATA CATTCCAGCT GCCCCAAAAG ACACATAATT TCTATGTGCT TGTCGACGAG	120
55	CIGATAGAGA TITTIGCATTT CCAGGGGAGC GGCTCTGACT TTTTGCACCT GCATAATCAG	180

	CIGIALCOC TOGASCICAA AGACAACGAS COGOCCITOC ITOCAGACOC TOGGITGATC	240
5	AAAGGCGAGC TOCOCTCCCC ATACTACGTT ACTGCACTCT CTTCATACAT CATTTTTGGT	300
	OCTOCTATTG TOOCGAGCGG CTGTAGGATA ATAGATGACT ACTOGGAGCA GCCCTTAAAG	360
10	GAGCAGGGAT TCACCATOCA CCACCGTGTA TTCTCTCTGA ACGGCACGCA ACTTTCATTG	420
	CTACGCCTGC TGAAACCCCC GCGTCCAGAA TCGCATCAGC AGGGTGAGAA GCTGGATACC	480
15	AACTOOCTAC AGAAGTOOGA GGATCCATAC CCAACGATCC AGGAACAACC AAATOCTGAA	540
	GCACGGCGG AATACGCTAG AGAACACGCC AGAGGTGAGC ACATAACGAT GATTGTTCCA	600
20	OGICADAGIA TITACCOCCAG TATAGAACTG ACCCIADATT ATADACTITCC TRAGITACCAC	660
	TACAAAAACT CATTIGCTAA TOOGITGA	688
25	(2) INFORMATION FOR SEQ ID NO:698:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 649 base pairs	
30	(B) TYPE: nucleic acid	
	(C) STRANDELINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
40	(A) ORGANISM: PAG1460UP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:698:	
	GATCCAACAA TTCCCCCCAGC CCCCCTCCAG CCGTCGTCTC CGTCCCCATCA AATGAGTCCA	60
50	COCCIGICIC AATCCCCCAC ACCIGCCGIC CATGCCCAC CICGAACTOC ATCCCCACG	120
	CAAACAGCTG GATAAACAGC CCGTTCTGCT CGCACCCCCG CCGCAGCTGT CCAAAGAGCG	180
55	CCTCCGCACC AGCTGCTATA TCATCGCCCC AGAAACTCTC TACGAATGCC CCCATCGCCG	240

	TGPACCICGT CGPAGFIGIG CATGICCOCIG CCTCTTCCCGG CTCAATTITIG ACAGTCTCGC	300
5	CCCCCACCCC AGCTCCGGAA COCTACGTAA TACAACACAC AACCAAATGC CCTACCCGAA	360
	OGTOCCAATIC GTOTTICTOCA COOCTOCOG CTOCCOCTTG COCCCAACCT CGTATOCTCA	<b>4</b> 20
10	AGAGTTOCTA CAGACTTTOG OCGACTCCCT AGCOGAGATT GCCCTOGTAC CGGGTCCGTC	480
	COSTICARTIC CARSTOCTICT STURCOCRAG CCRAGRACAR GROCCACOG GACACCOCA	540
15	ACACCATCTG GCATCGGCGC CGCCACAATG GTTTTCCTCA TAGTAAATAT CTCAAGCAGG	600
	CTGTCAAGCC ACTCTTTTTG CAGACAGCGG AACCGCCTGG GCGCCACAT	649
20	(2) INFORMATION FOR SEQ ID NO:699:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 688 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1461RP	
35	(ii) Oldfildii Indifolit	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:699:	
	GATCAAACCA CCACGOCACA TCATCATAGT TGATTAAATC AATTAGGTAA GGCAACCATA	60
45	GITGCAGACT TIGITTICIGI ACCATTITICI TOOGATTAAA GAAGTAGGGA GICACGAGGA	120
	AATGCACCGC ACATGCTTTG AGATTGGTGT TTTGGGATTT TAGAAGGCCA GTAACGAAGA	180
50	COGTIGAACCA OCTIGTICCAGC CATAGATTAT TTTTAACTOG ATGAACCTTIG TAGCACTCGA	240
	TGTATACGAC AATCGCCAAC CAGAGCAATG TCTCGTGCAA CGGGTTCTGG ATGACAAGCG	300
55	CACGOGGGT GCTCGTGAAT GGTAGGAGTT GGTTGCTTCC TATCCCACGG TTGCTAAATG	360

	COMMENTE TROSPECTIO GOSTICOGOS COMOCIGAL CITTAAAATIG TATITICAAGT	420
5	CCAACTOGTG ACCATAGCOG TOCACTAGTG ATAGCATGAG TGCCTCTAAC GGCAGAAGAA	480
	GCCCTTGCGG AAGCGAAACC ACCTCCCGGC ATTTGAGCAC CGCAGACATT AACTCCAAAA	540
10	OCCUCATION CCARGARATC TOTOCTORES ACTUATORS TUCTOCATICA TOCCOGAGGA	600
	AGTIGTATICAA AAGCCCGGGC AAACCCACGG GCACAGCCCG CCGCACATICC GCGTCCCCAT	660
15	TACAGIAGIC TATCCCACAG TIGITICAA	688
	(2) INFORMATION FOR SEQ ID NO:700:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 728 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDELNESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1461UP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:700:	
40	GATCOCCAG TITAAACITA AAGITGATAG AGITCCCGTC GTGCTCTCTG GATACAATAG	60
	ACCUCACUGA GIOGACCIOG COCTOCACCI ACTOCCCCC GIAGOCCCTG TOGICCCACA	120
45	TESCCCTTTC TAGGITGATC TTEGAGCCAG CTTTCCAGCT GCTGACTTCC GTCCCATAAA	180
	CIGITICIOS TOOGATOCOS ACCITIGAASC TATOOSCOST GAACIOOSTO ACOSTOAGOC	240
50	AGATACCATT GCATGCAATC GAGTCACCGA TGTGGCAATC CGCCAGTATC GGAGCCGCAT	300
	CCTTGATAAG GACTGACACA CCGTTGCCGC CTGCCTCGCT GGCATGGTTC TCCAAGTACT	360
55	CAGCAACAGT GOCAATGTGT TOCACTATAC COGTAAACAT COTATCAACT TOTATGGGCG	420

	MANAGETT COSTATOCCA TCTATOCATC TTCTTTTCTG CTACCGCGAG CTTTTTAAAC	480
5	TOGTAAGACA TOCATAAGGA AATOOCOGTT COCCATGTAG CTGACTAATA AAACTAGAAG	540
	ATACGACTAA CTATCTGATT ATACTTTAGG ACTATCTCTC CTTGCGCTGG TCACAGAAAC	600
o	ATCGFTGAGC AAGTCGCGTC TATCGGGAAA ATCACTTGGT TCCTTTGTCG TAGAGCTAAC	660
	TOCCIGAÇÃA OCTOGAÃÃOS OCTOTITITAA AGICTACTIC GAATOGIOGI GIACGICIOG	720
5	GTGCTGGC	728
	(2) INFORMATION FOR SEQ ID NO:701:	
20	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 701 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
?5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) OPICIARI COMPOR	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1462RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:701:	
40	GATCITAATT TAAAATTITA ATTAACTATT TATAATTIAG AAATATATAA TCTAGAGATA	60
	TATAATCITA AAATCATAGG TAAAAATACA TAAGATAGTA AGAATAAAAT TAGTAAAATA	120
45	AATAGAAAAC CATAAGITAA TIGATICATA AAGAAAAATG GAATTATITG TOOCATCTTA	180
	ATTITIATTA TITAATTGAT TATTATCTAT TTAACATAAA ACATTITAAA ATGITATAAA	240
50	ATAAATAACA AATTACTTAT ACAATATTTA TTAAATACTA TTTAATTTAA TTTTAATATT	300
	AAATATACCA TTTTTATTAA TAAATAGATT ATTAAGITTA TTAATATTAA GIGATATATA	360
55	ATTIAATTIA TATAAATIAT TIAATTIACT TCATTGATAT ATATAATTAT TAAATGIACC	420

	THEATAGIA THAITITHA TRAGICTAGE AATATTICTA TITAATAGIC TACCETTIAA	480
5	TICCATATTA CIACCTACTA AATATTTACC TAATAATATA TTATTAAGAA TACTTAAATC	<b>54</b> 0
	TAATAATITA TTATCTAAAG TATATAAATT AATTAAACIT TITTATTATT AITTAAAITA	600
10	TTATTAATTA GTAAATTATA TTTATTTATT TTATTAACAT AATTTTTTGG ATAATAATAT	660
	ATCATTATTA AATCGTAATT TATTAATAAT TATCTTAATG A	701
15	(2) INFORMATION FOR SEQ ID NO:702:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 728 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(Vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1462UP	
30	(a) Sizzifici. Prijigozop	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:702:	
33		
	GATCAATTAA TAAATOGFIT AACTAATAAA GITAATAATA AATCIATTAA TIATATAAAA	60
		00
40	CTACCTGATT TTATTGAATC AAATAATATT TTCTTAATGA ATACTACTAA ATCATCATCT	120
		120
	ATTGAGITTA TATTAAATIC ACCACCICIT ATTCATICAT TIAATACICC TCIAATTCAA	180
45	TCTTAAAATA TICTTAATTA TTAAATTATA TAATAAAAGT TAGTGGATAT AGITTAATTG	240
	GTAAAACATA TGTTTTAGGG ACATATATCT TCAGTTCAAA ACTGAATATC TACATATTAT	300
	NOTICE NOTICE AND ADDRESS OF THE PARTY OF TH	
50	ATCATTAATA TAATAACTCT TTAATTAGAG TOGTACCACA AGAATOCTGA AAGCATTAGG	360
	GGTGTGTACC TTAGCTCTCT AATTAAAGIT ATAAAATTAT CTTAACTAAT AAAAATAATT	420
	AATTAAATAA ATAAATAATTI AATTUAAA	
55	TATAATAAAT AAADAAAAA ATTIDTAAAA TITAAATTAA TIAATAAATA AATAAATTAA	480

	GITATATITA AATAGATCAA AATITCAACA ATITCCATIT CATITAGTAC TACCATCACC	540
5	ATGACCAATT GTTACATCAT TTAGTTTATT AGGTTTACTA TTAACTTTAG CTTTTACTAT	600
	ACATOGTATT ATTGGTAATA TITATCCTTT ATTATTATCT TTATTAGTAG TTTTATTACT	660
10	AATAACTITA TGATTTAGAG ATATGGTAGC TGAACTTACT TATTTAGGTG ATCATACTTT	720
	AGCTGTAA	728
15	(2) INFORMATION FOR SEQ ID NO:703:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 688 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
30	(A) ORGANISM: PAG1463RP	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:703:	
	GATCCCTGAG TCTGCTACCA AGGAGGTCGA GGAGGAGGAC ATCGATATCG AGCAATTGAA	60
40	OCAGGAGATG AAAGGCAACA AGGAGGCCTC TGCTTTGTAA GCTTGCTGTT TGCCGCTTGT	120
	CCTACCCAAT CGTTCCTCAG ACTATCTAAC TIGIATACAT CCCCCTATCG CCCCACCCCA	180
45	AGCCAACACT ATAATGIATA TGICAAGITA AATACATCAT ATATTATCTT GIGCCTCAAG	240
	GGICITAAAG AIGICATAGG ACAGICGCGI GCICAGACAC ACGAATATAA TCATAATAAT	300
50	AAATATATOG COGTCAGCTT CATGACCACG TCAAGCCTTG ATACCAGAAG ACACTTCTAG	360
	GAATTTCTCA ACCOCAGAGA AAACACTAGG GIGTAGGTCG TCATTCGTCA ACCACATCTG	420
55	CTCCTCGGTC CACAAGTTGG CCTCTGGTAC ATAGTCTGGT TCACCGACAC CCAATAAGCC	480

	ACCUIOCOCA OCCCAATOOC TOACACOTOG AAGCIGIAGI GICTICCACA CGICATCCAT	540
5	COCCTCCAAT ACCACATCCG ACACGTCGTT CGTGTCCCCT CGAGTACCAA TCATACCCAG	600
	TCTCTCCGTC CCGCGTGCAA CGGTAGCAGT TCAAGGGCCT GTACGTACAT GCGATGCTCT	660
10	CCATCAAAAT GTCGGAAGCA CGCTTGGC	688
	(2) INFORMATION FOR SEQ ID NO:704:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 704 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1463UP	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:704:	
35	GATCAAACAG TAGAAGTATT AGAGCTGCTT GCAAAGGGGG TCATAAACAA GAGAGCTGTA	60
	ATGICGACAA ATTAAACAGA AAAATATCAT TATTAGTOGA TAAATAACCA ACTTGCACTG	120
40	AGAGIATAGI TOTACATGIT TATTOCGTAA CAGAATTICT ATOCAAATAG TITAATTOCG	180
	TITTACTIAT CTACOGAGIA GCAGIOCAAG AACCTIGIAT CCCAAAATOC TAGAGOGACA	240
45	TOCAGATGTA TAGTAAAGCA ACGTCTGTTT CTTTGGATTT AGCAGCGTCA GGCGAACAAA	300
	AAAAATAGAA AGTCAACAGG GATTOOGGAAG TTATGACAGT TGATATGTTT GTCCATTIAGT	360
50	AAGICATTCA GITGATATGA GGTOCTTAAA TGTTTGTAAG AAGCAAGAAC GAAGAGAGAT	420
	ACAAAATGIG CAGITGIGAA TOGIGAAATT GACACCAGAG GACGICACTT CCCGITGCCA	480
55	CIGITIGCCA ATTOCTTCTC GAGCIOCTCA ACCTTGCCCT GTAAATCTCT ATTGACTTTC	540

	TITAGIAGIT CCAATICAAT AIGCGITICC TICCATCITC CATAGCIGAG CAGITICCC	600
5	ATCTCCTGGT TCTCTTTTGT CAACATTTCG AGTCGGACAA TCATCTTGTG AGCGAGGCT	660
	TCTTCGTCAT AACGCCCGAA TCGGGTAACG GAATTAGAGG GATT	704
10	(2) INFORMATION FOR SEQ ID NO:705:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 699 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1464RP	
25		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:705:	
	GATCGAAATA ACTITCCGCTG AAAACGCAGC AGAGGCAGCC AATGGTCAAA TOGAGCGAGA	60
35	ATATCCACGA TATTITCTAGG GTACTGTTGC TTGCCAGTTG GTGCTCGGAA ACATAACCCT	120
	CAATGGCGCC CAGTGTGTTG TACATACCCC ACACGGGAAA CAGACCCATG AATGACCCGA	180
40	AAACCACCAG CCACGCGCT AAGCCGCCAT CCGGGTATTC GTTGGAGTTA TCGAGATATG	240
	COCCUTATION TRACTICALOS TRACAGOGAS ASTOTOSTICA GOOGASTICG	300
45	TOSTIGGGCC ATCCCCAAAA AGCTCTTTGT CGCCCACAGC TGTGGCTCTG CCGCTGTCAG	360
	ACCATOGOCT CACCICTACG OCTACOGOCT CATCGCCATG COGTACTTCA ACOCTGTCCT	420
50	TGICCATCAC CACCATCGTT CCTAGCACGT ATGGCAGATG CTCCGAACCG CGTCAGCGCC	480
	ACCACAGACC ATCTATCTAC TTAAATACCT AATTATCTGG TGTCCAGCTA AAAATCCGAG	540
55	TATCAGTCAT CCTGTGGCGG CCTTATCACC CATTAGGGTC CGCTTTGCGG TAGTGCATTA	600

	CCGTCGGCGG GATTCATCCT CCAAAATGTC TCAAGCGATG CCTTGATTCC GAGTGTACAA	660
5	GGGCCAGATT CCAACGGGCC AGGAGGCAAC TAATAGAGG	699
	(2) INFORMATION FOR SEQ ID NO:706:	
10	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 710 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
15	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
20	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1464UP	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:706:	
30	CATCITICOCC TTTTTCITCA CACCOCCGIG CGIGIAGIAT IGITCCICCT TAAIGITICCA	60
	GITGAGGGG GACGAAGAGG GCGCAGAGGG GICIGGGCAG GCACGGGIGG AAAAGGCCCT	120
35	GICGGCCGT TOCAGGGCA GCGCGCGTC GICGTGGTCG TAGTCGTCAT GTTGGGGCCC	180
	GGGGGGGC CACTIGTGCGT CCAGGGGGTG GCCGTCGCAC GCCAGGGCCC ACAACTCGGC	240
40	GTCGCGGAAC TCGTACTCCT TCTGCGGGTC CTCGCGGGGG CGCTTGGCCG GCGGGTCCAC	300
	GOCACOGOCO GOCACCTICA GCCCGITOGA GATAATGAAC TIGIGITOGA COCAGCCCTT	360
45	COGATOCTIC TTTCCOCCAT TOCGITTOCG COCCOCCTIC TOCCCCTICCG OCACOCCCC	420
	GOCCGGCGCG GCATGCAATT CGTTCTCGTC TGGCCAGACT GGGCGGGGAT AAACTCGCCC	480
50	AGGATOGOGT CCACGITAGT GAGGTOGOGG TTGCCGGTCCT CTGCGGCTGC GTGGTGGTGG	540
	TIGGOGOGI CACCOCCTC CACCOCCTCC TOCTCCTOGG CCTTGGGCTC CTGCTCCGGC	600
55	ATGCCCCGTT CGGCTGCATG CCTCCAATCG ACTTCGACGT CGTACGATCC CATCCAACGA	660

	ACCCCGIAAC TIAICICCAA GIAIOCCTOC ATACCTATAC TOGICGITCA	710
5	(2) INFORMATION FOR SEQ ID NO:707:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 703 base pairs	
10	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1465RP	
20		
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:707:	
	GATOCACTIC TITIGGOGACA AGACATIOGA GGGOGGCAAC GACIGGGAAA TCTACAACGA	60
30	CCCCCCCACC ATCCCCCACA GCCTCCCCCTC CCCCCACGAC ACCCTCACGAC TCCTCACACA	120
	GCTGTTCGAC CTGTAGGGGC CGCCGCTAGC TAGTTCTTTG TAATTGCTCG ACATTTACAA	180
35	TGCATATTCC TATATACACC GCGCGCAGCG CTCAGCTGAG CAGCCGTACG TACGCCAGCA	240
	CCACCCCAAA CGIACCCCTG CACACCCCCA TCACCCACTG CATGACCTCC GTCTTGACCG	300
40	AGIOGATTIG CATCITCATA TTACIGACCT CCIOGICAAT TOSOGIGICA ATCTOCTIGA	360
	TOTOCAGATT GTOGTTOCTG GACTOCTOCC GGATGOGTOC CTTTTOCCAAC GACAGATCCA	420
45	OCTIGNACCO TECGITOGOC TICGIGNICI CCICIOGGNG COGGITICOGC AGCIGCICIA	480
	GETCETTTCS AATCCCCTCC TETTCETTCT GCATGCAGIG CATCTCCCTG CCGTCCCCCG	540
50	TCAGCAGTTG GTCCCCCAGT TTTGCAAAAT CCACCCGCTG CTGGTACGTC AGCTTCGTAA	600
	OCTICIOSOS OGACOCIASS TOCIOCGAÇA CATOCOTCAS OCCCCOSOSC ASTOCOTCOS	660
55	ACATGATATO CACGATOGCA TICGOCTIGOT GOCTIGOTIGA AGT	703

	(2) INFORMATION FOR SEQ ID NO:708:	
5	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 619 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
10	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
15	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1465UP	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:708:	
25	GATCCCCCAA TAGCTTCATT CCATCGTCTG GTCCCGTACC TCCTCCACTT CTCTTCCTCT	60
	TCTCTATGTT CGTTGCTCAC GGCCGGAAAA CCACTACAGC ACAAAAAATT CACAAGGTCC	120
30	GCCGCACCAG CCTTTTTAAT TAGCGCAATG GCAGCGAGTC CTGGTATATA AGGCAAAAGA	180
	COOCAGOOG ACAGOTACTA CAGOCTCATO GAGOCATOGT ATGITICOGOG ACAGTICOCOG	240
35	CAGGGGGCAG GACTAACCTT GATGITICGAT AGAATGCGTT GTACAACCAC GCGGTGAAAC	300
	AGAAAAAGIT OCTOGAGCAG GAOCTGAATC GATTIGAGCT COCOGTOGCG GCGCCGGTGG	360
40	GOCTOCAGGG TICCATATOG ACGGCACTGG TGGGACTGGA GCGCACAATT GAGCAGTATC	420
	AGCCCCAGGT GCCCCAAACC GCCAGCCGCC CCCAAGCCATGCC CAGCCGCTTGC	480
45	COCAMOTICAC GGAGTICCOCA ACGAACOCCO COCCOCCGTT CCACGGGCTG CCCCCCGA	540
	GCATGCAGCC GETGCCETTC CAGACCGGGC CGGCAGCGCCC GGAGGGCCCC GTGAACCAGC	600
50	CGGCGGGGGG GGCGCGCAC	619
	(2) INFORMATION FOR SEQ ID NO:709:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGIH: 715 base pairs

	(B) TYPE: mucleic acid	
5	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1466RP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:709:	
20	GATCTCTTAC TTTTCCTACT CACCAATGTC TTTAACAGAC ACCCAGAGTC ACGGCCGGCA	60
	CONTATORO COROCTOSOS CONTOCOSOS CONTROLINAS TOSCOSOCIO GRACIOSOSO	120
25	TAGICTCACA GCAACGGAGC TIGCTCCAAT TGGGCTGCAT TCTCCCGACC ACAGTCTGTT	180
	TGICAGGIGA CTCTCAGCCG TCCCCAATGT ACATTICTAT TTATCTACIT CTTGCCCCCT	240
30	TECCOCCACC ACATCOGGTG CCGGGCAGCA CACCGGACCGC GCATCGCGGC CCTGGGGTTC	300
	GTAGAACTOC OCACAGCACG TGTACAGTOC CTCCACTOCC GCCGCGCAAC GGCCCTCCTC	360
35	STACCCISIG COTTICAGAC ATSCCTISSAT COCACATISCC TESSECCTISC ATSSESSETS	420
	TCCCTCTGCG CTGCGCCGCC TATTGTCCAT GTTTTGTGTT CTATCTGTTG GCCGGTACCA	480
40	CGTTGTTGTA CCAGAGTACA TTGTCGCCGT GACCCCGTGT AATGTCACCC CGTGGGCCAC	540
	AGATGACCCT GCCACATGCC TCATTTCTTT GACCGCACCG TGCCGCGAGA CCGCCCACAT	600
45	GGGCCGTGCG CACTCCCGACG ACACCCACGG GGCGGCACTG CAAGGGTCGC AGGTGCGCAT	660
	GAGTCAAAAC AAACCAGGTG TGGCGCTGGG CGGGTGAAAA TCGACTCATA GAGAC	715
50	(2) INFORMATION FOR SEQ ID NO:710:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 694 base pairs	
5 <b>5</b>	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1466UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:710:	
	GATCHIATTA ATTITGATGG TGCTATATTC TAAATTCAAG TAATGATAGC GCGTGATGCG	60
20	GIACGIACCI ATACATATAA COCACAGITIC ACCATOGICT ATGCGIGIAT GAAAATCACT	120
	CCASCCCTCC GACACCCCAC GIGIAATCTA GIGAGTTICA AGTICTICCT CCTCATCCCC	180
25	AGAAAGITOG CCCCCCCCCC TGAGGITCIT GAGCCCCCC TTGAGCTGCG CGATAAGGCT	240
	ATTOTOCOTT TGAGCATGCA TGCGGATACC CTCTAGAGAC ATATGAGCCG AATCTGCACC	300
30	ATCIAAACCA TETTCOCTET TOCTOCCAET COCACCTOCC ACTITOCCAC TOCACACACC	360
	TETCTETCCA TETTTETAAG AATCETCGET CETTGCCCAG TTGGAATTCA TGGTTCCCAT	420
35	AGTGTGCAAG ATTTTCTCCT CTTCTGTTAG TTCCAGATGG GTACCTGTCA GATTGATCAA	480
	GCACCTGCCC CTTTTACGCC GCCACACCTT GCCCACAAGA GAGTGCCCGC TTGCCGTCGC	540
40	TICACCAAGG TITIGITAATGG AGGIGIGAGA TCTCGGAGGIC CTTGGTAGTC TCAGACACGA	600
	AGCACCOGCA TCATGTATCC ACTTCGCAAC AAGCGAAGTC CAGCCACACT GGTGTGATGC	660
45	OCCCAAGCCC CTACCAGTGT CACCATOGAA GTAT	694
	(2) INFORMATION FOR SEQ ID NO:711:	
50	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 690 base pairs  (B) TYPE: nucleic acid	
55	(C) STRANDEINESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: DNA (genomic)	
5	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1467RP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:711:	
15	GATCOCAGAC TCCCCCCGGAG AGACTITICOC ACCTCGGGCCA CAGGTCTTGA AAGAGAGCTC	60
	COCCOTTCC GICCCAGACT CTTGTTTATC ATGTCCGTAA GACCACCGTT CGTCCCACCT	120
20	ACCCCTTCT TGTTCGTGTT TCCACCAATT GATGGAATTT GAGACGTGAA CCTCTGCGGA	180
	TTCRRKCTAT TGAGCACACC ATTGGCACCA CTTGAGCCCC TTCGCTCTGC CATCCCTAAT	240
25	CGICCTATCC TACGGCCGC TAATAAGITA CTACCAGACT CIGGCCCTCA TCIGGGACTG	300
	ATGITATOGI CIOCAGOCAG ATCCIGITIG IGACCOGATO GAAATCATOG AGTACGAATA	360
30	ACCACGIGAC CATTATTCAC GIGATGAATT TOOCGGTCCC TGTTGCCCGAC TCTTACTCCA	420
	OGITAACCAT GACTAGATOG OCATACCTCA GATACCTTAT TCATOGGATC COGAGTTOCC	480
35	GCGTCGGCCG AACCGCCCGG TGAATCTGTG CTGACGACCT AAAAAAATAGT GTGCGCAAGC	540
	TICCITAATC TGTGAGATOC ACACTGACAA ACTTGAAGOC TGAACCATCA AAGCGATACG	600
40	CCTCATGCAC GTGCTCAATA AGGTCCAGGA AGTCTCGCAA TGGGGCAAGC AGACGGTAGA	660
	TTGCAAGACA CAGACGATTG GGTTGTGCCA	690
45	(2) INFORMATION FOR SEQ ID NO:712:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 700 base pairs	
50	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
55		
	(ii) MOLECULE TYPE: DNA (genamic)	

	(VI) ORIGINAL SOURCE:
	(A) ORGANISM: PAG1467UP
5	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:712:
10	
	CATCGTCCGA GTGCAAATCC ATACCAAAAA TGTGGACCCA GGTACGGGAT TCGAACTTCT
	CONCINENT THOUSAND CONCERNS A THOUSAND
15	CCAACAAAAA TAGOCTCAGT GAAGTGCCCCA ATTGCCTTAT AGTCGTTTTG CAGAGCATAT
	AGAAATGTOG GACAAGOOG TOOOOOOCT TGTOOGACOC GACOGAAGAA GOGATCTOOG
	TOTAL TOTAL STATE OF THE STATE
	COOCAATTAC COCOCTICACA COCACOCOTIC COCAACACAA AAACCTICAAC CCACTITCTIC
20	
	CCATGAGCGA GATGCAGCAG CCAATACCTA TCCCAATGGT AAACGAGGG GTCCAGATGG
25	CCCAATGGCG GAGGGCAACA GGGCCCGCGT CCTTTTTGCG CGGTCTGCCG TGCTGTTTCT
	TOCACTICAC GGICAGCICG GITTCATAGC COGACTOGGA CICGITIGCAA AGGITIGTIGCA
	CIGHIGAN AGINGIGA
	OGTOCTICAG CAGGOGGIGC TICTOGIGGI GGITGGACAT GATTATAGGG CTGCAGTATA
30	
	CICGGAIGCA TITIGOGIGOG GIGIAGOGCI TCAGGAGAGC CGCCAGOGIG CICTICIGGC
35	CCTTCTGGCA CACGGGAATC ACGGTGGGGC AGGGCGCCTT CTCGCACAGG CCGTCCAAGA
	GCTCTGGCGC CTGCGCTATG TCGTGGAAGA CCACCATAAC CGCGAGGTAC CCCTGGCCCA
	TOTAL CONTRACT CONTRA
40	CGTCCCAGCG CGTGACCATG CCCAGGTTCT TCACGTCAAA
40	
	(2) INFORMATION FOR SEQ ID NO:713:
	(i) CTCVTTT CTTTT CTTTTT
45	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 689 base pairs (B) TYPE: nucleic acid
	(C) STRANDEINESS: single
50	(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

## (A) ORGANISM: PAG1468RP

5		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:713:	
10	CATCTOGTOG CTCATTGTOG ACCTGCAAAA AGTGTTCAGA AGGAAGGCAA CATGTGTTT	, 60
	TAATCCTACG OCCGIOOCCT CAGAGATTGT TCACTCAATG TCGTTCATCA TTATGAATGG	120
15	CTCCCCCCCC CCTCCCCCCC TCCAACCCCCC CCCACACGCC CTCCCCCCCCC CCCCCCCCCC	180
	CTGGGCCACG CAGGGTCCAA AACCCACCCA AACTCACCGC GCCCACCCGG CTACACCGCC	240
20	GCCAGCACGT CACGTGCGGT TACCCGCCCT GCCGGCACTG AAAATTTTTTC GCCGCCAACA	300
	CTATCOCOCC CGAAAAAGCA ATTTGCCOOC CAACCACACA ACCATCTGTT ACCGAACAGG	360
25	ACAGGACTCA TOCCCOGFTC CCTTCTTTAT TEATTTACTA GCTCCACATA GATATTTTTG	420
	ATATTATAT GGIGIGITTT CCTCCGCACG CCGCAACCCA GCACTTAGCA GACCACGGG	480
30	OCAGGGACTG ACACCCAGCC AGAACAGAAC AACAACAGGC GACCTTACAA TGAGCATGGA	540
	AACGCCCCCT GTAGATATCG ACAACATCAT CGACCGCTTG CTGGAGGTGC GGGGCTCGAA	600
35	OCCOSSICAC CAGGIOGACC TOGAAGAGCA CGAGATCCCC TACCTGTOCT CCAAGGCCCG	660
	CAGCATCTTT ATCAAGCAGC CCATTCTTC	689
40	(2) INFORMATION FOR SEQ ID NO:714:	
	(i) SEQUENCE CHARACTERISTICS:	
45	(A) LENGTH: 620 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1468UP

	(XL) SEQUENCE DESCRIPTION: SEQ ID NO:714:	
5	GATCTCAGAA TTATCOGCTA GCAATTGATA TTAGCATACT TAATTGGTGC TAAATACTTT	60
	GOCATCOCAT CTAGACATAG GAAGTAACCT CAAAAAAACCT ACOCAGATAG TAAACCTOGA	120
10	AGAGAGATTG CGCAACAACA ACGOCCAGTT GGAAAATAGA CCACCACTTG ACCCTGTCAT	180
	TIGIAGACIC ASCAGIGITC CIGIGIGIGC GITCOCCAAT CICCATGIAC TGITGCTCGT	240
15	TCATTACTTC CATTGTGAGC ATGGAGAGCT TGCGCACCGC ACCCTCTAGC GTCTCCGAGC	300
	TOGAATCAGC GOCATCOOOG GAGAGAACAC CGTAGGTATT AAACGTGACA TOCTTAGTCA	360
20	GGTAGCCCGA ATTIGTCGTTC GCAAAGCAGT ACTGGTATTT GCCATCTGTA GGCGCCTTCA	420
	ASSICAACTC ACCOTOCGAC CACOCACOCT OCOCATOCAG CACTGACOGT COGTCAATOC	480
25	CGTACACCAG CAGGICTCCA GACAGCTGTT GATGTGATTG TGGGTCTCTG TCGCCGAATT	540
	GATAAGTGAT TGTCAGCACG TCCCCGCCTT TCAACTGCTC AAAGAAACAG CGCCGCCCGT	600
30	AGGGGGAAG AAGTACATTG	620
	(2) INFORMATION FOR SEQ ID NO:715:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 686 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
15	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1469RP	
	V-7 SAMENTALL INSTITUTION	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:715:	

	GATCAACTAC ATCTGCGAGC AGCAGCCGAA TTGTAAGGTG GCCATCATAG CATATGACAA	60
5	GIGOCTOCOT TICTICAACC TOCOCCCOGA GICCAGCCAG OCACAGGAGC TGATTGTGTC	120
	CGASCICAGA GAAGICITCC TOCCOCTGTA CAGCOGCCTC TTCGTGAGGC CTGCGGAGGC	180
10	AATGCATGTC ATACAGGACA CGTTGGTCAA GCTCGAGTCG TTTATCCAGG ACGACAAGCT	240
	CTCGCACGOC GCCGAGOCCT GCTTCGGGTIC GCCGCTCGAG GCCGCGCTGC TGGCGCTGGA	300
15	CACTOCCACC AATOSTAATG GCGGCAAGAT CATTGCGACT CTGAACAGGC TGCCCACCGT	360
	GGGCAACGGC AATCTGACGC TGCGGCGGCA CGACGGCCTC AAGAAGAGCC TGAAGTGCCGA	420
20	CAACABCTTC TACACCGCGC TGGCGCACAG GATGCTGAAG GCGTACGTCG GCCTGGACCT	480
	CITICTOCACA GOCAGOGOCT TOATGGACTT TOCCACGOCTC GOCCACCCCG TOCTGGCCAC	540
<i>25</i>	CTCCCCCCACT ACTCCAACTT CCACCTCCAC CCCACCACTT CCCCCTCCCT	600
	CAACCACATG CTGCACCCCG TCAGCAGCAC CGTCGGCTAC CAGGCGCAGC TCAAGGTGCG	660
30	CTOCTCCTOG GOOCTGTCGT CAGTCG	686
	(2) INFORMATION FOR SEQ ID NO:716:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 572 base pairs	
	(B) TYPE: mucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1469UP	
50		
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:716:	
	CATCOCOCCA OCACCACTAG ACATCACAG CAATCACAGT GATTATCTCC TOGTTACCTT	60
55		

	CAAACTCITC ACTCTCCICA AGAACTTGIT ACCTGATGAC TCCTTCTTAT TGTCTGTGTC	120
5	ACGCGCCCC GIGIAGGCGI CITICGICGIC CICCTICICG TCCICAACAT ACCCACACIG	180
	GETCTTAGTIC AGCTTCAGGT TOCCGTTCCT GGGGTCGGGG CCAATCGCCG ACGCGGACGG	240
10	AGGGCTTTTC GCCAGCCTGT GGCTCAGAGA CTTCTTCCTG CCCACCGTGC TCTGCTTCAT	300
	COCCTCTATA OCCACAGGG CCGCCGGCGC GCCGTCGAGG AACGTCGTGG AGCCAAGCCC	360
15	CTGTGTCACG GOCCCATGCA CAAGGTCCGC GGTTACCTTG GCGTCGAACT GCGTCACCTC	420
	CCAATGGTTC TTGATAGCGT TCACGGTCGA CGACGAGGC TCGCCGACGT CGCGGGCGA	480
20	ATACAGGTAC GAGTOGTOGT COTOGTOGAT GOOGAAGACO TOGTTCATOG CAGACTTGTG	540
	TOCOGTOGCC CCCACAACGT CCACTTCGGC CC	572
25	(2) INFORMATION FOR SEQ ID NO:717:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 699 base pairs	
30	(B) TYPE: nucleic acid	
	(C) SIRANDEINESS: single	
	(D) TOPOLOGY: linear	
35	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1470RP	
40	(A) CASRAGAI. PROI 4/ORP	
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:717:	
45	GATCTTOCTG CTATCCAGAA ATGGGAAGIT CTTAGACRAC GGGGAATTAA GCCCCTTTTC	60
50	CAATATTTIG AGCGTCGTTT CATAGCTCGG AAGACGCAGC AGAAGCCCCC CCAGTAGTGT	120
	CTGTTCATGT TOGCTCATGA AAGGTGTCTC TATCAAATCT AGCTCCATCA TOGCAGAGTA	180
55	GITATTATCT TICITOCAAG ACAGACOCAC ATGCCCCAAC TTCGTCAGGA TTACAGTAAA	240

	ATAATOGTAG AACCOCOGAC TCACAGAATC GACGACOGCT GGAAATGAAG TOGGCCCGTA	300
5	GAAGATOGIG COCCCCIOCT TCTCTATCAC AAGATOGAAC TOCGAAAGIC TGTTCACOOG	360
	GGACACCGTG CCCATAACGT GCTTCTGCAT GAACAGCTGC GGTACCATCT CGCTCTTCAT	420
10	CCGCCCCACC TCACTCTCAA CCTCCTCCACT CCCTCCCACC ACCTCCACAT TCCCCCTTCC	480
	AGCTGAACAG CTCCCGTGAG TTCACGTCGT GCGTAAACTC AGACAGGTAC ACACACTCGG	540
15	GCAGGCCCTT CCCAATACAT TTAGAGCACT TCGGCCGCGC CTTGTTGCAC TTGACGCGCC	600
	CCTTCCCCCA CAACACCCCAC CACTTCCCTCA CCTTCCCCCCT CCTTTTCCACA ATCTTCCCCAT	660
20	COGACTICTOC CATCCCOCCA CCTTCACCAA AATGACTAG	699
	(2) INFORMATION FOR SEQ ID NO:718:	
25	(i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 655 base pairs  (B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genamic)	
35	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1470UP	
40		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:718:	
45	GATCGCGGAC GTGGAACACT GGCCGGAGAT GCGCGGGGGC ATCCTGGTGG TTTCTGCGGA	60
	CCGCAAGGAC ACGCCATOGA CGAGCGGTAT GCAGCAGACG GTGCACACGT CGGACCTCTT	120
50	CAAGGAGCGC GTCGCGACGG TGGTGCCGGC GCGGTACGCA CAGATGGCGG CGGCGATCCG	180
	COCCCCCAC TICCCCACCT TICCCCCCCCT GACCATCCAC GACTCGAACT CCTTTCACCC	240
<i>55</i>	CACCIGOCIG GACTCATTIC COCCGATCIT CIACAIGAAC GACACTICGC GCCGGATTGT	300

	CAAGCTGTGT CATCTGATCA ACGAGTTCTA CAACGAGACC ATCGTGGCGT ACACGTTTGA	360
5	CGCGGGTCCG AACGCGGTGC TCTATTACTT GGCGCACAAC GAGGCGGGC TCTGCGGCTT	420
	CCTCTCTCCC GTCTTTCCCC CCAACGACGC CTGGCAGCACC ACGTTCTCGA CGGAGCAGCG	480
10	CGCCACTTCG CCGCCAGTT CGACGAGTGC GTGCGCGGCA AGCTTGCGAC GGACCTGGAC	540
	CACCACTICC ACACACCACT TCCCCCCCTC ATCTTCACCA ACCTCCCCCAC	600
15	ACACTAAATC CTCGCTCATC GACCCCGAGA CGGGCCTGCC CCGCTGACGC TATTC	655
	(2) INFORMATION FOR SEQ ID NO:719:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 708 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
25	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
30	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1471RP	
35		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:719:	
40	GATCAATTAA CTATCTAGAT GAGICTAATT AATTAATATA CTTAAAAGTC COGTTAATAT	60
	CATTAGCTAC CCTATCOGAA CAGACCGTCT GCTACTAGGC CGAAAGGGTA AAGCAGTTGT	120
45	CAGTCAGTAC TROCTGTTCC TRATEGRATE CONGRESSIAT TETTTGTCAC	180
	TOGACTACOG COCCTOCCOC CTTOCACAGO GTACCCATGA TTCTGAACOC CAAGGTACCA	240
50	CACCITCCIG CCACATCICC TCGACCICTT CCAAAGICAA ACCCITIGIC TCGGGGACAA	300
	AGAAGAACAT GTAGAAGAAC GCAAAGATCA AACAACCCAT GAACACGTAG CCGTAGTAAA	360
55	ACCIGATOSC ATTOGTAATG TATOGTGTAA AGAAGOOGAT CAAAAAGOOC CATATOCAAT	420

	recession occurrance Anaceering Ciricancier Inangocana Gierecanaa	480
5	CAATGACATA COCAATTOOG OCCCAGGTAG TIGCAAAGAA GAAAAATGTA GAGOCAGGTA	540
	AAAACAATCA TAGCATTGCC TGCCGGTCTG GAAGAAGGCT GATCGGGTCC ATTGGGCCAT	600
10	AGTOTTGTCA CACCAACGGA GOCAAAAATA ACCATACAAA CGGCCATTGC CGCGGCACCG	660
	TAGAAGCAAA CATTICCTICC TGCCAAATCT ATCGACAGIG TTACATIG	708
15	(2) INFORMATION FOR SEQ ID NO:720:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 718 base pairs	
20	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1471UP	
30		
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:720:	
	GATCTTCGCC TICTTCTACA TGTTCTTCTT TGTCCCAGAG ACAAAGGGTT TGACTTTGGA	60
40	AGAGGICGAG GAGAIGIGGC AGGAGGGIGI CGICCCAIGG AAGICCGAGI CCIGGACICC	120
	TTCCTACAAG AGAAATCCTT ACCAGACTGA GGAGGTGAAG CCAGAGAAGA CCTGGGCTTA	180
45	AAAACTTTAA ACTACAAACT TTTTIGITICT GCTAATCATC GGGTTAAAAC CTAAACCTAA	240
	TCTATGTTCA TTAATATTGT TATGACGTTC ACGAGATAGC ATATGTAAAT TACTATTAAA	300
50	AATATGCGAT TAATCTGTAT TTATTAGTIG TAATTGCAAT GCCATATGAT ACTGCAAAGC	360
	AATACATGCC GAGATAACCA ACGCCACTGA GOCGGGACTG GGCCCCTTCT CCGGCCCGGC	420
55	CAACATOCCT GTOCTTOCTIC GOCCGCGTGC CCGTCGCCGG CCAGCCGCAT GCCCGTCGTC	480

	GGICALCOCC CCACITICAA ACTITIGIAAT CGAGCAGGAA ATTAAGATIC GITATAAATG	540
5	ATATCAAATT TTTCGTCGTT TCTTTTCAGT GAGTAATATT GTTCCGGCAC CGCACGCCGA	600
	TGATGCCGCT ACATCGCACA GGGCCAAAGC ACAGGTGCTA AACTATTGCT TAGTTGGCGT	660
10	CGTTGAGCTC GTTTATCCTT AGTGGAATAT CTGCAGCATA TTCAATATCA AGTCTGAA	718
	(2) INFORMATION FOR SEQ ID NO:721:	
15	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 695 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
25	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1472RP	
30		
30	(vi) STATE PROPERTY AND ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY AND ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY AND ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY ADDRESS OF THE PROPERTY AN	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:721:	
35	GATCTATCTC CCAGCTTAGA GAGACCGTCC GGATGTAAGT GATACCCAGA CAGCCAATGA	60
	TACTOGTCAA GITTTGTAGT TITTATAAGAA AACATATATT AAACOOCTAA AGACAGAAGG	120
40	CGAAAAGCCC GACTITTATG GOCGTAGAAG TCGTGAAAAA GOCCAAAAAC TATATTTCCA	180
	CITAGOGCIC CICCITCCIC ACGIAAACOC GCATCATCAT ACGCCTICIG TGAGICAAGA	240
45	GCACTACGAC ACGCCGTGCA TTCCCTCATA CAACCTTGCC AACACATGAT CATGTCCAAG	300
	GATATTOCTA CCACCCCAGA ACTIGICOGAA CCAGACAAGT ACTICGITICA CCAGCCCCAT	360
50	TIGCIGCIAC AAGAAATCAC CTOCACGITA GACTCCATCC TGAACAACTT AAATGGCCTG	<b>4</b> 20
	AATATTTCCC TGGAGAACTC CATCGCAGTA GOCAAAGAGT TTGAGAGOGT GTCCGAGCTT	480
55	TOGAAGGTCT TITTACGACOG ACTICOCGAAC GGAGCGCCTC CTGGAGTTGC CGCCAGCCAAC	540

	COSTOSTCTIC ASCACCTISCC CACTIGAGOCC GTCGCCGCGC ACCAGAATTOC TGCAGGGGGC	600
5	AATAGTGACG CACCAGCGCC ATCGCAGTAG CGTTTGCACT CTGCCCTGGC TTTTACACCGG	660
	TOCACCCACA TTOCOCTICTA CTTTTATGTG TCATC	695
10	(2) INFORMATION FOR SEQ ID NO:722:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
15	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
25	(A) ORGANISM: PAG1472UP	
	(xi) SEQUENCE DESCRIPTION: SEO ID NO:722:	
30	(AT) SEQUENCE DESCRIPTION. SEQ ID NO. 122:	
	GATCTCGATT GAATGCCAAT GAAGGTTTAT GGCCGTCACG GGAGGTATAA CAGACTTGTA	60
35	ACGACTITIG GTAAGACCCA COGTGAGGAA GATAGCTOGT TTAGCAGCGA CGATGAGAAC	120
	CACGGCAGAC CAGTTAGCGA CGACACAACC AAACTCAGCC TGAGCCAAGA TOGATGCAGC	180
40	GAATTACCOG ACCAGACCAT ACGTCCCCAAT ACAAAACCTC CCCCCCACCC AACCCAGACC	240
	GATCCOGTIGT COCAGTITICT GCAACCCCCC GCATCCCCCC ACAACCCCAC AAGACCACCA	300
45	ACATGOGATT CTACAGAATA TAGAGAGAGT GOCAGTCAAG AGITTCTAAA CGCTGTGAAC	360
	GITGIGCAGG GCATAGIGIC TICICICAAG CCIGCAAAAG AGGIAGITIGA GCACTGGGGG	420
50	GASCTTCAGG ATGTGCCAGA GGATCGGGGC AATAACGGGC AGGCGGTCTA TGGCAAAACA	480
	AGAACATOCT TOCAAAAAOCG GAAGAGGATT CTGACACCGA AGCTGCTGCA CATGAGTCTG	540
55	ACGAACCOCT OCACAGOOCG ACGAAGCACT ATCOCGGCAC TITTAATGAGC TOCGTACGAT	600

	GOCCACACI CITAAGIACA GOCAAGAICI GGACITIATA TIGICOGACA ACTOCATGAC	660	
5	GACACCOGAA CATAGACOCA CCACATOCTO COCTTOTOTO TOGATATOAT GAACAACGA	719	
	(2) INFORMATION FOR SEQ ID NO:723:		
10	(i) SEQUENCE CHARACTERISTICS:		
,,	(A) LENGTH: 675 base pairs		
	(B) TYPE: nucleic acid		
	(C) STRANDEINESS: single		
15	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: DNA (genomic)		
20	(vi) ORIGINAL SOURCE:		
	(A) ORGANISM: PAG1473RP		
25	(Xi) SEQUENCE DESCRIPTION: SEQ ID NO:723:		
	CATCOCATCA TOCTICTACAC CAAGCGCGAC GTCTGCGGCCG CGCCCACCCC CGCCGCCCTC	60	
30	CACCOCTOOC ACOCCCAGAC COOCCACCAC TACATOCTCC TCGACCOCCG CACCOCCCG	120	
	GACCCCCCCC COCCICCTCCCC CCCCCTTACC ACCCCTTACC ACCCCCCCCC	180	
35	GOCGCCCTCC CCCTCGGCTA CCGCCTGCTC GTTGCGGGCCA TGCCCCAACGT CGGCAACTCC	240	
	ACCITICATICA ACCICCITCOG COCCICOGOC ACCICCOCCC COCCCAACCT CCCCCCCACC	300	
40	GEOGROCIACE COGGOGICAE GOGGOCTACE AGTGAGTOGG TOCOCATOGC CGATCACOGC	360	
	GOOGGOGICT TCATGCACGA CACOCCOGGC GTOGCCCTGC COGCCCGGCC CTCCTCCGTG	420	
45	CCCCCCATICC TCCCCCTTCC TCTCCCCCCC TCCCTCCCC CCCCCC	480	
	ATCCAGGOGG ACTACTGCTC TACCTCCTCA ACCTTCAGGG CCTGGCCCCC TCCTAGGCCG	540	
50	CCTACAGCCC CCCCACCAAC GACATCGCCG CCCTGCTGGC CGCCGTGTGC ACCCGGCCACC	600	
	SCCTACGCTC CGAGACCGCA SCCGCCCTGC ACTGGCTTGC CATCCGGGCC CCGGGGCCTCT	660	
55	GCCTGCAACC GGAAG	675	

(2) INFORMATION FOR SEQ ID NO:724:

5	<ul><li>(i) SEQUENCE CHARACTERISTICS:</li><li>(A) LENGTH: 703 base pairs</li><li>(B) TYPE: nucleic acid</li><li>(C) STRANDEINESS: single</li><li>(D) TOPOLOGY: linear</li></ul>	
15	(ii) MOLECULE TYPE: DNA (genomic)  (vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1473UP	
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:724:	
25	GATCTIAGACG GAGTTATTAT GCCGCGGCAC CTCCAGCGAC TGATACTCAA GAATGTGCGC	60
	TCCGTGCGGT GGTGGACGTT CCCAGAGATC CACGAAATTA CGCTAGATCC TAATACGTTT	120
30	ACCAAGAAAC AGGGCTTTGT GGGAACTATA CACGGGCCAG ATCAGGATGG GGTGGAAGTG	180
	CCCCACATAA ACACCCTCT CATGAGTCAG GACACATACT TCCACTTTGA TAGTCTTTTG	240
35	AGGGCCAGGT TCCAGAACCT CAACTACATC AGTCTGCACA ACGTTTCCGA GGAAATTACT	300
	GOCATCATAG TOCCTCACCG ACTGTATTOC AATGGCCGCA TCAGCATTOC AGGCTGCGTC	360
40	GIGAAGGGG TIGIAATGAT CTAAACTTGC CCGGATATCC CTATTGAGAA ATAAACACAT GGGTGAAGIT ATACATAGGC GCGGAAGAAG CCGCTTGAAT ATTGATAGAC CGAATAGTGC	<b>420</b> <b>480</b>
	GATCAATGTA ATTAAATAGA TAGGTTACAG CCCTACCGGG CTGGCATTTG GTCCGAGATT	540
45	GETCTGCCTC TACCAAGTCA GOCAGTTACC GGAGGGTGAA GTAGTAGGAC ATCATAACTC	600
50	ATAAAAAACG TTACATTCGT TGTOCTTGTC GOGAAATCAG TAATCATOCA GGTOCGTCGT	660
	GAAACCGAAG GAAACGTAAT GOOGTOGAAT AAGTAAAAGA TOC	703

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(2) INFORMATION FOR SEQ ID NO:725:

	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 716 base pairs	
5	(B) TYPE: mucleic acid	
	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1474RP	
15		
20	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:725:	
	GATCGITCAG TITAATCACC TGGGACGCAC TGCCTTGCGG TTCCAGCACT GCCTGAAACT	60
25	TGGCCAGGCG TTGCATCACG GCATTAAGCT CCTGTACATC GCGCTCGTGC TGGGCCTCCA	120
	GCTGCAAGCG CAGTTCAGCG CTGATATGCT TCCCCCCCGG TGTAGACATC TGCCGCCAAGC	180
30	TAGOGTAGOT GOCCGACCOC COCAGOGGG AGCTGCCCCC GCCCTTGTCA GCCGTCTTCT	240
	GTGCCCCCAT TAGTGGCCGT ATCATCGTCT CGATCCCGCC GTTTGCCCATC ATCGGTATGG	300
35	GIGIGITIGIA ATCGICAATT ACCOCACTOC AGTCCTCGIC CAGGICCGIA AAATACTIGI	360
	CTTTTTTGCC GCCAGGGTGG TTAGACCGGC CCGTGGTGTT GCTCCGAAGC GGGCTCAAGT	420
40	SCACGOCGOG GIGGCIGCIG CIGIGGCICG ACAGGCACGC TGCATAGICI GCGACCICCI	480
	GATGOCOCTA ATATTCCCAT COCTATCTOC AGOCTCCAGC GATGOCGACG CCAGCTGATT	540
45	CGACTICOCC GATGACOGOC TCTTCCACGA CTTGATCAGC GAGCCCACAA GCGACGAAGA	600
	TCATCAATTT CACTITIGGT ACATTTCTTT GCACCCATTC CCATTATGGG GAACCGTCCT	660
50	GATAGCCATC ACAATGTATA GCTCGCTACT CTGAACCGCG TGGCAACCAC TGCAAC	716
	(2) INFORMATION FOR SEQ ID NO:726:	
55	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGIH: 699 base pairs

	(B) TYPE: nucleic acid	
5	(C) STRANDEINESS: single	
•	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1474UP	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:726:	
20	GATCGAATTC TCACAGGCCA GTACCTGCGT ATTACAGGTT TGCCATAGTA TGATTAGAAC	60
	CGTAAAGCCC AAGAATCCCA GCCCCAAGAG AGCTCTGGAG AAAAAAGAGC CGAAATTGAC	120
25	GGAGAACGIG AAGCAAGCGC TTTTAATTCC TGGCCAAACT TCGAATAAGC TCTTGCACGA	180
	TETTIATOCTE GACCITOCTE GACTICAAGAA GCCTGATGTG AAGCOCTTCA COCCGAAGAA	240
30	CCACCITICGT CCGITTICAGG ATGCGTCGGG TGTCCGAATTT CTCAGCCGACA ACAATCACAG	300
	CICGITIGGIG GIGGICTICCT CCAACTCGAA GAAGCGGCGC AACAACTTGA CATTCATAAG	360
35	GACGITIGGG TACAAGGITT ACGACATGAT GGAGCIGCAG ATTGCAGAGA ACTACAAATT	420
	OCTAGOGRAC TICCOGRAGO AGRACOTTICO AGROGOTTO ARACCGRIGI TITICCTICCA	480
40	AGGIGGGGCA TICGACTOTO ACCOLAGIATA CAAGCAGGIC AAGTOTTIGT TOCTOGACTT	540
	CTTCCGCGGT GAGGTGACCA AGCTGCAAGA CGTTGCAGGG CTTCAGCATG TGATAGCAAT	600
45	GACGATCCAG GCCCACTITIG AGGATGCCGA GCCATTGCCC AACGTCCTTT TCCGCGTCTA	660
	CAGGCTTAAG ACGTACAGAA GCAGCCAAGG TGGTAAGAA	699
50	(2) INFORMATION FOR SEQ ID NO:727:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 749 base pairs	
55	(B) TYPE: nucleic acid	

	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) Original Source:	
10	(A) ORGANISM: PAG1475RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:727:	
	GATCOGACCA ACGAGCOCAT CTOCAGCCAC ATCOTTGATA ACGTCACCAT GATCGACGAA	60
20	ACCEAGGAGG ACCAGGGCGC AAAGAAGGGC GCCTTTGCTG TTTGAAGCCG GATCCTGCGG	120
	CGITCAACCG TAAATAGICT TATAGCCAGC ACCCCAGGCG CCGGCCGGIT CCTATGIAGI	180
25	CCTGCAATCG CTCGCTTGCT AGCCGCACGA TCACAGAATA CAGCTACTTT ATCCTAAATC	240
	CACTOCTATO AAAATATOOA GOOGGACAT TIGTICICIG TOTOGTOGGA TGTGGGGGTC	300
30	GCCATTIGTIGG AGTIAGGGCCG CAACTICGGAC AGCCACCACA GGTICGCCATC ACAGCTIGCCG	360
	GICCOGIGIC CGICCCIGGA ATCCTGCTCC AAGCCCTTCT GGTCAAAGCC AGCCAAGCTC	420
35	CCCTGTCTGA TGGCGTCCTC GACCGCTGCG TCCAGCAAGT CCTGGTATGG ATCTGCGCCG	480
	ACCCTICTOG GOGCCCCAGG CGTIGIGIGA ACCCAGTCGC ACAGAGAGGG TGTCGCTGTT	540
40	AGCGCAACAG ACGAGGCGCC TGTGCCGGCC GCATGGGCCG CCGTGCCGAA TGCGTGCCGG	600
	TICATGIAAT TOCTOCCCTG GICCGATGIG TATTGIGTCT GCGAACGGGA AATCGGGGAC	660
45	GCAGGAACGT TOGCCTOGCC GCCATCGTTC TOGCAGCTCT TOGGTTGCGG CACCAAAGCC	720
	TCCTTCTGCA GCATCCGCCC TGAGCCGTT	749
50	(2) INFORMATION FOR SEQ ID NO:728:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGTH: 740 base pairs	
	(B) TYPE: nucleic acid	

5	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
10	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1475UP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:728:	
	GATCITICCGI CCCCAGTACG GICGICTCTT CCAGATATNA CCACCCAGCG CAACTGIATC	60
20	AAGCTAACCA ACACAGTKCG CACGCTTTTC GAGCCGAGCT CAGGCGCGAG GTGAACCAGC	120
	TCTGAGACAG ACAGACGCCC CTTGTTCAGA AGTAGCTCAA TAACACGTCC GGCTCGCTCG	180
25	CCGAGGIGCG ACCGCGCTAC CTCTGTGTAC AGGAAGGTTT CAGGACTCAA TGTCCTCATC	240
	TCCAGTGTCG ATACCGGCAC CTCCGCAGCA CGCTCGTTTT CGACTTGTCC ACCTGCAGCA	300
30	CCCATAGATC CETTCATTAT OCACTAGGAC CTCCCCTCA CTCAAGCCCA GCGCCGTCTG	360
	GAACGCAATA CTCGCTAGTG CTAGTTCCCA CCTAATATCT ATCTCATCGC CCATCGAGCA	420
35	OCCOCCACC TAAAAAATCA CCACTGCGCG CTCACCACGC ACGGTTCACT AAATACGAAA	480
	CAGTIGITCG TCACGIGITG CTCACGIGAT TITACCCGGC CCGIATAATA TCGGGITCTC	540
40	AGCGCGCCGA GCCAAGCACA CITICCTGTAT CATRACAAAC CAGCACAGGC GGTAGGAGCT	600
	ATCOSCAGAG TCCCAATACC CITISCTACTG TICACATTAG GIGGITICAAA TGAGIGICTG	660
45	TITAGIGGIT ACCAAGAGIG TGGCCACAGC CACAITGGGG ATCIACACCG GGATGGIGGI	720
	AACGCGGCAG TIGGICCITC	740
50	(2) INFORMATION FOR SEQ ID NO:729:	
	(i) SEQUENCE CHARACTERISTICS:	
55	(A) LENGIH: 707 base pairs (B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
10	(A) ORGANISM: PAG1476RP	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:729:	
	CATCGTATOG CTAACTGTAA TATOGAAAGA AGCACAGACA TCCCCGGAAAA ATGACATCTC	60
20	AGTGACACTO TICAACAAAT CATAAGAAGA AAAGTATGTG ACTAATGCTT GCAGAAAAAT	
20		120
	AAATTOCTOG CTACCAGTAA GOGATGITAG TAGOGTGCCA TOGCATTCAA TAAATOGTAA	180
25	GAGATACGIG GGIGGIATCI CGATGCITITI GAGGIACGCA AAAATIGGGC CATATAAAATC	240
	CATCTICAAT GGIAGCCITT TOCATATOGA TICTICAAGA AGICTGITTA TAAGTICTIT	
		300
30	ATCAGAATOC TOCATAGACT GATOCAGGAG AGCACTTAGC ACATGCCCTT TATTCCTAGG	360
	ATAGAGCAAA TATTCTTTGA ACGAAGCTGG GICTTTCCGG AAGICAGGCT TCATACCATA	420
35	AAGGTACATG TATACATTCC TTGCGACATC CATATCCTCA ATACTGCTTT CAAGCATCGC	
33	THE THEOREM CATALOGICA ATACIGCTIT CAAGCATOC	480
	AAGGTAAAAT TOGTAGGAAA ATTOGGGTAC CCAGGAATGC TGITGAAATT GOGTOCAGAG	540
40	TITICIATECT CICTICOCCT CCITCCTICC CACCOCCAAC ACCAACTICG CACACAACCA	600
	GCGICTGACA GGGAATCAAG ACCATCTGIT GAGGGAATTT GOGTGAGAAG GCGATCAAGC	660
45	ASCITICAÇÃO CAACITICCAS GGAATCIAAS CIGACAAGCC CAGCIAC	707
	(2) INFORMATION FOR SEQ ID NO:730:	
50	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 635 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEINESS: single	
55	(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: DNA (genomic)

5	(vi) ORIGINAL SOURCE:  (A) ORGANISM: PAG1476UP	
10		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:730:	
15	GATCTGAAAC TAACAACAGC AGTGOGTGAA OCAAGAGGCA TTGGAGGCGT ATGACGGCGT	60
	GIOGCAAGOC AAGTACACTA TOGOCTTGOG OCAGACCAAC ATGAGCTTTG TGAACCACOG	120
20	CGAGGACATC TACTOGATGT GTTTGACOGC GTGCTCGAAC TTGATGAAGA ACTACGATAT	180
	CAAGCCGGAA AGCATCGGCC GCCTCGAGGT GGGTACGCAG ACGTTGCTTG ACAAGTCGAA	240
25	GICCGIGAAG ICIAITITIGA TOCAGITIGIT COCCAGAAC ACCCACITOG ACCGIGICGA	300
	TACOGIGAAC GOCTOCTATG GOOGTACTAA COCGITGITT AACTOCTIGA ACTOCATIGA	360
30	GICCAGITICG TOOGACOGTIC GIGACOCAAT CGITGITTIGT GGIGACATCG CAATCIACGA	<b>4</b> 20
	CAAGGGTGCC GCCCGGCCCA CTGGCGGTGC GGGAACTGTC GCTCTCCTGA TCGGTCCAGA	480
35	COCCCCATT GICTITICACT CTG190GTGG CTCGTACATG GAGCACGTCT ACGACTTCTA	540
	CAAGCCTGAC TTCCGCAGTG AGTATCCATA CGTGGACGGC CACTTCTCAC TAACATGCTA	600
40	OGTCAAGGGC OGTOGACCAG GCTTACCGGC OCTTA	635
	(2) INFORMATION FOR SEQ ID NO:731:	
<b>4</b> 5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 719 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDELNESS: single	
50	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
55	(vi) ORIGINAL SOURCE:	

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## (A) ORGANISM: PAG1477RP

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(xi)	SEQUENCE DESC	CRIPTION: S	SEQ ID NO:73	1:	
GATCTTTOO	G AGGGACCACT	CTGCAATCC	AGAAGACTAG	AGCAGTTGTC	TAGGACAACA

15 20 25

TATTICAAAGG CCAATAACGC CAAACAATAC GITAAAGITG GCTGCCAGIT TITICAACACA
CTACTACAAC ATTATGAGGG CATAAAGGTG CITICTAGATG ATAGCAAAAAT CATTCCTCAG
CTCGCCAGTA CTCTCTATAA GGCTATGGAA GGGCATATTT TACCCAGTAA GCTCTTCTCC
TCTTGGGCTC TCCAGAATAC GITATGTGGC TCCTACTTCA AATTCCTCGG ATTGCTAATG

AAGITTATAA GGAGACTICT GGIGITTTAC CGICCTTTIC GATACOGAIT CICGACAGIA

AAATCTAAGG AAGGAATCAA TATATTAGAA AAATGGAACA TGTTCACTGT CATCTATAAA 420

ATGITICACC CATCACCCCT AGCGGAAGAA TATITIGITIAC TCATGCTTCC AGAGTIGGAC 480
CTCTCTCACA GCATACATTG TAGGATTATT TTTAGCAAAG CGCTAGTCGA CAGTAGAGAA 540

GTCATAAGGA TCAATGCTAC CAGGGTTTTA GGCGAAATGA TCAGCAGGGT CAAATTATCT 600

GATCCCACTC TOGAAGAGIT CATGITAAAC CTGTTOGTCG CTCAGTTGTA CGATTTATCG 660

AGTICAAGTICG TAGCAGTICGC CGACCAGATA CTIGTACCATT ACTIGTITAAG TCAAAGTAT 719

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# (2) INFORMATION FOR SEQ ID NO:732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pai

(A) LENGIH: 726 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

50

3000 CD ......

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: PAG1477UP

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:732:	
5	CATCCGAATG TCCTTAGTCT GTGGGAAGGA ACCGATGGTG GTGGTTGGGA ATAGCGGGAG	60
	CTIGAAAAIT GOCTOCTOCT CCTTGAGACG CTCCCCGAAT GGTGCGGCTC TCGTGGATAG	120
10	CTTCTCGTTC AAACCAGCAA CACGTCCTGG ACAGCAGGAT CGTTGGTGAT CGCAGAGGGG	180
15	GCACGCGCAG CAATCGAGTC TGCATTTGCC TTCAACTCAG AGGAAAAGTC TTCGCCAGAA	240
	GOGITICITAG OGAGGACAAC AACCICATOC AGCITICIGOG TIGCAAAAGA GAACCAGICC	300
20	TIGATOTOTO OCTOCAAGOC AGACTOGTIT TOCAAGTOAA CTOGAGTGTG CAACAAGGAA	360
	GAGGACGIGG CAACAATAAC GOGGICCCCT CCTAGITTICT CAATTGCCTT AGAAATAGIG	420
25	GCAGCCGACT TCGCGAAGIC ATTCTTCCAG ATGTTTCTAC CGTCAACAAC ACCTACAGAC	480
	AACGACTOGT TITICOCCAAC GATCOCTAGA ACGICGICCA ACTOCTCTOG GTTTCTCACC	540
30	AAGTCGAAAT GTAGGCCAGC CACTGGAAGA TCCACAAGCG CCTTCAAGTT CGGAACGACT	600
	GICCCGAAGT AGGIGGICAA CACAATGICG AGAGACTITT CCCCACCTAT ATGITCATAA	660
35	GCGGICTTAA ACGCAGACTG TACGTCCTCT GCAAGATCTA AGACCAACAC AGGCTCATCC	720
	AGCTGA	726
40	(2) INFORMATION FOR SEQ ID NO:733	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGIH: 675 base pairs	
15	(B) TYPE: nucleic acid	
,,,	(C) STRANDEINESS: single	
	(D) TOPOLOGY: linear	
50	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1478RP	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:733:	
5	GATCATTATG CATTITATGA TATACACTGC TATCAAAGAC GACCAGTGGG TAGTGAATAC	60
10	ACACCOSCTG GCAGACACAA CCAATGCCCA GGATGAGGCT ACTGAGGACG ACTTAGAGGA	120
	CCTCGTTAGT ACCACTCCAC ACACCGCCCA TOCTACTAGC GAGTGAAGAG GTATTTTACC	180
15	TGACCITTGG AATATATAGG TAGGIGATGA GCTTTACAAT ACGIATTGGC TAACAATGAA	2 <b>4</b> 0
	ATGCAGGAAC TCCTCAAGCT CTTTAAGTTC TGTAAAAAGG GTATCAAAAA CCGTTTTTCC	300
20	ACCOCTIGTET COGTAAATGA CCTCGATTAT CCCATTCCAA TAGTTCCTCC TCTTCAACGT	360
	CAGATCTATG ACCCCTTTTG CCCCGAGGCT GCTACGCAGT TCGCTGCGTG GCATGCCGAG	420
25	CATCTIGICA AATAGOCCIA TCIGITIGIT TAGOCTAGOG ATGITCOCCT CACGAOCATG	480
	CACCGIATOG COCTOCCTIC GITGIGGAAG CACCTOGATG GACGAACCAG GAACAATGIT	540
30	CAAGACGCAC TCCGTAACAA CTCTTTTAAC CACCTGTAAG TAGTTTCTAT GCCTTATTCT	600
	ACCCAAAACA GGICTTAATA GGAGAAGGIC ACCATCAGCT CTATATTTAT GCTTGGAAGT	660
35	TOCTOOCTIG ACCCC	675
	(2) INFORMATION FOR SEQ ID NO:734:	
40	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 706 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
45	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
50	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1478UP	

	(xa) SEQUENCE DESCRIPTION: SEQ ID NO:734:	
5	GATCTGAGTA TCAAGATACC ATGAGCGATT CITGCTCACT CTTGTACGGG ACTGCCCCGC	60
	TTATCCAAGT GCAGACAAGA TGCAACATGC ATACTGGCAG ACCAGGCCCT CTGGATCATC	120
10	GAGTTOCTTT AAGCAACATA GTAGGAGGCT TCGAAGGAGG AGTTCTTCGG CTACCTATGT	180
	AAGAGATOCA OCOGATOGTT ACTOCTOGTC ACGTOCTAGA ATCATATACC ACOGAAAAGT	240
15	GGATATGITG CTTGCCCTTT AGATATGGCA GITTTGCCAC CCTACTTGAC ACAGCTGTAA	300
	CAACGITICAC TAAGGATAAA CAAGAGCTAC TGTCAACOOG CTATCCATAC AATGACATCT	360
20	GATCTAATGG AGGIGGACTC GGCCCATACA CCGCATGTTT ATAGCGCAAG CAAGGACAAC	420
	GITCACAAGT TIGICCAICT CCTICCCCAG GICICCAAGA CIACIATAAC ATICCACICC	480
25	COCTATGIGI OGAAGICICI TOGOGAGCIA AIGICITIOC OCAAGGAGCI OCAGCAGCAG	540
	ACCCTCACCA TCCTTATCAC GCTCCTATAT COGGACGACT CGGCATTGAA GGTGCCATTG	600
30	CTTCCTGTGC TGAACCAGAA CTCAAAAGCA GOGTGGAGGA TGCGGGAGGCA TTCCAGGGCA	660
	AGTACCCCCC AGACTITIATIC AGCTGACTGC TGACGGCAAG ATTGAC	706
35	(2) INFORMATION FOR SEQ ID NO:735:	
	(i) SEQUENCE CHARACTERISTICS:	
40	(A) LENGTH: 695 base pairs	
40	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: DNA (genomic)	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:735:

(A) ORGANISM: PAG1479RP

(vi) ORIGINAL SOURCE:

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	CHICAGOTTA CABIAGCATT GICTOCCAG GITOCCIGOC TOAATTITAT CCCGGCCCTC	60
5	GAAGAACTOC AACTOGAAGA GGAAGTTOGT GCGGCACTGG CATAAATTGT CTATGCCCAG	120
	CCCCIGITGG CAGAACGCAT GCITGCACTC TGCAAACIGC TGCACCTCGA ATTCGCCGGAT	180
10	CAACAGCTGT AGCTCCACGA GCGCATCCTT GGTAAGCCTG CTGCCTCCGG AGCGGTCGGC	240
	GCACCETTTE TOGATECATT CETTEATCTC CTCTETTAGE TTGCCGTCTE TCGTCGGCGA	300
15	ATTOTOGAAA AGOGTOGGGC GCACTATOTO COTGCCTGAA GGCACCTTGT TOTOCCTTGTT	360
	COGCTOGTOG TITTICGTAGG GOGAGGTGAC TGATGATGAA TCATTCATAA AGCTGTTTTT	420
20	ATTCCCCACC CTCCCCTTCC CCTCCACCTT CACCTCAAAT TGTTTCAACC CCCTCTTATA	480
	AGGICTITIC TOCATTATTA TAGCACTATG CCAAGATCCA GATGIGGCAA TOTGGGATTA	540
25	CTAGACCTET TECECCACCA TOCACTICIC TTATATACAC TESCACTTIC TETCTCACAC	600
	AAAGACGIAA AATTOOGACT ACGAAAAGGG AGTCOCCAAA CAAGTOGCAA ACGTTGTAAA	660
30	ACCATACTGT ATATTTATAC TATTACTAAT TATCT	695
	(2) INFORMATION FOR SEQ ID NO:736:	
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENCTH: 716 base pairs (B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
40	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: DNA (genomic)	
45	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: PAG1479UP	
50		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:736:	
55	CATCOBBBCA THACBETISCS CATCHACGAG GABGACATHG TOBBBCGACCA GBBCCBGGACG	60

	CALCHALACG GOCACCOCCA GAAGCIOGGT TCGHACCGGG CGCGGGCCGG GCCCTTCTCC	120
5	AACACGCTGT CCAACCTGCT TCCCAGTATC AGCGCGAAGC TGCACCACAA CCGGAAGGGC	180
	GGCACGGGGA AAGTCGCGGC GTCTGCTGCG GACGGGGAAGCGGG GTCTACGGTG	240
10	GTTGCGGGAG AGATGGCGGG CAGCATCACG CCTCCGCAGG ACCTACATAA CGTGGTCAGC	300
	TICCOGGAGO CATACOGGOT TOCACAGOCA COCACTIOGA OCGAATOGIA TACGIATOGI	360
15	TCTOGATACA GTOCCCACCT GCAGCCCACA GTCTCCAACC CTGCTACGCG GACTCGGAAT	420
	AATACTGTAT CTTCCCAGAT TACTTCCCTT TCAAGCATCG GCCAGCTGGG AACCCCCAGC	480
20	ACGAGCAACA TCTGGACCAA CAATGGCTCA AGCCCGGCAG ATCCAATCAG CAACATGCTC	540
	ACCACCACT TCAACCCCAT CCCCCTCCCC CACTTTGGCC AGTCCAACTA CTACGACGTA	600
25	ATCACGCAGC AGCAGCCTCC GCAGTOGACG AACTCACTGA ATGTGCCCTC CGGGGGTAAT	660
	ATTICIOGGA AAAACGIACT CGITCICAAT CTAATGCTTC TAGCATATAC GCAGAT	716
30	(2) INFORMATION FOR SEQ ID NO:737:	
	(i) SEQUENCE CHARACTERISTICS:	
25	(A) LENGTH: 748 base pairs	
35	(B) TYPE: nucleic acid	
	(C) STRANDETNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(vi) ORIGINAL SOURCE:	
45	(A) ORGANISM: PAG1480RP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:737:	
	GATCCTCTGA GOCGAGCCCT ATCCCAAGTT TATTCCAACT TCTTGCCGAA AGGTAACAAA	60
55	CCGITTATTI ACAIGAGITT ACACATAACA CCGGAGAATG TIGAIGITAA TGIGCATCCT	120

	ACAAAGOGIG AAGIACGATT TITGIATGAA GAAGAGCIAA TAGAGOGCAT TOGIAATTIG	180
5	CICCATGAGC GGITATCTCA GCTGGATACT TCGCGAACTT TTAAACCGGG CTCTTTGACA	240
	CCTGGGAAAC ATAGTTCAAC TGTGTCCTGC GCATTCCGGC AATCAGCGAC CCCCGCAAGT	300
10	ACACAACCAA AGGCAAAAACG TOCAGAAAAC ATGCTTGTCA GGACTGATGG TAGCCAAGCT	360
	AAAATTACTA ATTATGICAG AGCAAGTCAA AGCTCTACCA GCTCATCCIT TTCCACTTCT	420
15	TTAAGAAAGA AATCACATGC GGCAGCAAGT GATGAACTTG GCAGCATTGG CGAGGACTCC	480
	CAAGATACAG CAACATOGAT GACAACCTCT ACACAAGAGC CTAATCATAC CAAGTCTAGA	540
20	OCCATITIAA CCITATIGAA TAAIGAGIAT GAAGICGIAC AOCOGGAAAG AACOGAAGIA	600
	AATCTCACCA GCATCAAAAC TCTAAAGCAG GAAGTAGACG AAGATATGCA TAAGGGAATT	660
25	AACAAGIGIC TITGCAGATA TGACCTATGT TGGIGTCGTT GATGCAACAA GGCGACTTGC	720
	ATCTATACAG CATGGTTTAA AGTTATTT	748
30	(2) INFORMATION FOR SEQ ID NO:738:	
	(i) SEQUENCE CHARACTERISTICS:	
35	(A) LENGTH: 727 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: DNA (genomic)	
	(ri) ontonny ocen-	
	(vi) ORIGINAL SOURCE:	
<b>4</b> 5	(A) ORGANISM: PAG1480UP	
50	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:738:	
	GATCOCCTICA TOOGATACAT AAACCACOGA ATCAATGAAA AOCTCOCTTA CGAACAGTITI	60
55	GGATCTGTAC COGAGAAGGG CTACTATATT CCTCCCACAA TATTTCTGGA CGTTCCTCAG	120